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FEATURES

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Adams, C., Addo-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Adams, C., Addo-Oduola, B., Banks, T., Banck, J., Buck, J., Benton, J., Buck, J., Burkett, C., Buren, M., Brown, M., Bryant, N.P., Burkett, C., Burell, K. L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., Davila, M.L., Davis, C., Denn, A.L., Ding, Y., Dulh, H.H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elnal, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garrell, J.H., Guorell, J.H., Haves, A., Harlis, C., Harris, K., Hart, M., Havlak, P., Haves, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
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    Ward-Moore,S., Warren,R., Washington,C.,
    filliams,G., Wallamson,A., Walezzk,R., Wooden,S.,
    Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
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INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUTMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOWME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
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Pred. No.
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source

FEATURES

CDS

, Shooshtari, N.,

Query Match Best Local S

Matches

BASE COUNT ORIGIN

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ROD 11-JUN-2001
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Pred. No. 13;
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Best Local Similarity
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                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their.order in this sequence record is
                                               Consensus quality: 152255 bases at least Q40 consensus quality: 158448 bases at least Q30 consensus quality: 164461 bases at least Q30 Estimated insert size: 15555; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
 Assembly program: Phrap; version 0.990329First call to findPhrapList.
                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                 contig of 13782 bp in length
gap of unknown length
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contig of 9405 bp in length
gap of unknown length
contig of 4694 bp in length
gap of unknown length
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Center clone name: CH230-516
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Gaps

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AF302076.1 GI:10505361
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ilarity 95.0%;
Conservative
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Shirotani, K. and Sai
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REFERENCE
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TITLE
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KEYWORDS
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AF157106
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                                                                                                                                                                                                                                                                                                                           Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                    Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and
   musculus neprilysin-like peptidase alpha mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                         1 (bases 1 to 2583)
Shirocani, K., Tsubuki,S., Iwata,N., Takaki,Y., Harigaya,W.
Maruyama,K., Kiryu-Seo,S., Kiyama,H., Iwata,H., Tomita,T.,
Iwatsubo,T. and Saldo,T.C.
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Sciurognathi;
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J. Biol. Chem. 276 (24), 21895-21901 (2001)
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1.1e+02;
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Pred. No. 1.1e+
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="endopeptidase"
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Eukaryota; Metàzoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 2601)
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Shirotani, K. and Saido, T.C.
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                 AF302075.1 GI:10505359
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Mus musculus
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Best Local Similarity
Matches 19; Conserv
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AF157106
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KEYWORDS
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                                                                                                                                       AUTHORS
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LADNONVNGFSSLGENTADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINY
AQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCR
IW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="SEP(delta); metalloprotease; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKMVG
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Ikeda,K., Emoto,N., Raharjo,S.B., Nurhantari,Y., Saiki,K.,
Yokoyama,M. and Matsuo,M.
Molecular identification and characterization of novel
membrane-bound metalloprotease, the soluble secreted form of which
hydrolyzes a variety of vasoactive peptides
J. Biol. Chem. 274 (45), 32469-32477 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-JUN-1999) International Center for Medical Research, Robe University School of Medicine, 7-5-1 Kusunoki, Chuo, Robe
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Mus musculus neprilysin-like peptidase beta mRNA, complete cds
AF302076
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
1 (bases 1 to 2652)
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Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T.,
Iwatsubo, T. and Saido, T.C.
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J. Biol. Chem. 276 (24), 21895-21901 (2001)
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Pred. No. 1.1e+02;
0; Mismatches 1;
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'organism="Mus musculus"
'db_xref="taxon:10090"
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/db_xref="GI:6467401"
                                                                                                                                                                                                                                                                                                 2 (bases 1 to 2601)
Ikeda, K., Emoto, N. and Matsuo, M.
Direct Submission
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AF302077 2694 bp mRNA linear ROD 11-JUN-2001
Mus musculus neprilysin-like peptidase gamma mRNA, complete cds.
AF302077
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DQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRWDLMELQEREGLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMONYLVWRLVLD
RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSTVRELIEKIRSVEVDNLDELNWMDESKKKAQEKAMNIREQIGYPDYILEDNNKHL
DEBYSSLTFYEDLYFENGLONLKNNAQRSLKKLREKVDQNLMIIGAAVVNAFYSPNRN
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                                                                                                                                                                                                                                                                                                                        /translation-"MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIGKOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                 Neuroscience Laboratory, Brain
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Shiotani, K., Taubuki,S., Iwata,N., Takaki,Y., Harigaya,W., Maruyama,K., Kiryu-Seo,S., Kiyama,H., Iwata,H., Tomita,T., Iwatsubo,T. and Saido,T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most phosphoramidon sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
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                                                    Wako-shi, Saitama
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protein_id="AAG18447.1"
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  Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuros
Science Institutute, RIKEN, 2-1 Hirosawa,
351-0198, Japan
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Pred. No. 1.1e+02;
0; Mismatches 1;
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    2652
/organism="Mus musculus"
/db_xref="taxon:10090"

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25. .2364
                                                                                                                                                                                                         note="endopeptidase"
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                                                                                            Location/Qualifiers
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Best Local Similarity 95.0%;
Matches 19; Conservative
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Mus musculus
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AUTHORS
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MEDLINE
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AF157105 2892 bp mRNA linear ROD 25-NOV-1999
Mus musculus soluble secreted endopeptidase mRNA, complete cds.
AF157105
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PRENGNWLDDWSUNFSARHFQQQSQCMIYQYGRFSWELADNQWVNGFSTLGENIADNG
GVRQAYKAXLEWLADGGKDQRLDGLNLIYAQLEFINYAQWGGSYRPEFAVQSIKTDV
HSPLKYRVLGSLQNLPGFSEAPHCPRGSPMHPWKRCRIW"
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DILABELEYILKGYLEDSTSLRHPADGSRNPCENRYLNRSCMNGSVIEKBSEPLLSVLKWVG
GWPYAMDKWNETMGYLERQIAVLNSOFNRRYLIDLFIWNDDONSSRHYIYIDQPT
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                                                                                                                                                                                                              HLANATVPQEKRHDVTALYHRMDLMELQERFGLKDRVSLCSPGCPGTHSVDQAGLELG
                                                                                                                                                                                                                                       NPPASDSRVLGLKGFNWTLF1QNVLSSVEVELFPDEEVVVYG1PYLENLED11DSYSA
                                                                                                                                                                                      LGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELET
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J. Biol. Chem. 274 (45), 32469-32477 (1999)
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FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLD
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (08-JUN-1999) International Center for Medical Research,
Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
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PLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARILENMDGSRNP
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/product="neprilysin-like peptidase gamma"
/protein_id="AAG18448.1"
/db_xref="GI:10505364"
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/protein_id="AAR13152.1"
/db_xref="GI:6467399"
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Pred. No. 1.1e+02;
0; Mismatches 1;
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/db_xref="taxon:10090"
281. 2578
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Boileau, G. and Desgrosallers, L.
New metalloproteases of the neprilysin family
Patent: WO 0047750-A 12 17-AUG-2000;
BOILEAU GUY (CA); DESGROSEILLERS LUC (CA); UNIVERSTIE DE MONTREAL
                 KSTVRELIEKIRSVFVDNLDELMMMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHL
DEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWIIGAAVVNAFYSPNRN
                                                QIVFPAGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNMLDWWSN
                                                              FSARHFOQOSQCMIYOYGNFSWELADNONVNGFSSLGENIADNGGVRQAYKAYLRWLA
DEGKOORLPGINLTYAQLFFINYAQWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
LPGFSEAFHC PRGSPMHPMKCRIW"
1774 c 774 c 774 t
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FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLA
RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLY IKRAFSKDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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PLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNP
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Pred. No. 1.1e+02;
0; Mismatches 1;
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Pred. No. 1.1e+02;
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Sequence 12 from Patent W00047750.
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/db_xref="taxon:10090"
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llarity 95.0%;
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RESULT 10 AF176569

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ALEGOE829 203286 bp DNA linear ROD 05-APR-2002 Mouse DNA sequence from clone RP23-10M12 on chromosome 11, complete sequence.
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AF176569 2925 bp mRNA linear ROD 11-MAY-2000
Mus musculus neprilysin-like metallopeptidase 1 (N11) mRNA,
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Ghaddar,G., Ruchon,A.F., DesGroseillers,L. and Boileau,G.
Direct Submission
Submitted (09-Aug-1999) Biochemistry, University of Montreal, 2900
Edouard Montpetit, Montreal, Que H3T 1J4, Canada
Location/Qualiflers
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Pred. No. 1.1e+02;
0; Mismatches 1;
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/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="testis"
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/gene="N11"
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AL606829.13
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                                                                                                                                                                                                                      on Apr 7, 2002 this sequence version replaced gi.18250804.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, GANISSPROT: Tr:, TREMBL; WP:, WORNPEP; Information on the WORNPEP
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Mus musculus chromosome 4 clone RP23-15L19, *** SEQUENCING IN
PROCRESS ***, 2 unordered pieces.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                              Direct Submission
Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@ssanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep.RP23-10M12 is
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constructed by the group of Pieter de Jong,
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
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56507 a 42785 c 43119 g 60875 t
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Pred. No. 90;
0; Mismatches
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1 (bases 1 to 208249)
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95.0%;
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Best Local Similarity 95.0°
Matches 19, Conservative
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                                                                                         Chapman,J.
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                                                                                                                                                                                                                     Insert size: 208149; sum-of-contigs
Insert size: 219051; 2.3% error; agarose-fp
Quality coverage: 12.41x in Q20 bases; sum-of-contigs Quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               runs of N, but the exact sizes of the gaps are unknown.
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                                       Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator; 11% of reads Chemistry: Dye-terminator Big Dye; 88% of reads Chemistry: Dye-terminator Big Dye; 88% of reads Consensus quality: 207834 bases at least 040 Consensus quality: 207956 bases at least 030 consensus quality: 208060 bases at least 020
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137404. 208249
/note="assembly_fragment:01838
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a 53647 c 51328 g 49076 t
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Pred. No. 90;
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                          Summary Statistics
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Center project name: bM15L19
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Submitted (02-MAR-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA on Jul 28, 1999 this sequence version replaced gi:4836860. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases. Pl library location:
                                                                 Embydroidea; Drosophilidae; Drosophila; nuscomorpha; nuscomorpha; Drosophilidae; Drosophila; Bater, B. Blazej, R.G., Chalker, S.E., Apbayani, A. Arcalna, T.T., Batter, E., Blazej, R.G., Butenhoff, S., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hankle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Rarra, K., Kearney, L., Lee, B., Lee, B., Lip, Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R. G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D. E., Galle, R., George, R. A., Harris, N. L., Hoskins, R. A., Houston, K. A., Hummasti, S. R., Karra, K., Karra, K. Karra, K. Karra, K. Karra, K. Macda, P. Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M. A., Macda, P., Pefiffer, A. R., Woshrefi, M., Nixon, K., Pacleb, J. M., Park, S., Pefiffer, B., Poon, L., Sequeira, A., Sethi, H., Shir, E., Sairskas, R. R., Wan, K. H., Weinburg, T., Zhang, R., Zieran, L. L. and
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18780 c 19359 g 22875 t 640 others
                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                        Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence: It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 82665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 511 bp in length
gap of unknown length
contig of 1555 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 665 bp in length
gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of unknown length contig of 575 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-MAR-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA on Jul 28, 1999 this sequence version replaced g1:4454435. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases. Pl library location:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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contig of 22581 bp in length
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contig of 727 bp in length
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Pred. No. 3.4e+02;
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gap of unk
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2 (bases 1 to 25478)
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Matches 18; Conservative 0; Mismatches 1; Indels
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Pred. No. 3.1e+02;
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Best Local Similarity 94.7%;
Matches 18; Conservative
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	457 24 0 1004 23 0 3130 22 0 4179 22 0 6779 23 0 9234 22 0 22452 22	15.8 79.0 395 22 ABA08497 Human 15.8 79.0 1419 16 AA079154 A. ac 15.8 79.0 1419 24 ABA08955 Human 15.8 79.0 2936 21 AAA09315 Human 15.8 79.0 2936 24 ABK13306 DNA e. 15.8 79.0 3163 20 AAX60266 Human 15.8 79.0 3714 24 AAD33552 Human 15.8 79.0 4714 24 AAD33552 Human 15.8 79.0 4896 24 AAD36547 HUMAN 15.8 79.0 4896 25 AAD3667 HUMAN 15.8 79.0 4896 25 AAD3667 HUMAN 15.8 79.0 4896 25 AAD3667 HUMAN 15.	3 79.0 4896 24 3 79.0 7746 22 3 79.0 12683 22 3 79.0 12683 22 3 79.0 12744 22	15.4 77.0 8785 23 ABLI5582 15.4 77.0 11293 22 ABA17918 15.4 77.0 22107 22 ABA17921 15.4 77.0 22107 22 AAK79542 15.4 77.0 22109 22 ABA17922 15.4 77.0 22109 22 AAK79543 15.4 77.0 22111 22 AAK79540	RESULT 1 AA228811 ID AA228811 ID AA228811; XX AC AA228811; XX DT 01-FEB-2000 (first entry) XX	cardiovascular disease; neurodegenerative disease; growth hypothalamic-hypophyseal axis; endocrine disorder; probe; Synthetic. Rattus rattus. FR2777291-A1.	XX
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	n 5.1.6 Compugen Ltd. earch time 125.659 Seconds (Without alignments) updates 358.431 Million cell updates		4370478	/genesegn-embl/NA1980.DAT:*/genesegn-embl/NA1981.DAT:*/genesegn-embl/NA1982.DAT:*/genesegn-embl/NA1983.DAT:*/genesegn-embl/NA1985.DAT:*/genesegn-embl/NA1985.DAT:*/geneseqn-embl/NA1986.DAT:*/geneseqn-embl/NA1986.DAT:*/	geneseq/geneseqn-embl/Nk1987.px;; geneseq/geneseqn-embl/Nk1988.DaT;; geneseq/geneseqn-embl/Nk1989.DaT;; geneseq/geneseqn-embl/Nk1990.DaT;; geneseq/geneseqn-embl/Nk1991.DaT;; geneseq/geneseqn-embl/Nk1991.DaT;; geneseq/geneseqn-embl/Nk1993.DaT;; geneseq/geneseqn-embl/Nk1995.DaT;; geneseq/geneseqn-embl/Nk1995.DaT;; geneseq/geneseqn-embl/Nk1995.DaT;; geneseq/geneseqn-embl/Nk1995.DaT;; geneseq/geneseqn-embl/Nk1999.DaT;; geneseq/geneseqn-embl/Nk1999.DaT;; geneseq/geneseqn-embl/Nk1999.DaT;; geneseq/geneseqn-embl/Nk1999.DaT;; geneseq/geneseqn-embl/Nk1999.DaT;; geneseq/geneseqn-embl/Nk1999.DaT;; geneseq/geneseqn-embl/Nk1999.DaT;;	nesegn-embl/NA2002.DAT:*cted by chance to have a of the result being priniscore distribution.	Description Rat membrane Soluble secre Rat membrane CDNA encoding Drosophila me Drosophila me Drosophila me Drosophila me Drosophila me Drosophila me
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	Ger Copyright (c) nucleic search, usi July 8, 2003, (US-09-647-780A-5 20 1 tggagggcagttggctgtg IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Total number of hits satisfying c Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 10 Maximum Match 10 Listing first 45	z		Y the	March Length DB 100.0 2286 24 100.0 2286 24 100.0 2925 20 92.0 2925 21 84.0 3439 23 84.0 7620 23 84.0 9695 23 84.0 9820 23
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us-09-647-780a-5.rng

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membrane metalloprotease designated neprilysine II (NEPII) gene (AAZ28810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and itssues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wayman CP, Phillips SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted endopeptidase; SEP; endocrine; vasotropic; analgesic; enzyme; gynaecological; antisense-therapy; male erectile dysfunction; MED; female sexual dysfunction; FSD; female sexual arousal disorder;
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds
                                                                                                                  Sequences AAZ28811-Z28827 represent probes for detecting the rat
               New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardiovascular disease -
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Pred. No. 3.5;
; Mismatches 0; Indels
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164..2286
/*tag= a /note= "Encodes catalytic domain"
                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 2 A; 3 C; 10 G; 5 T; 0 other;
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                                                                                  Claim 3; Page 20; 29pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted endopeptidase;
                                                                                                                                                                                                                                                                                                                                                        1 Similarity 100.0%;
20; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-155042/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PFIZ ) PFIZER LTD.
(PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
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                                                                                                                                                                                                                                                                                                                                          Query Match
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AAD28130
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female sexual arousal disorder

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The invention relates to an isolated and/or purified nucleic acid ancocding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male arectile dysfunction (MED) or female sexual dysfunction (FSD) (e.g. female sexual arousal disorder (FSD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such as premature ejaculation, anorgamia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is SEP consensus DNA sequence found in human, mouse and rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the gene for the rat membrane metalloprotease designated neptilysine II (NEPII), which is involved in (h)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to screen for inhibitors, cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20; DB 24; Length 2286; Pred. No. 5.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat membrane metalloprotease NEPII gene.
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Disclosure; Fig 6; 167pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617 TGGAGCGGCAGTTGGCTGTG 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%;
Matches 20; Conservative
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Schwartz JC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "neutral endopeptidase metallopeptidase-like
                                                                                                                                                                                                                                                                                                                                                                   Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;
NEP-like enzyme; protein production; protein secretion;
neurological disease; Alzheimer's disease; pain; psychiatric disorder;
fertility; bone disease; abnormal phosphate metabolism; ss.
                                                                                                                                                                                                                                                                                                                                      cDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a murine neutral endopeptidase metallopeptidase-like enzyme, designated NL-1. The specification also describes NL-2 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders. NL enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide processing by the NL-3 enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oduction and secretion of foreign proteins and active using chimeric constructs containing the foreign protein
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders -
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                                                   Length 2765;
                                                                                    Indels
               684 A; 735 C; 787 G; 559 T; 0 other;
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Pred. No.
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332..2629
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                                                                                                                1 TGGAGCGCCAGTTGGCTGTG 20
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                                                100.0%;
100.0%;
                                                                                                                                                                                                                                AAA63763 standard; cDNA; 2925
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                                                                                                                                                                                                                                                                                                (first entry)
                                                                                 Conservative
                                Query Match
Best Local Similarity
.....hes 20; Conservat
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P-PSDB; AAB08130.
               Sequence 2765 BP;
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                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 3905
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    Length 2925;
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Pred. No. 1.8e+02;
); Mismatches 2; Indels 0;
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                                            Indels
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                                            0; Mismatches
Score 18.4;
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                      Pred. No.
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                                                                                                              936 TGGAGCGACAGTTGGCTGTG 955
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                                                                                     1 TGGAGCGGCAGTTGGCTGTG 20
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  92.0%;
95.0%;
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2000US-0614150.
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Best Local Similarity 90.00
These 18; Conservative
Query Match 92.0
Best Local Similarity 95.0
Matches 19; Conservative
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P-PSDB; ABB59038.
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(ABB57737-ABB72072)
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11-JUL-2000;
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ID ABL1411
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26-MAR-2002

ABL14154;

Drosophila;

7-SEP-2001.

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specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 3959; 21pp + Sequence Listing; English
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Pred. No. 1.9e+02;
0; Mismatches 2;
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The sequence data for this patent did not form
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Local Similarity 90.0%;
les 18; Conservative
                                                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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11-JUL-2000; 2000US-0614150.
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pharmaceutical, gene; ss
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P-PSDB; ABB59056.
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P-PSDB; ABB59037.
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                                                                                                           NO 36944
                                                                                                                                                        developmental biology; cell signalling; insecticide;
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pharmaceutical; gene; ss.
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Pred. No. 1.8e+02;
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90.0%;
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                                                                                                                                                                                     pharmaceutical; gene; ss.
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P-PSDB; ABB70051.
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les 18; Conserva
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26-MAR-2002

ABL03159;

RESULT 7
ABL03159
ID ABL0

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Query Match

Gaps

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Indels

Length 7620; 0 other;

18

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                        colated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9695 BP; 2668 A; 2438 C; 2581 G; 2008 T; 0 other;
                                                                                                                  Claim 1; SEQ ID NO 3902; 21pp + Sequence Listing; English.
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k; Pred. No. 1.9e+02;
0; Mismatches 2;
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                        New isolated nucleic acid
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                                                                        interactions
                                                 genes
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6436 TGGAGCAGCAGTTAGCTGTG 6455 1 TGGAGCGGCAGTTGGCTGTG 20 g ó

ABL03158 standard; cDNA; 9820 BP (first entry) 26-MAR-2002 ABL03158; RESULT 9

Drosophila; developmental biology; cell signalling; insecticide; Drosophila melanogaster expressed polynucleotide SEQ ID NO 3956. pharmaceutical; gene; ss

Orosophila melanogaster.

W0200171042-A2

27-SEP-2001.

WPI; 2002-122018/16.

P-PSDB; ABB90350.

23-MAR-2001; 2001WO-US09231

2000US-191637P. 2000US-0614150. 23-MAR-2000; 11-JUL-2000;

(PEKE) PE CORP NY

Myers EW; Li PWD, Venter JC, Adams M,

2001-656860/75 P-PSDB; ABB59055 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell capable of detecting 1000 or more genes from brosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA The invention relates to an isolated nucleic acid detection reagent Claim 1; SEQ ID NO 3956; 21pp + Sequence Listing; English. solated nucleic acid from Drosophila and New isolated interactions denes

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antiallergic; hepatorropic; antidiabetic; antilnflammatory; antiulcer; vulnerary; anticonvulsant; antiborestraia; antibunal; antiporastitc; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nootropic; neuroprotective; antiviral;
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                         Length 9820;
                                                                                                                               Sequence 9820 BP; 2698 A; 2466 C; 2628 G; 2028 T; 0 other;
                                                                                                                                                                                                                      Indels
sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                      Score 16.8; DB 23;
Pred. No. 1:9e+02;
0; Mismatches 2;
                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 1321.
                                                                                                                                                                                                                                                                                      6561 TGGAGCAGTTAGCTGTG 6580
                                                                                                                                                                                                                                                               1 TGGAGCGGCAGTTGGCTGTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                    ABL90759 standard; cDNA; 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2001; 2001WO-US16450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                         84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-2002 (first entry)
                                                                                                                                                                         Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200190304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL90759;
                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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Gaps

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Indels

Length 9695;

84.0%; 90.0%;

18; Conservative

Best Local Similarity Matches 18; Conserv

The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discretes e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; Note: The sequence data for this patent did not form part of Claim 4; SEQ ID NO 1321; 2081pp + Sequence Listing; English. disorders

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Matches

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RESULT 11 ABL09885

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the sequence data for this patent did not form part of the printed pecification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more. genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nsecticides, therapeutics and pharmaceutical drugs. The invention liscloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                         Orosophila melanogaster expressed polynucleotide SEO ID NO 24134
                                                                                                                                                                                                                                                                                             developmental blology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 24134; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.4; DB 23;
Pred. No. 2.7e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA sequence SEQ ID NO:14100.
                                                                               ABLO9884 standard; cDNA; 3178 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH15715 standard; cDNA; 3230 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2124 TGGAGGGCAGCTGGCTG 2107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      discloses genomic DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TGGAGCGGCAGTTGGCTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.0%;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                         oharmaceutical; gene; ss
                                                                                                                                                                                                                                                                                                                                                                          Orosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY
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                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                             Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
2
                                                                                                                                   ABL09884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /enter
                              RESULT 12
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                                                         ABL09884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH1571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
        format directly
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID NO 24137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.4; DB 23; Length 1004;
Pred. No. 2.4e+02;
0; Mismatches 1; Indels 0;
                                                                                                                           Score 16.4; DB 24; Length 457;
Pred. No. 2.3e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 24137; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                he sequence data for this patent did not form part of the
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printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                               Sequence 457 BP; 73 A; 163 C; 119 G; 101 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                         ABL09885 standard; cDNA; 1004 BP
                                                                                                                                                                                                                                                                  11111111 | 1111111 | 247 GAGCGCAGCTGGCTGTG 264
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                                                                                                                                                                                                                                      3 GAGCGCCAGTTGGCTGTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li PWD,
                                                                                                                                                         Local Similarity 94.4%;
les 17; Conservative
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Best Local Similarity 94.4%;
Matches 17; Conservative
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2000US-0614150.
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Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4PI; 2001-656860/75
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11-JUL-2000;
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genes from Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nteractions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wenter JC,
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                                                                                                                                   Query Match
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss

Gaps

; 0

Indels

Length 3178;

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Homo sapiens EP1074617-A2

07-FEB-2001

27-AUG-1999; 11-JAN-2000; 02-MAY-2000; 39-JUN-2000;

Ishii S,

39-JUL-1999;

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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodyrersity and for nutritional purposes. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cow; fruit fly; yeast; hamster; macaque; horse;
commuco, monkey; dog; sea urchin; expressed sequence tag; ES: diagnostics; forensic test; gene mapping; genetic disorder; blodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; tomato; monkey; dog; sea urchin; expressed sequence tag; ES diagnostics; forensic test; gene mapping; genetic disorder; blodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4179 BP; 767 A; 1323 C; 1224 G; 865 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.4; DB 22;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n XB, Wang Z,
Werhman ·T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1609 GAGCGGCAGCTGGCTGTG 1626
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2000US-0631451.
2000US-0663870.
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Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-476164/51.
P-PSDB; AAM23988.
                                                                                                                                  Cricetulus griseus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cricetulus griseus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention.
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17-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-2000;
                                                                                                                                                                                                                                                     32-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH98669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH98669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 [all-length cDNas defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 2.7e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sogai T, Nishikawa T, Hayashi K, Saito K, Yi
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3230 BP; 579 A; 1041 C; 977 G; 633 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hamster EST-derived coding sequence SEQ ID NO: 504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID 14100; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                              99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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ilarity 94.4%;
Conservative
                                                                                                                                                                                    28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                  99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                     2000JP-0241899
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                                                                                                                                                                                                                                                                                                                                                                                                                                (HELI-) HELIX RES INST
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hes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ull-length cDNAs
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AAH98647;

MX EX BX SX

RESULT 14 AAH98647

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Query Match Matches

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Gaps

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Indels

Length 4179;

Asundi V;

Chen R,

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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention.
                                                                                                                                                                                                                                       Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                         Tang YT, Liu C, Zhou P, Qian XB, Wang Z,
Cao Y, Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                          Claim 1; Page 543-545; 1275pp; English.
25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                              WPI; 2001-476164/51.
P-PSDB; AAM24010.
                                                                                         (HYSE-) HYSEQ INC.
```

Chen R, Asundi V;

Gaps Length 4180; Indels Sequence 4180 BP; 768 A; 1323 C; 1224 G; 865 T; 0 other; Score 16.4; DB 22; Pred. No. 2.8e+02; 0; Mismatches 1; Ouery Match 82.0%; Best Local Similarity 94.4%; Matches 17; Conservative

ò Dp

Search completed: July 8, 2003, 02:18:48 Job time : 127.659 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 01:24:03; Search time 27.6098 Seconds

(without alignments)
222.151 Million cell updates/sec

1 US-09-647-780A-5
Sequence: 1 tygagcggcagttggctgtg 20
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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2: /cgn__b/prodtal/lina/b_CoMB.seq:*
3: /cgn__b/prodatal/lina/b_COMB.seq:*
4: /cgn__b/prodatal/lina/ba_COMB.seq:*
5: /cgn__b/prodatal/lina/pcTuS_COMB.seq:*
6: /cgn__b/prodatal/lina/pacKfiles1.seq:*
Pred. No. is the number of results predicted by chance to ha

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			æ				
<u>ц</u>	Result No.	. Score	Query Match	Query Match Length	88	ΩI	Description
		15.8	79.0	541	4	US-09-465-558-31	Sequence 31, Appl
	O	15.8	79.0	1195	-	US-08-535-230A-1	1,
		3 15.8	79.0	2936	4	US-09-166-350-6	9
	v	4 15.2	76.0	479	₹	US-09-465-558-25	25,
	0	5 15.2	76.0	536	4	US-09-465-558-63	63,
		5 15.2	76.0	1079	<u>`</u>	US-08-270-583-1	1, A
		7 15.2	76.0	1079	Н	US-08-783-889A-1	٦,
		9 15.2	76.0	1102	٣	US-09-067-089-1	-
		9 15.2	76.0	1297	9	5187077-23	
	Ä	0 15.2	76.0	1297	9	5427925-21	Patent No. 5427925
	c 1:	1 15.2	76.0	1468	4	US-09-465-558-69	Sequence 69, Appl
	1	2 15.2	76.0	1554	m	US-09-109-205-4	4,4
	ij	3 15.2	76.0	1554	7	US-09-443-184-46	46,
	c 1,	4 15.2	76.0	1558	4	US-09-123-030-7	7, 8
	H	5 15.2	76.0	2265	ч	US-08-242-689-1	٦,
	Ä	6 15.2	76.0	2265	4	US-08-468-583-1	'n
	H	7 15.2	76.0	3218	4	US-09-221-017B-255	•
	ī	8 15.2	76:0	43360	4	US-09-453-702B-206	Sequence 206, App
	Ä	9 .15.2	76.0	4	4	US-09-453-702B-261	261,
	ñ	0 15.2	76.0	4403	4	US-09-103-840A-2	2, A
	7	1 15.2	76.0	4411	4	US-09-103-840A-1	'n
	0	2 14.8	74.0	, ,	,	US-08-791-495-1	7,
	ر د	3 14.8	74.0	.345	4	US-09-199-637A-256	256
	~	4 14.8	74.0	384	4	US-09-199-637A-254	Sequence 254, App
	Ŕ	5 14.8	74.0	592	4	US-08-896-164-80	80, A
	ت د	6 14.8	74.0	752	-	US-08-725-182C-1	Sequence 1, Appl1
	0	7 14.8	74.0	752	m	US-09-013-150-1	Sequence 1, Appli

Sequence 1, Appli Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 192, App	Sequence 191, App	Sequence 190, App	Sequence 189, App	Sequence 252, App	Sequence 102, App	Sequence 128, App	Sequence 64, Appl	Sequence 1, Appli.	Sequence 2, Appli
US-09-359-503-1 US-09-062-422-1	US-09-396-184-1	US-08-937-263B-1	US-08-791-495-6	US-08-791-495-8	US-08-791-495-4	US-08-359-850-3	US-09-199-637A-192	· US-09-199-637A-191	US-09-199-637A-190	US-09-199-637A-189	US-09-199-637A-252	US-09-199-637A-102	US-08-961-527-128	US-09-453-702B-64	US-09-199-637A-1	US-09-103-840A-2
4 4	4	4	Н	н	7	7	Ť	4	4	4	4	4	4	4	4	4
752	752	752	755	755	1002	1002	1653	1827	1920	1932	1938	2101	13440	31728	42235	4403765
74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0	74.0
14.8 14.8	14.8	14.8	14.8	14.8	14.8	14.8	. 14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8
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ALIGNMENTS

OCATION: (517)..(518

LOCATION:

FEATURE

Query Match

Matches

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NAME/KEY:

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DB 4; Length 2936;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                      APPLICANT: Scanlar, Matthew
APPLICANT: Scanlar, Matthew
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd
APPLICANT: Jager, Elke
APPLICANT: Muth, Alex
TITLE OF INVENTION: Renal Cancer Associated Antigens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MOTAKINO:
APPLICANT: MOTAKINO:
APPLICANT: MOTAKINO: LAYO O.
APPLICANT: OFOZO: UT. FAMIL M.
TITLE OF INTENTION: TETTAKINDROFOLATE METABOLIC ENZYMES
FILE REFERENCE: BB1322 US NA
FURRENT APPLICATION NUMBER: US/09/465,558
CURRENT FILING DATE: 1999-12-17
EARLIER APPLICATION NUMBER: 60/112,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.2; DB 4;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.8; DE
Pred. No. 82;
0; Mismatches
                                                                                                                                                                                                                       FILE REFERENCE: L0461/7051
CURRENT APPLICATION NUMBER: US/09/166,3503
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: US 09/166,350
                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1058 GGTGCGCCAGTTGGCTGAG 1076
                        , Application US/09166350A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ce 25, Application US/09465558 No. 6436657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGAGCGGCAGTTGGCTGTG 20
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85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.0
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 76.0
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-166-350-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unsure
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LENGTH: 479
                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: NO. 57078470 NO. 5707847disk of NO. 5707847th America, Inc
: 405 Lexington Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                              Length 541;
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                                                                                                                            DB 4;
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Methylesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.8; DE
Pred. No. 75;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Christgau, Stephan
Kofod, Lene Kofod
Andersen, Lene No. 5707847boe
Kauppinen, Sakari
                                                                                                                          Score 15.8;
Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    leldt-Hansen, Hans Peter
udolfsen, Gitte
                                                                                                                                                                                                               263 TGGNGCGGCAGTTGACGGTG 244
                                                                                                                                                                                                                                                                                                                Patent No. 5707847
                                                                                                                                                                                             1 TGGAGCGCCAGTTGGCTGTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELECOMMUNICATION INFORMATION TELEPHONE: 212-867-0123
                                                                                                                        79.0%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTORNEY/AGENT INFORMATION:
NAME: Valeta, Gregg A
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.0°
Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                         Best Local Similarity.
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unsure
                (520)
                                              ; NAME/KEY: un
; LOCATION: (5
US-09-465-558-31
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APPLICANT

0; Mismatches

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                                                                                                                                                                                         Length 536;
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08270583

Patent No. 5629193

GENERAL INFORMATION:
APPLICANT: HUDSON, ET AL.
TITLE-OF INVENTION: Serum Paraoxonase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: CRELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                       Score 15.2; DB 4;
Pred. No. 1.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                            289 TGGCGCGCAGTTGACGGTG 270
                                                                                                                                                                                                                                                          1 regaececaerrescrere 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONCURRENTLY
                                                                                                                                                                                       Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIKEEA. CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEIC ACID
                                                                    unsure
(525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                   unsure
(520)
                                                                                                                        unsure
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                                                                                                                                       ; LOCATION: (531)
US-09-465-558-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-270-583-1
                                                                  NAME/KEY: U
LOCATION:
FEATURE:
NAME/KEY: U
FEATURE:
NAME/KEY:
LOCATION:
                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                   RESULT 6
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                                                                                                                                                                                    APPLICANT: MOTAKINYO, LAYO O.
APPLICANT: OTOZCO Jr, Emil M.
TITLE OF INVENTION: TETRAHYDROPOLATE METABOLIC ENZYMES.
FILE REPERENCE: BB132 US NA.
CURRENT APPLICATION NUMBER: US/09/465,558
CURRENT APPLICATION NUMBER: 05/112,734
EARLIER APPLICATION NUMBER: 60/112,734
EARLIER FILING DATE: 1999-12-18
NUMBER OF SEQ ID NOS: 70
SOFTWARE: MICTOSOft Office 97
SEQ ID NO 63
LENGTH: 536
                                    284 TGGCGCGCAGTTGACGGTG 265
                                                                                                                   US-09-465-558-63/c
: Sequence 63, Application US/09465558
: Patent No. 6436657;
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (406)
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us-09-647-780a-5.rni

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Gaps
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Patent No. 5427925

Patent No. 10126

DOUGLAS J.; RING, JULIE A.; METCALE, DONALD; NICE, EDOUARD C.; NICOLA, NICOS A.; SIMPSON, RICHARD J.; MILLSON, TRACY A.

TILLE OF INVENTION: RECOMBNIANT METHOD FOR MAKING.

LEUKEMIA INHIBITOR FACTOR

NUMBER OF SEQUENCES: 38

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/58,979

FILING DATE: 06-MAY-1993

FILING DATE: 06-MAY-1993

APPLICATION NUMBER: 948,614
                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5187077

APPLICANT: GEARING, DAVID P., GOUGH, NICHOLAS M.; HILTON
DOUGLAS J.; KING, JULIE A.; METCALE, DONALD; NICE, EDOUARD C.; NICOLA, NICOS A.; SIMPSON, RICHARD J.; WILLSON, TRACY A.
TITLE OF INVENTION: LEUKEMIA INHIBITORY FACTOR
NUMBER OF SEQUENCES: 41
                                                                                                                                                DB 3;
.4e+02;
les 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.0%; Score 15.2; DB 6; ilarity 85.0%; Pred. No. 1.4e+02; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.2; DB 6;
Pred. No. 1.4e+02;
0; Mismatches 3;
                                                                                                                                                Score 15.2; DE Pred. No. 1.4e+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/294,514 FILING DATE: 09-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 TTGAGAGGCAGTGGGCTGTG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 69, Application US/09465558
; Patent No. 6436657
                                                                                                                                                                                                                                                                            39 reseccecresrescrere 58
                                                                                                                                                                                                                                       1 TGGAGCGCCAGTTGGCTGTG 20
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APPLICATION NUMBER: 667,159
FILING DATE: 11-MAR-1991
                                                                                                                                                Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (38)..(1102)
US-09-067-089-1
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 17; Conserv
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; LENGTH: 1297
5187077-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 1297
5427925-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query, Match
                                                                                                                                                                                                                                                                                                                                                                 5187077-23; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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                                                                                                                                                                                      CARELLA, BYRNE, BAIN, GILFILLAN CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hudson, Peter L.
APPLICANT: He, Wei W.
APPLICANT: Huben, Steven M.
TITLE OF INVENTION: Serum Paraoxnase
FILE REFERENCE: PF124D2
CURRENT APPLICATION NUMBER: US/09/067,089A
CURRENT FILING DATE: 1998-04-27
EARLIER APPLICATION NUMBER: 08/783,889
EARLIER FILING DATE: 1997-01-16
EARLIER FILING DATE: 1994-07-05
NUMBER OF SEQ ID NOS: 6
                                                                       GENERAL INFORMATION:
APPLICANT: PETER L. HUDSON, ET AL.
TITLE OF INVENTION: Serum Paraoxonase
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/08/783,889A
16 JAN 1997
                                   Sequence 1, Application US/08783889A
Patent No. 5792639
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/270,583
FILING DATE: 5 JULY 1994
ATTORNEI/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09067089A Patent No. 6140093 GENERAL INFORMATION:
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                                                                                                                                                                                                                         6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                              33,073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1079 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
EQ ID NO 1
LENGTH: 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201-994-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                         CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                              07068
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APPLICANT: Biddlecome, Gloria
TITLE OF INVENTION: Genes Encoding Neuronal Voltage-Gated Calcium Channel
TITLE OF INVENTION: Gamma Subunits
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                                                                            Length 1554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lal, Preeti
TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
FILE REFERENCE: PC-0007 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                  Indels
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orners INFORMATION: Incyte ID No. 6372431 1810320CB1
US-09-443-184-46
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Pred. No. 1.5e+02;
0; Mismatches 3;
                                                                          Score 15.2; DB 3;
Pred. No. 1.5e+02;
                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/443,184A CURRENT FILTING DAFE: 1999-11-19 NUMBER OF SEC ID NOS: 138 SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: US APP. 09/123,030
CURRENT APPLICATION NUMBER: US/09/123,030
CURRENT FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                        US-09-443-184-46
; Sequence 46, Application US/09443184A
; Patent No. 6372431
                                                                                                                                                                                           657 TGACGCGCCACTTGGCTGTG 676
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Patent No. 6365337
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cunningham, Mary Jane
APPLICANT: Zweiger, Gary
APPLICANT: Raser, Matthew R.
APPLICANT: Panzer, Scott
APPLICANT: Seilhammer, Jeffrey J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%;
                                                                        76.0%;
illarity 85.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Murinae gen. sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baughn, Mariah APPLICANT: Azimzai, Yalda
PROSTUT12
1810320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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LENGTH: 1554
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  · LIBRARY:
                    ; CLONE:
US-09-109-205-4
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                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                76.0%; Score 15.2; DB 4; Length 1468; 85.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
UNRENT APPLICATION DATA:
                APPLICANT: MOTAKINYO, LAYO O.
APPLICANT: OFOZCO Jr, EM11 M.
TITLE OF INVENTION: TETRAHYDROFOLATE METABOLIC ENZYMES
FILE REFERENCE: BB1322 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yue, Henry
TITLE OF INVENTION: HUMAN SCAD FAMILY MOLECULES
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Incyte Pharmaceuticals, Inc
                                                                                      CURRENT APPLICATION NUMBER: US/09/465,558
CURRENT FILING DATE: 1999-12-17
EARLIER APPLICATION NUMBER: 60/112,734
EARLIER FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Microsoft Office 97
LENGTH: 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                   270 TGGCGCGGCAGTTGACGGTG 251
                                                                                                                                                                                                                                                                                                                                                                                                             1 TGGAGCGGCAGTTGGCTGTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET WUMBER: PF
FELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corley, Neil C.
Baughn, Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lal, Preeti
Guegler, Karl J.
Gorgone, Gina
                                                                                                                                                                                                                                                                                                                              Ouery Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                  TYPE: DNA
CRGANISM: Triticum aestivum
US-09-465-558-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-109-205-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT
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0; Gaps

Length 2265;

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Score 15.2; DB 1;
Pred. No. 1.5e+02;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                           Search completed: July 8, 2003, 09:30:59 Job time: 38.6598 secs
                                                                                                                                                                                                                                      1008 UGGAGCUGCACUUGGCUUUG 1027
                                                                                                                                                                                                              1 TGGAGCGGCAGTTGGCTGTG 20
                                                                                                                         Ouery Match 76.0%;
Best Local Similarity 60.0%;
Matches 12; Conservative 5
MOLECULE TYPE: mRNA FEATURE:
                                         NAME/KEY:
COCATION:
US-08-242-689-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mernods and Compositions for Early Detection and Treatment of Insulin Dependent Diabetes Mellitus
                                                                                                                                                                                                                                 Length 1558;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,689
                                                                                                                                                                                                                                 Score 15.2; DB 4;
Pred. No. 1.5e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Atkinson, Mark A.
APPLICANT: Maclaren, No. 56459981 K.
APPLICANT: Kastern, William
IITLE OF INVENTION: Methods and Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
JITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/746,443
FILING DATE: 16-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/569,324
FILING DATE: 17-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US, 07/427,051
FILING DATE: 25-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/283,633
FILING DATE: 13-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
                                                                                                                                                                                                                                                                                                                                                         1350 regreegeegeriegerere 1331
                                                                                                                                                                                                                                                                                                                  1 TGGAGCGGCAGTTGGCTGTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08242689; Patent No. 5645998; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UF PELECOMMUNICATION: 1ELEPHONE: 904-375-8100
                                                                                                                                                                                                                                 Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2265 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                             ; NAME/KEY: 3'UTR
; LOCATION: (1361)..(1558)
US-09-123-030-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                            NAME/KEY: CDS
LOCATION: (390)..(1361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: M
TITLE OF INVENTION: D
TITLE OF INVENTION: M
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear.
                     OCATION: (1)..(389)
    NAME/KEY: 5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-242-689-1
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Compugen Ltd.
GenCore version 5.1.6
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July 8, 2003, 19:09:54; Search time 115.512 Seconds	(without alignments)	273.390 Million cell updates/sec
19:09:54		
8, 2003,		
July		
Run on:		

US-09-647-780A-5 Title: Perfect score:

1 tggagcggcagttggctgtg 20 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1105431 segs, 789497651 residues Searched:

2210862 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq _NEW_PUB.seq NEW_PUB.sec Published

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence 1487, Ap	Sequence 1489, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 5830, Ap	Sequence 159, App	Sequence 3, Appli	Sequence 3, Appl1	Sequence 1723, Ap	_	Sequence 6786, Ap	Sequence 3025, Ap	Sequence 12815, A	Sequence 5691, Ap	Sequence 26751, A	Sequence 109, App	4	Sequence 1224, Ap	Sequence 9095, Ap
ΙD	US-09-764-868-1487	US-09-764-868-1489	US-09-781-558-1	US-09-957-683-1	US-09-764-891-5830	US-10-205-823-159	US-09-900-449A-3	US-09-781-558-3	US-09-878-574-1723	US-10-156-761-1	US-09-960-352-6786	US-09-867-701-3025	US-09-918-995-12815	US-09-864-761-5691	US-09-918-995-26751	US-09-244-694-109	US-09-974-300-6034	US-09-917-800A-1224	US-10-198-846-9095
BB :	6	σ	10	10	σ	σ	σ	10	10	σ	10	10	σ	10	თ	10	10	10	6
Query Match Length DB	22452	22452	3348	4197	5746	7808	34668	74586	384	9025608	. 296	307	332	478	482	206	510	.516	531
Query	82.0	82.0	79.0	79.0	79.0	79.0	79.0	79.0	77.0	77.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0
Score	16.4	16.4	15.8	15.8	15.8	15.8	15.8	15.8	15.4	15.4	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2
Result No.	1	7	m	4	5	9	7	æ	O	10	c 11	c 12	13	.c 14	15	c 16	c 17	c 18	c 19

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Sequence 9074, Ap	Sequence 4837, Ap	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 6700, Ap	Seguence 107, App	Seguence 107, App	_	Sequence 107, App	Seguence 1223, Ap	Sequence 183, App	Seguence 802, App	Sequence 23, Appl	Seguence 86, Appl	Sequence 2118, Ap	Sequence 90, Appl	Sequence 94, Appl	Sequence 4, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 272, App	Sequence 342, App	Sequence 5342, Ap	Sequence 56, Appl
US-09-864-761-9074	US-10-156-761-4837	US-10-222-577-11	US-10-222-578-11	US-09-790-045-11	US-10-156-761-6700	US-09-924-340-107	US-09-992-600A-107	US-10-000-489-107	US-10-000-986-107	US-09-938-842A-1223	US-09-746-783-183	US-10-037-270-802	US-09-802-640-23	US-10-171-581-86	US-09-880-107-2118	US-08-823-386-90	US-10-205-951-94	US-10-017-273A-4	US-09-905-846-1	US-10-017-273A-5	US-09-905-846-5	US-10-044-090-272	-	US-10-128-714-5342	US-10-205-951-56
10	б	6	6	10	6	σ	6	σ	σ	5	σ	σ	6	σ	10	10	σ	σ	10	σ	10	12	σ	Ф.	σ.
588	810	884	884	884	918	1520	1520	1520	1520	1527	1528	1554	1570	1600	1738	2469	2799	2893	2893	2975	2975	3331	3408	3409	3421
0.97	76.0	0.97	76.0	76.0	76.0	76.0	76.0	0.97	. 76.0	76.0	76.0	0.92	76.0	76.0	76.0	76.0	76.0	76.0	0.97	0.92	76.0	76.0	76.0	76.0	0.92
15.2	15:2	.15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	.15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2
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ALIGNMENTS

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    refer to PALM or file wrapper

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT322
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                 Score 16.4;
Pred. No. 8
                                                                                                                           CURRENT APPLICATION NUMBER: US/09/764,868 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1489, Application US/09764868
Patent No. US20020168711A1
Application US/09764868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22357 GAGCGGCAGTTGGCTGAG 22374
                                                                                                                                                                         Prior application data removed NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                   SOFTWARE: Patentin Ver.
SEQ ID NO 1487
LENGTH: 22452
                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-764-868-1487
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                                                                                                                                                                                                                                                                                           TYPE: DNA
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Gaps

consult PALM or file wrapper

Score 15.8; DB 9; Pred. No. 1.8e+02; 0; Mismatches

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Sequence 5830, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOOR
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-0117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 159, Application US/10205823
Publication No. US20030108963A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1835 TGGAGAGCCAGTTGGCTGT 1853
    3273 GGAGCTGCAGCTGGCTGTG 3291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGGAGCGGCAGTTGGCTGT 19
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NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5830
LENGTH: 5746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oersch, Sebastian
amatkar, Shubhangi
Tonsey, Angela M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlegel, Robert
Monahan, John E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endege, Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                        RESULT 5
US-09-764-891-5830
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-764-891-5830
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
ITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
ITLE OF INVENTION: AND USES, THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
TITLE OF INVENTION: 55063, a No. US20020123098Alel Human NMDA Family Member
TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: MNI-191
CURRENT APPLICATION NUMBER: US/09/957,683
CURRENT FILING DATE: 2001-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
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                                                                                                                DB 9; Length 22452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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89.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2;
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                                                                                                                                                         Mismatches
                                                                                                              Score 16.4;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 48
SUFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/781,558 CURRENT FILING DATE: 2001-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/199,811
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/641,426
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                                                                                                                                                                                                                        22357 GAGCGCCAGTTGCCTGAG 22374
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                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09781558 Patent No. US20020034778A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGAGCGCCAGTTGGCTGTG 20
                                                                                                            Query Match
Best Local Similarity 94.4%; Pr
Matches 17; Conservative 0;
                                                                                                                                                                                                  3 GAGCGGCAGTTGGCTGTG 20
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                           :0020034778A1
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Beasley et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LE REFERENCE: CL000756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
; LENGTH: 22452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: HUMAN
US-09-781-558-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 4197
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LICANT: Anderson, Dustin
LE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
LE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
LE OF INVENTION: THERAPY OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 7808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : FastSEQ for Windows Version 4.0
                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/205,823
                                                                                                                                                                                     NT FILING DATE: 2002-07-25
APPLICATION NUMBER: 60/307,982
FILING DATE: 2001-07-25
APPLICATION NUMBER: 60/314,356
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APPLICATION NUMBER: 60/341,746
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2 GGAGCGCCAGTTGGCTGTG 20

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APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT APPLICATION NUMBER: 09/9333,535
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9025608;
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Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max correst information: Clone ID: LIB3028-034-Q1-B1-D2 US-09-878-574-1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.4; DB 9;
Pred. No. 1.2e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SAKAKİ, YOSHIYUKI
APPLICANT: HATTORİ, MASAHIRA
IITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                              Sequence 1723, Application US/09878574 Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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Best Local Similarity 94.1%; Pr
Matches 16; Conservative 0;
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94.1%;
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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SEQ ID NO 1723
LENGTH: 384
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Best Local Similarity
Matches 16; Conserv
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SEQ ID NO 1
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF ZOOL 2001 2000, 449A
CURRENT APPLICATION NUMBER: US/09/900, 449A
CURRENT FILING DATE: Z001-07-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 34668
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APPLICANT: Beasley et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: C1000756
CURRENT APPLICATION NUMBER: US/09/781,558
CURRENT FILING DATE: 2001-02-13
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
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                                                 Indels
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Pred. No. 1.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.0%; Score 15.8; DB 9; Best Local Similarity 89.5%; Pred. No. 1.6e+02; Matches 17; Conservative 0; Mismatches 2;
89,5%; Prea. ....
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COTHER INFORMATION: n = A,T,C or G
US-09-781-558-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09781558 Patent No. US20020034778A1
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Best Local Similarity 89.5%;
Matches 17; Conservative
       Best Local Similarity 89.5
Matches 17; Conservative
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US-09-900-449A-3
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-12815
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Matches 17; Conserv
                                                                                                                                                                                        Query Match
                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC ACID AND FAI DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAI DEPOSITION
TITLE REFERENCE: 16511.006/37-21(10298)C
CORRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 296;
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APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
KUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASTSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.2; DB 10;
Pred. No. 3.9e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 29-LIB34-015-Q1-E1-H1
US-09-960-352-6786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.2; DB 10;
Pred. No. 3.9e+02;
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                     Sequence 6786, Application US/09960352
Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020132237A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 TGGAGCGTCGGTTGGCTTTG 198
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                                                                                                               APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.0%;
Matches 17; Conservative
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SEQ ID NO 6786
LENGTH: 296
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; ORGANISM: Homo sapien
US-09-867-701-3025
                                                                  GENERAL INFORMATION:
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-09-960-352-6786/c
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US-09-918-995-12815
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LENGTH: 307
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PPLICANT: Chen, Wensheng
ITLE OF INVERTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
ILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                         Score 15.2; DB 9; Length 332;
Pred. No. 3.8e+02;
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                0; Mismatches
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PESTSEQ for Windows Version 3.0
SEQ ID NO 12815
LENGTH: 332
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LING DATE: 2000-08-03
LICATION NUMBER: GB 24263.6
LICATION NUMBER: US 60/236,359
LICATION NUMBER: US 60/236,359
LNG DATE: 2000-09-27
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PPLICATION NUMBER: PCT/US01/00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION NUMBER: PCT/US01/00664
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IOR FILING DATE: 2000-02-04
IOR APPLICATION NUMBER: US 60/207,456
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APPLICATION NUMBER: US 60/234,687
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Patent No. US20020048763A1
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PERVINE: Homo sapiens

PERVINE:
OTHER INCOMATION: MAP TO ACO04752.1
OTHER INCOMATION: EXPRESSED IN LUNK, SIGNAL = 13
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AQ292016 nbxb0041E
AG68830 nbxb0077H
BE469456 IpHdk0183
AA093253 110282.se
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4044-75 Mouse El4.5 retina lambda ZAP II Library Mus musculus cDNA,
BI989738
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AA948928 LD27627.5
BH521881 BOGKF43TF
AL296196 Tetraodon
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Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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/organism="Mus musculus
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BJ184876
                                                                                                                                                                                                                                   8, 2003, 00:47:28; Search time 1013:95 Seconds (without alignments) 319.453 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32308132
                               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16154066 seqs, 8097743376 residues
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Maximum Match 100%
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em_gss_pro:*
em_gss_rod:*
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:snw_ssb_me

em_gss_mam

em_dss_pln

em_estfun: em_estom:*

qb_est5:

gb_est3:

em_esthum:

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600 509 538 565 601

92.0 87.0 87.0 87.0 87.0

18.4 117.4 117.4 117.4

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Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing 0 (2000) and then cultivated on the BCD medium containing 0 (2000).
                                                                                                                          Life Technologies); Average insert size: 1.8 Kb; Insertion site: TACGTCCACTGAATTCTGACTG---- Other information regarding entire library may be found at http://pga.swmed.edu/Data/Libraries/microarray_cdna_libraries.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ173933 normalized full length cDNA library, chloronemata, caulonemata and malformed buds Physcomitrella patens subsp. patens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jita,T., Shin-1,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.
Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comparison of the moss Physcomitrella patens genome with flowering
                                                                                                       RNA preps
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/clone_lib="normalized full length cDNA library,
chloronemata. caulonemata and malformed buds"
/tissue_type="mixture of chloronemata, caulonemata and
malformed buds"
                                              /dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps
(Manniatis); Cloning Technique: CWA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Bukaryota; Viridiplantae; Ztreptophyta; Embryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
  /clone_lib="Mouse El4.5 retina lambda ZAP II Library"
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/db_xref="taxon:145481"
                                                                                                                                                                                                                                                                                                                                                                   Score 18.4; DB 13; Length 600; Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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111 Yata, Mishima, Shizuoka 411-8540, Japan
21: 81-559-81-6856
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Center For Genetic Resource Information
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Best Local Similarity 95.0%;
Matches 19; Conservative
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Inpublished (2002)
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BJ173933
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DEFINITION
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VERSION
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A backbone of the vector is pBluescript II, that was in vivo excised from a modified 185 phage vector (Mo bi Tec, Germany). XhoI excised from a modified 185 phage vector (Mo bi Tec, Germany). XhoI digested-5' end of CDN is ligated to Sall site of the vector, and the BamHI digested-3' end including poly-A tail is ligated to BamHI site of the vector. CDNN inster could be amplified with conventional T7 and T3 primers. This normarized full-length CDNA library was generated basically according to the method described in Genome Research 10, 1617-1630 (2000), Carninci, P. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing 0.5um BA (benzylaminopurine) for 8 to 13 days under the continuous light.
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BJ184876 normalized full length cDNA library, chloronemata, caulonemata and malformed buds Physcomitrella patens subsp. patens BJ184876
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Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
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chloronemata, caulonemata and malformed buds"
/tissue_type-"mixture of chloronemata, caulonemata and
malformed buds"
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Bryopsida, Funariidae, Funariales, Funariaceae, Physcomitrella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Tadasu Shin-1
Center: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yats, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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Pred. No. 1.7e+03;
0; Mismatches 1;
Score 17.4; DB 13;
Pred. No. 1.7e+03;
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                                                         Mismatches
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ilarity 94.7%;
Conservative 0
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Unpublished (2002)
                              Local Similarity 94.7
les 18; Conservative
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AZ367683
LOCUS
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ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

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A backbone of the vector is pBluescript II, that was in vivo excised from a modified lPs phage vector (Mo bi Tec, Germany). XhoI edigested-5' end of CDNA is ligated to Sall site of the vector, and the BamHI digested-3' end including poly-A tail is ligated to BamHI site of the vector. CDNA instert could be amplified with conventional T7 and T3 primers. This normarized full-langth class of the vector is primers. This normarized full-length class in Genome Research 10, 1617-1630 (2000), Carninci, P. et al. Protonomata were blended by the PoLyTRON, and then cultivated on days under the continuous light.
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                                                                                                                                                                                                                                              ljita,T., Shin-1,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.
Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
                                                                                                                                                                                                                                                                                                                                Comparison of the moss Physcomitrella patens genome with flowering
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National Institute of Child Health and Human Development, National
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/clone_lib="normalized full length cDNA library,
chlorommata, caulonemata and malformed buds"
/tissue_type="mixture of chloronemata, caulonemata and
malformed buds"
                                                                                                                               Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipldae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Physcomitrella patens subsp. patens"
/db_xref="taxon:145481"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Pred. No. 1.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
CDNA clone pphb41106 5', mRNA sequence.
BJ187554
BJ187554.1 GI:18355495
                                                                                                        Physcomitrella patens subsp. patens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Institute of Genetics
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1 (bases 1 to 660)
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ilarity 94.7%;
Conservative
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Fujita, T., Shin-1.T
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Best Local Similarity
Matches 18; Conserv
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VERSION
KEYWORDS
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AUTHORS
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BQ521069
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                                                                                                                                                                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Walss, R. and Wright, D., Walss, R. and Wright, D., Walss, R. and Wright and French and Stokes grown scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Sciurognathi; Muridae;
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Pred. No. 1.7e+03; ·
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0117 row: M column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B, Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: plasmid enus
High quality sequence stop: 565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="taxon:10090"
'clone="UUGC1M0117M01"
                                                                                                                                             Chordata;
                                                                                                                                                                 (ammalia; Eutheria; Rodentia;
( bases 1 to 565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                               AZ367683.1 GI:10481479
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ilarity 94.78;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                      Jnpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606 Pax: 801 585 7177
                                                                                                                    Mus musculus
                                                                                       nouse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
Best Local Similarity
Matches 18; Conserv
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Vertebrata; Euteleostomi;

BASE COUNT ORIGIN

DEFINITION

RESULT 5 BJ187554 LOCUS

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Gaps

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Length 601; Indels

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Best Local S
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ORIGIN
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TITLE
JOURNAL
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KEYWORDS
SOURCE
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AQ688530
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                  DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          786 bp DNA linear GSS 03-DEC-1998 nbxb0041E05f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0041E05f, DNA sequence.
                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV-SPORT6.ccdb; Site_1: NotI; Site_2: ECORV; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 Kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
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/clone_lib="CDGI Rice BAC Library"
/tissue_type="Leaf"
/lab_host="Leaf"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
Ehrhartoideae; Oryzeae; Oryza.
I (bases 1 to 786)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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Pred. No. 1.8e+03;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                    /dev_stage="embryo, stages 20-27"
/lab_host="DH10B (phage-resistant)"
                                                                                                                   Plate: LLAM11852 row: P column: 22
Seg primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                   /organism="Silurana tropicalis"
/db_xref="taxon:8364"
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Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                                                                        'clone="IMAGE:5335941"
'clone_lib="NICHD_XGC_Emb7"
'tissue_type="tailbud"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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Location/Qualifiers
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'cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4530'
                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 GGGCGCAGTTGGCTGTC 195
CDNA Library Arrayed by:
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1 Similarity 94.7%;
18; Conservative
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     141
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AUTHORS
TITLE
JOURNAL
COMMENT
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AQ292016
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KEYWORDS
SOURCE
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Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Organ saliva, Nipponbare variety. The library contains 36,864 clones with an average insert size
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           the whole library for colony screening."

189 c 183 g 248 t
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nbxb0077H20r CUGI Rice BAC Library Oryza sativa genomic clone
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world. Half of the world population especially those inhabiting highly populated areas of the humid tropics
                                                              and subtropics, rely on rice as their primary source of
carbohydrate. MonocotyLedonous rice is a diploid plant
(2n-24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
lindIII; Rice is one of two most popular grains in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 786;
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/tissue_type="Leaf"
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Pred. No. 1.9e+03;
0; Mismatches 1;
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Tel: 864 656 7288
Fax: 864 656 4293
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Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
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Location/Qualifiers
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'clone="nbxb0077H20r
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18; Conservative
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Oryza sativa
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Liew, C.C.
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Best Local 8
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ORGANISM
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BF891199
LOCUS
      RESULT 10
AA093253
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AUTHORS
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KEYWORDS
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(2n-24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 1285.5kb providing 10.9 haploid genome equivalents: The deep coverage allows the isolation a particular sequence with a probability of 99.9% Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 bp mRNA linear EST 28-JUL-2000 IpHdk01836 Head kidney cDNA library Ictalurus punctatus cDNA 5' similar to Ribosomal protein 136a, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcriptome analysis of channel catfish (Ictalurus punctatus):
Gene catalogouing and profiling from the head kidney
Unpublished (2000)
Contact: Liu 2J
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ostarlophysi; Siluriformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="lctalurus punctatus"
/db_xref="taxon:7998"
/clone_lib="Head kidney cDNA library"
/note="Organ: Head kidney; Vector: pSport1; Site_1: Not1;
Site_2: Sall"
87 c 113 g 71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Meopterygii; Teleostei; Ostariophysi; Siluriforme
Ictaluridae; Ictalurus.
1 (bases 1 to 397)
Cao.D., Kocabas, A., Ju, Z.; Karsi, A., Li, P., Patterson, A. and Liu
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 Swingle Hall, Auburn University, Auburn, AL 36849, USA Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag auburn.edu
Seq primer: Ml3 Reverse.
Location/Qualifiers
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Pred. No. 1.9e+03;
0; Mismatches 1;
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Pred. No. 2.3e+03;
0; Mismatches 0;
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llarity 100.0%; P
Conservative 0;
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BE469456.1 GI:9559947
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Best Local Similarity 94.7%;
Matches 18; Conservative
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203 Swingle Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  channel catfish.
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Best Local Similarity
Matches 17; Conserva
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ORGANISM
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BE469456/c
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251 TGGAGCGGCAGTTGGCT 235

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1 (bases 1 to 265)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G. H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Slmpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
mRNA linear EST 24-OCT-1996
Lambda ZAP Express Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."
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mRNA sequence.
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                                                                                                                                                                                                 Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza; S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini; Hominidae; Homo
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PM3-MT0110-191000-007-b11 MT0110 Homo sapiens CDNA, 1
BF891199
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Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG
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Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                          75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cliew@rics.bwh.harvard.edu
                         10282.seq.F Human fetal heart,
                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 214)
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Mammalla; Eutheria; Primates;
                                                                                                                                                                                                                                                                                             CDNAs from fetal heart (1996)
Unpublished (1996)
Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                         Brigham and Women's Hospital
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                                             cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF891199.1 GI:12282658
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20202663
                                                                                                AA093253.1 GI:1638722
                                                                                                                                                                                                                                                                                                                                                                                                     Harvard Medical School
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90.0%;
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Seg primer: T7
Class: shotgun.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: marrow; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 .716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-MT0110-19000-007-bl1&t3=2000-10-19&t4=1)
Seq primer: puc 18 forward=1
High quality sequence stop: 69.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Um. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 bp DNA linear GSS 04-OCT-200
1M0244G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0244G11 R, DNA sequence.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., 18lam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
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Pred. No. 2.5e+03;
0; Mismatches 2; Indels 0;
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Length: 10000 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MT0110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stringency conditions.
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                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Adult'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGGAGCGCAGTTGGCTGTG 20
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90.0%;
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Pax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/) The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732144[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                             /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aguaro, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
A random sequencing approach for the analysis of the trypanosoma
cruzi genome: general structure, large gene and repetitive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
CP(1650) San Martin, Prov. de BS AS. Argentina
Tel: 54-11-4580-7255 ext 309
                                                                                                                                                                                     'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Trypanosoma cruzi.
Eukaryota; Eujenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 332)
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                                                                                                                /clone_lib="Mouse 10kb plasmid_UUGC1M_library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.0%; Score 16.8; DB 17;
90.0%; Pred. No. 2.7e+03;
tive 0; Mismatches 2;
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                                                                        /clone="UUGC1M0244G11
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/strain="C57BL/6J
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performed as previously described to the source of the Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
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/clone_lib="NCI_CGAP_Sub8"
/lab_host="Hild8 (Life Technologies)" the modified
/lab_host="Hild8 (Life Technologies)" the modified
polylinker; Site_l: Not I; Site_2: Eco RI; NCI_CGAP_Sub8
is a subtracted library derived from NCI_CGAP_Sub8. The
NCI_CGAP_Sub8 library derived from NCI_CGAP_Sub5. The
NCI_CGAP_Sub8 library had 2.5 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub5 was used
as a tracer in a subtractive hybridization with a driver
comprishing: a pool of clones from NCI_CGAP_Sub5 was used
as a tracer in a subtractive hybridization with a driver
comprishing: a pool of clones from NCI_CGAP_Sub4
(IMAGE clone Ids 273283-273415, 3068040-3069191; 25% of the
driver population), a pool of clones from NCI_CGAP_Sub4
(IMAGE clone Ids 2723592-273936; 25% of the driver
population), NCI_CGAP_Sub6 (pool Afrayor population), and
NCI_CGAP_Sub7 (IMAGE Ids 3069192-3072238, 3081864-3084550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand CDNA and therefore this may represent a bonafide poly A tail. CDNA Library Preparation: M.B. Soares Lab Clone distribution: M.B. Soares Lab Clone distribution: M.B. Soares Lab Clone distribution information can be found through the www-bio.lnl.gov/bbrp/image/image.html
Seq primer: Mil Forward
POLXA-Yes.
                                                                                                                                              /cell_type="epimastigote"
/note="vector: pBs(") (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 Kb range was gel purified and cloned into the dephosphoryated Hincil site of the vector"
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1-H-B14-aps-b-06-0-UI.S1 NCI_CGAP_Sub8 Homo sapiens cDNA clone MAGE:3088450 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                       Score 16.8; DB 17; Length 332;
Pred. No. 2.7e+03;
0; Mismatches 2; Indels 0:
                                                   'organism="Trypanosoma cruzi"
                                                                                                                                                                                                                                                                 site of the vector"
6 c 115 g 72
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/db_xref="taxon:9606"
                                                                                        /db_xref="taxon:5693"
/clone="G10E17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
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BF511828.1 GI:11595126
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1 Similarity 90.0%;
18; Conservative
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-NN0079-140 400-334-all&t3=200-04-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 418.
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1 (bases 1 to 418)
1 (bases 1 to 418)
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1 bases 1 to 418,
1 carcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,P.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare Simpson,A.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORESTES PCR (U.S. Letters Patent application Ludwig Institute for Cancer Research)
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                                                                                                                                                                                                                                                                                                                                                                                                    AW898919 404000-334-all NN0079 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was made by cloning products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human, transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue mRNA and cDNA amplification were performed under
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                                                                                                         Score 16.8; DB 12;
Pred. No. 2.9e+03;
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Pred. No. 2.9e+03;
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                                                                                                                                                               0; Mismatches
                                163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
TAG_SEQ-None found"
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FEATURES

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/organism="Mus musculus"
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YKAYLQWLAEGGRDQRLPGLNLTYAQLFFINYAQYWGGSYRPEFAIQSIKTDVHSPLK
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nep 11 membrane metalloprotease and its use for screening inhibitors useful in therapy
Patent: WO 9953077-A 1 21-OCT-1999;
INST MAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLADDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOWME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
Location/Qualifiers
Patent: WO 9953077-A 6 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)

LOCATION/Qualifiers
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Schwartz,J.C., Gros,C., Ouimet,T., Rose,C., Bonhomme,M.C. and Facchinetti,P.
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/db_xref="taxon:10117"
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Pred. No.
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AUTHORS
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TITLE

FEATURES

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1 AGTTCCCACTTGGGGCCCATG 21

Matches

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AF302075 2583 bp mRNA linear ROD 11-JUN-2001
Mus musculus neprilysin-like peptidase alpha mRNA, complete cds.
AF302075
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LADNONNNGFSTLGENIADNGGVRQAYKAYLRWLADGGKDQRLGGLNLTYAQLFFINY
AQWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPWKRCR
IW"
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                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                      1 (bases 1 to 2583)
Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T.,
Iwatsubo, T. and Saido, T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most phosphoramidon sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
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AF157106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="neprilysin-like peptidase alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-SEP-2000) Proteolytic Neuroscience Science Institute, RIKEN, 2-1 Hirosawa, Wako-sh 351-0198, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.4%; Score 19.4; DB 10;
ilarity 95.2%; Pred. No. 18;
Conservative 0; Mismatches 1;
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Laboratory, Brain

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FSARHFQQQSQCMIYQYGNFSWELADNONVNGFSTLGENIADNGGVRQAYKAYLRWLA
DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRK
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Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saltama
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 2694)

2 hirotani, K., Tsubuki,S., Iwata,N., Takaki,Y., Harigaya,W.,

Maruyama,K., Kiryu-So,S., Kiyama,H., Iwata,H., Tomita,T.,

Iwatsubo,T. and Saido,F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases J. Biol. Chem. 276 (24), 21895-21901 (2001)
                                                                                                                                                       Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory,
Science Institutute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
351-0198, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                        'product="neprilysin-like peptidase beta"
among thiorphan-, and
                     phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
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Pred. No. 18;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             'protein_id-"AAG18447.1"
                                                                                                                                                                                                                                                                                          /organism-"Mus musculus
                                                                                                                                                                                                                                                                                                        db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                              /note="endopeptidase"
                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                             2 (bases 1 to 2652)
Shirotani, K. and Saido, T.C.
Direct Submission
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illarity 95.2%;
Conservative
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Best Local Similarity
Matches 20; Conserv
                                                                                           11278416
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ORIGIN
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AF302077/c
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TITLE
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AUTHORS
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MEDLINE
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SOURCE
                                                                                                                                                                                                                                                FEATURES
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Mus musculus neprilysin-like peptidase beta mRNA, complete cds.
AF302076
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AQWGGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPWKRCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIVTLGVFYSIALRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="SEP(delta); metalloprotease; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNSRYSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKMVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :VEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELN
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                                                                                                                                                                                                                           membrane-bound metalloprotease, the soluble secreted form of which
hydrolyzes a variety of vasoactive peptides
J. Biol. Chem. 274 (45), 32469-32477 (1999)
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Maruyama,K., Kiryu-Seo,S., Kiyama,H., Iwata,H., Tomita,T.,
Iwatsubo,T. and Saido,T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-JUN-1999) International Center for Medical Research, Robe University School of Medicine, 7-5-1 Kusunoki, Chuo, Robe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                       1 (bases 1 to 2601)
Kreda,K., Emoto,N., Raharjo,S.B., Nurhantari,Y., Saiki,K.,
Yokoyama,M. and Matsuo,M.
Molecular identification and characterization of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="soluble secreted endopeptidase delta"
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Pred. No. 18;
0; Mismatches 1;
                                                                                           Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurognat
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organism="Mus musculus"
db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="AAF13153.1"
db_xref="G1:6467401"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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    GI:6467400
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95.2%;
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Shirotani, K., Tsubuk:
                                                                                                                                                                                                                                                                                                                                           (bases 1 to 2601)
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                                                 Mus musculus.
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20; Conserv
  AF157106.1
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KEYWORDS
SOURCE
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ORIGIN
                                                                   ORGANISM
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AUTHORS
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AUTHORS
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  VERSION
KEYWORDS
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Gaps

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Indels

Length 2652;

DB 10;

ROD 11-JUN-2001 complete cds.

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ORIGIN
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AX033272/c
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VERSION
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                                                                                                                                                                                                                                                                                                                      LGMPSREYYFOEDNNHKVRKAYLEFMTSVATMLRKDONLSKESAMVREENAEVLELET
HLANAVPOERRHDVTALYHRNDLMELOERFCIKDRVSLCSPCCPGTHSVDOAGLELG
NPASDSRVLGLKGFWTLFTONVLSSVEVELFPDEEVVVYGTPYLENLEDIIDSYSA
RTMONTLWRKLVLDSTGSLSQRFKEARVDYRKALYGTYVEFVRRECYSYVNSNMESS
KTMONTLWRKLVLDESSQRFKEARVDYRKALYGTYVEFVRRECYSYNSNMESS
KTMONTLWRKLYLLESSGRFKEARVDYRKALYGTYVEFVRRECYSYNSNMESS
KGSLYIKRAESKUSSKGTVRELIEKIRSVFVDNLDELMRMDEESKKKAOEKAMNIREDI
GYPDYILEDNNKHLDEYS SSLIFY EDLYFENGLOALKNNAQRSLKKLREKYDONLMII
GAAVVNARYSDNRIAUJVFPAGTLIOPPFFSKDOPOSLNFGGIGWYIGHETHGFDDNGR
NFDKNGNMLDWWSNESARFOOGSOCMIYOYOFFSWELADNONVNGFSTLGENIADNG
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                                                                                                                                                                                                                                     /translation="MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIALRD
                                                                                                                                                                                                                                                       SSLKSDICTTPSCVIAAARILENMDOSRNPCENFYQYACGGMLHHYIPETNSRYSVF
DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKMYG
GWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus Eutheria: Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2892)
Ikeda, K., Emoto, N., Raharjo, S.B., Nurhantari, Y., Saiki, K., Yokoyama, M. and Matsuo, M. Aharacterization of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus soluble secreted endopeptidase mRNA, complete cds
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Direct Submission
Submitted (08-UN-1999) International Center for Medical R.
Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 2694;
                                                                                                                                                                    /product-"neprilysin-like peptidase gamma"
/protein_id="AAG18448.1"
/db_xref="GI:10505364"
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/note="SEP; metalloprotease"
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                                                            /organism="Mus musculus"
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/organism-"Mus musculus"
/db_xref-"taxon:10090"
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/db_xref="G1:6467399"
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                                                                                                                           'note="endopeptidase"
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Best Local Similarity 95.2%;
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351-0198,
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                                                    DQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRADLMELQEREGLKG
FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLV\LD
RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
                                                                                                                                                                                           QIVFPAGILQPPFFSKDQPQSLNFGGIGMVICHEITHGFDDNGRNFDKNGNMLDMWSN
FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSLGENIADNGGVRQAYRAYLRWLA
DGGKDQRLPGLNLIYAQLFFINYAQVWCGSYRPFFAVQSIKTDVHSPLKYRVLGSLQN
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Boileau, G. and Desgroseillers, L. New metalloproteases of the neprilysin family
Patent: WO 0047750-A 12 17-ANG-2000;
BOILEAU GUY (CA); DESGROSEILLERS LUC (CA); UNIVERSTIE DE MONTREAL
                                                                                                                                      KSTVRELJEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYJLEDNNKHL
DEEYSSLIFYEDLYFENGLQNLKNNAQRSLKKIREKVDQNLWJIGAAVVNAFYSPNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT 21-SEP-2000
CMNQSVIEKRDSEPLLSVLKMVGGWPVALDKWNETMGLKWELERQLAVLNSQFNRRVL
IDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHKVRKAYPEFWTSVATMLRK
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QYACGGWLRHHVIPETNSRYSVFDIIRDELEVIIKGVLEDSTSQHRPAVEKAKTLYRS
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DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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Sequence 12 from Patent WO0047750.
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/db_xref="GI:10280088"
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332. .2629
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FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLA
DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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Chaddar,G., Ruchon,A.F., DesGroseillers,L. and Boileau,G.
Chaddar,G., Ruchon,A.F., DesGroseillers,L. and Boileau,G.
Direct Submission
Submitted (09-Aug-1999) Biochemistry, University of Montreal, 2900
Edouard Montpetit, Montreal, Que H3T 1J4, Canada
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="neprilysin-like metallopeptidase 1"
protein_id="AAF69247.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="testis"
1. .2925
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Pred. No. 18
                                      936 AGTICCCACTIGAGGCCCAIG 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          936 AGTTCCCACTTGAGGCCCATG 916
  AGTICCCACTIGGGGCCCAIG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGTICCCACTIGGGGCCCAIG 21
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                                                                                                                                                                                                                          AF176569.1 GI:7769082
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hes 20; Conservative
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                                                                                                                                                                                  complete cds.
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Best Local S
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                                                                                                 RESULT 9
AF176569/c
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ORIGIN
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                   ACCESSION
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MEDLINE
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KEYWORDS
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BCT 19-JUN-2002

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RESULT 10 AE000795/c LOCUS

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Development, Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEYRQCLTVKRVKKGTLVDIGADKLALCREKLTVNRIMSFRVVRLGKEILIEPDEPED
RYMGYEVLDTRRNLAESLKTVGADVVVATSRNASPITSILDEVKTRMRGAREAAILFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal proteins; similar to, sp:LN:RL3_METJA AC:P54014, p() 2.1E-95, pid=53%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'translation-"MARHHOPRKGSVAFSPRKRAARETPRVKSWPQVDEPGLLALAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TETKDDLRRKLTPPADDYDQEAAIEKIRSNMEYVADVRVIVHTNPRLASVPKKKPEVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECGLGGKTPEEKFEYALEILGKDVRASEIFSEGAFVDAIAVTKGKGFQGPVKRWGIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :YHDDADGEARFIRDILTYMDTPQYLRRKVFPIMRELKHVGILPPLRTPHHPTGKPVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNPDGGFVRYGLVRNDYVMIKGSVPGPTKRLVVLRKAIRAAGKQEEAPQINYISTASK
                                                                                                                                                                                                                                                                      Smith, D. R., Doucette-Stamm, L.A., Deloughery, C., Lee, H., Dubois, J., Aldredge, T., Bashirzadeh, R., Blakely, D., Cook, R., Gilbert, K., Harrison, D., Hoang, L., Keagle, P., Lumm, W., Pothier, B., Qiu, D., Spadafora, R., Vicaire, R., Wang, Y., Wierzbowski, J., Gibson, R., Jiwani, N., Caruso, A., Bush, D. and Reeve, J. N. Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonym: Methanobacterium thermoautotrophicum str.deltaH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Function Code:14.01 - Unknown, Conserved protein; similar to, sp:LN:YL31_HALMA AC:P20571, p()=1.2E-16, pid=27%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Methanothermobacter thermautotrophicus str.
                                                                                                                Methanothermobacter thermautotrophicus str. Delta H. Archaea; Buryarchaeote; Methanobacteria: Methanobacteria; Methanobacteria; Methanobacterials; Methanobacterians at 1 (pases 1 to 1000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (10-AUG-1997) Genomics and Technology Develo
Therapuetics Corporation, 100 Beaver Street, Waltham,
02154-8448, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="ribosomal protein L3 (E.coli L3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="conserved protein"
'protein_id="AAB84510.1"
1 of 148) of the complete genome. AE000795 AE000666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:187420"
/clone="MTH"
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                                                             AE000795.1 GI:2621036
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/gene="MTH2"
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/translation="MAKVKYAYKEEDRSGTARASATHLKISPKHAVEICREIRGMELE
KAKKYLEEVIRMERPVAFKRYNRKVGHRRGLNGWASGRYPVKAAGQILKVLENAEANA
EYKGLDTEKLRIIHISSHRGPVIRGWIPRAFGRATPFNTPTTHVQIVLGEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-"MAILRSEEIREMDGEELQKKLDELKAEYARYISKSAAAGIHENP
GKMREIRRTIARVLTIMNEK"
                                                                                                                                            Ribosomal proteins; similar to, sp:LN:RS3_METJA AC:P54034, p. 07.8.5E-53, pid=39%"
                                                                                                                                                                                                                                                                                                                                                                                               QRGMHFRRVAYTTMRRIMAAGAQGVEVTISGKIRGARSATAKFTDGYIKKCGEPSVKH
VREGFATVQLKPGVLGVYVRIMPPDVVLPDKVEIEDPRVTETPAEEASEASEASESEVEDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Function Code:10.04 - Metabolism of Macromolecules, Albosomal proteins; similar to, sp:IN:RL29_METJA AC:P54035, p()=4.5E-15, pid=58%" /codon_start=1
                                                                                                                                                                                                                                                                                                                         /db_xref="G1:2621055"
/translation="MIEKDFVVEGLRRTRIDEY_EKELERAGYGGMDVQVTPMGTMVV
                                                                                                                                                                                                                                                                                                                                                                       VYAERPGMVIGRGGKTVRAITQKLKNKFDLENPQVEVKEVDVPELNPKIMAHKIAAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Function Code:10.04 - Metabolism of Macromolecules, Ribosomal proteins; similar to, sp:LN:YRP1_METVA AC:P14021, p()=4.8E-27, pid=55%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MKICDVCGLPEBLCVCEEIAREVQTLKVYTVRRRFGKVMTIIEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="35 bp direct repeat includes part of MTH8 (ribosomal protein S3); 97% ID to interval 5450-5416" complement(5416. .5450)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="35 bp direct repeat includes part of MTH8 ribosomal protein S3); 97% ID to interval 5396-5362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Product="ribosomal protein L35 (E.coli L29)"
Protein_id="AAB84529.1"
                                                                                                                                                                                                                                                                             /product="ribosomal protein S3 (E.coli S3)"
/protein_id="AAB84528.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                             EVEDLEEIEDLEEVEDLEEVEDLEDTEAEKKDADGEESEK"
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/protein_id="AAB84511.1"
/db_xref="G1:2621038"
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Canis familiaris BGT1 gene, exon
D42027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(5362. .5396)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (5416.
                                                                                                                                                                                                                                                            /transl_table=11
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5546
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753. .6058
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/gene="MTH10"
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                                                                 4723. .5499 /gene="MTH8"
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/gene="MTH8"
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95.0%;
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qene="MTH9"
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D42021S07/c
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                                                                                                                                                                                                                                                                                                                                                    2768. .3070
/gene="MTH4"
/note="Function Code:10.04 - Metabolism of Macromolecules,
Ribosomal proteins; similar to, sp:LN:RL23_METJA
AC:P54016, p()=3.3E-19, pid=41%"
                                                                                                                                                                                                                                         PWGPDPMAGKRTSAQSYGAGRGVAMVPRIKNGSRAAFVPQAVGGRRAHPPRFQKNYHE
RINRKERRLAIRSAVAATARKDLVEARGHRIENVPQLPLVVDDELSMIKRTADTREVF
RKLGIMDDIVRAREGKKIRAGKGKMRGRKYRTPRGPLIVVGDDKGITRGARNHPGVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="Mokrelisorrgrgtptyreashrrgkikyraydsiesegslkg
VVDIMHDPGRTAPVARVKFENGEERLIIAPEALMLNEEVPGGGVKRVKPGNSLPLSE
PEGTPIYNIENRPGDGGKLVRSSGTYASLITHDADKAVIELPSGELKALNPQCRATV
                          Ribosomal proteins; similar to, sp:LN:RL4_MBTJA AC:P54015,
                                                                                                                                                                                                                     'translation="MKIKVYSLEGEAIDEMELPEIFNEEFRPDVIKRAVLSAQTARVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'trans lation="mmny sskegytvy imdpyav imkphyteksmni idonnelafvy
RKSTKKDVRRAFEELFAVKVERVNTQVTPRGQK IAY IKLAKEHSAEDIAVKLGVF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVAGGGRREKPFLKAGKKYHALRAKGKKSVTVRGVAMNAVDHPHGGGNRQHPGRPTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="WTH5"
Note="Function Code:10.04 - Metabolism of Macromolecules,
Xibosomal proteins; similar to, sp:LN:RL2_METVA AC:P21479,
(()=2.18-79, pid=56%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Function Code:10.04 - Metabolism of Macromolecules, Ribosomal proteins; similar to, sp:LN:RS19_METJAAC:P54018, p()=2.1E-40, pid=57%"
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IGCYFGEFAPTRKKVEHGDPGMGATRFSMFVPLK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="ribosomal protein L23a (E.coli L23)"
protein_id="AAB84524.1"
db_xref="GI:2621051"
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protein_id="AAB84526.1"
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/protein_id-"AAB84527.1"
                                                                                                                                                 product="ribosomal protein L4 (E.coli L4)"
protein_id="AAB84523.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="ribosomal protein L8 (E.coli L2)"
protein_id="AAB84525.1"
                                                                                                                                                                                                                                                                                                               VRVENLNAELLAPGTHPGRLTVFTRSAIEKLDELFQ"
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                                                                                                                         /transl_table=11
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/gene="MTH6"
3835. .4245
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'gene="MTH5"
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qene="MTH6"
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/gene="MTH7"
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LDWAVHSFRITNCELQDTTQIHTHMCYSNFNDIHSIIDMDADVITIENSRSDEKLLS
VFREGVKYGAGIGPGVYDIHSPRIPSAEEIADRIDKMLAVLDTNILWVNPDCGLKTRK
                                                                                       TVPAMEMTKWFDTNYHF IVPELGPNTKFSYASHKAVNEYKEAKALGVDTVPVLVGPVS
YLLLSKPAKGVEKGFPLLSSLLBSSILPVYKEVIAELKAAGASWIQFDEPTLVLDLDSDK
                                                                                                                                                                                                                                                     AFTANGWVQSYGSRCVKPPIIYGDVSRPNPMTVFWSKTAQSMTSRPMKGMLTGPVTIL
                                                                                                                                                                                                                                                                              NWSFVRNDOPRFETCYOIALAIKKEVGDLKAGGIQVIQIDEAALREGLPLRKAEHAFY
                                                                                                                                LAAFSAAYAELESVLSGLNVLVETYFADVPAESYKTLTSLSSVTAYGFDLVRGTQTLG
                                                                                                                                                                                    AVDLVNETKLDSEIKSWLAFAAQKVVEVDALAKALAGQKDEAYFAANAAAQASRKSSP
                                                                                                                                                                                                       RVTNEEVQKAAAALKGSDHRRGTNVSARLDAQQKKLNLPILPTTTIGSFPQTVELRRV
                                                                                                                                                                                                                                  RREYKAKKISEBEYVTAIKEEINKVVKLQEELDIDVLVHGEPERNDMVEYFGEQLSGF
                                                                                                                                                         LVTSAGFPAGKYLFAGVVDGRNIWADDLATSLSTLQSLEAVVGKDKLVVSTSCSLMHT
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1 (bases 1 to 34864)

Evans,G.A.; Bradbury,P., Brignac,S., Bumeister,R., Burbee,D., Bvans,G.A.; Davdbury,P., Brignac,S., Bumeister,R., Burbee,D., Franklin,T.L., Garner,H.R.; Gordon,M., Gotway,G., Grant,O., Hahner,L., Harris,J., Hinson,S., Megarity,C., Narayanaswamy,U., Newton,J., O'Brien,K., Ollver,T., Patel,P., Probst,S., Rayner,S., Ward,T. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-JUL-1997) Genome Science and Technology Center, University of Texas Southwestern Medical Center at Dallas, 5323 Harry Hines Blvd, Dallas, TX 75235-8591, USA On Jul 25, 1997 this sequence version replaced gi:1737204.
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Human Chromosome 11 Cosmid cSRL97a6, complete sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-NOV-1994) Masaru Takenaka, Osaka University, First Department of Medicine; 2-2 Yamadaoka, Suita, Osaka 565, Japan (E-mail:masaru@medone.med.osaka-u.ac.jp, Tel:06-879-3632,
                                                                                                                                                                                                                                    Fakenaka, M., Bagnasco, S.M., Preston, A.S., Uchida, S., Yamauchi, A.
                                                                                                                                                                                                                                              Kwon, H. M. and Handler, J. S.
The canine betaine gamma-amino-n-butyric acid transporter gene:
diverse mRNA isoforms are regulated by hypertonicity and are
expressed in a tissue-specific manner
Proc. Natl. Acad. Sci. U.S.A. 92 (4), 1072-1076 (1995)
95166770
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Wang, H. and Bohnert, H.
Direct Submission
Submitted (25-OCT-2001) Plant Sciences, University of Arizona,
                                                               Takenaka,M., Preston,A.S., Kwon,H.M. and Handler,J.S.
The tonicity-sensitive element that mediates increased
transcription of the betaine transporter gene in response
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Zea mays methionine synthase mRNA, partial cds.
AF439723
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                                                                                                                                                           Biol. Chem. 269 (47), 29379-29381 (1994)
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0; Mismatches 2;
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/product="methionine synthase"
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/db_xref="taxon:9615"
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/organism="Zea mays"
/db_xref="taxon:4577"
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/gene="BGT1"
/citation=[1]
/number=6
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Wang, H. and Bohnert, H.
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ilarity 90.5%;
Conservative
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PRI 25-JUL-1997

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Gaps

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Indels

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represent the correct sequence.

Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.

The nucleotide sequence of this BAC clone was generated by combining Monsanto and Genoscope sequencing data.
                                                                                                                                                                                                                                                       Submitted (09-JUL-2002) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG 29-APR-2002
                                      Embryophyta; Tracheophyta
                                                                                                                                                                                                                                                                                                               On Jul 11, 2002 this sequence version replaced gi:20372839. IMPORTANT: This sequence is unfinished and does not necessarly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3931 bp contig from 1 to 53931

7812 bp contig from 54032 to 71843

7238 bp contig from 71944 to 84181.

NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                            Demange, N., Wincker, P.
                                                       Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
1 53931: contig of 53931 bp in length
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Oryza sativa chromosome 12 clone Monsanto-0J1374_A04, ***
SEQUENCING IN PROGRESS ***, 5 ordered pieces.
AL731891
AL731891.1 GI:20372841
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN.
                                                                                                        Choisne, N., Orjeda, G., Cattolico, L., Demange, N., Wincke
Segurens, B., Pelletier, E., Scarpelli, C., Salanoubat, M.,
Weissenbach, J. and Quetier, F.
Orysa sativa chromosome 12 sequencing
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71844 71943: gap of 100 bp
71944 84181: contig of 12238 bp in length.
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Pred. No. 1.2e+02;
                                  Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa
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/sub_species="japonica
/db_xref="taxon:4530"
                                                                      Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 84181)
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                                                                                                                                                                                                                                                                                              : www.genoscope.cns.fr)
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90.5%;
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Matches 19; Conserv
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Pred. No. 1.2e+02;
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HTG; HTGS_PHASE2; HTGS_ACTIVEFIN
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Matches 19; Conservative
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Submitted (29-APR-2002) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
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Oryza sativa.

Oryza sativa

Oryza sativa

Eukaryotza, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Wagnollophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 99239)

Cloisne, N., Orjeda, G., Cattolico, L., Demange, N., Wincker, P.,

Segurens, B., Pelletier, E., Scarpelli, C., Salanoubat, M.,

Weissenbach, J. and Quetier, F.

Oryza sativa chromosome 12 sequencing
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represent the correct sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1584 bp contig from 1 to 11584
6246 bp contig from 11685 to 47930
9114 bp contig from 48031 to 8144
829 bp contig from 97245 to 97073
066 bp contig from 97174 to 99239.
NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ombining Monsanto and Genoscope sequencing data.
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84.8%; Score 17.8; DB 2; Length 99239;

Best Local Similarity 90.5%; Pred. No. 1.2e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0;
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'sub_species="japonica'
'db_xref="taxon:4530"
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97242 AGCTCCCTCTTGGGGCCCATG 97222

<u>, 6</u>

Search completed: July 8, 2003, 03:34:22 Job time: 236.102 secs

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Human immune/haema
Human foetal liver
Zea mays DNA fragm
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Human cDNA clone H
Human secreted pro
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Human PRO10 nucleo
Human PRO12 nucleo
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Copyright (c) 1993 - 2003
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Listing first 45 summaries
                                                nucleic search, using sw model
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Post-processing:

Database

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Total number

Searched:

1mmune/haema

immune/haema

heparin cofa

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:

gcgdata/geneseg/genesegn-embl/NA1997

/SIDS2/gcgdata/geneseg/genesegn-

/SIDS2/gcgdata/geneseq/genesegn-emb1/NA2000.DAT:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT

Rat membrane metal Rat membrane metal Soluble secreted e CDNA encoding neut Zea mays DNA fragm Human MDDT encodin Stomach cancer rel Human secreted pro Human polynucleoti Description SUMMARIES AAZ28810 AAD28130 AAA63763 AAC41442 ABQ72543 ABL64430 AAC74249 AAI58283 AAZ28812 B 2765 2286 2925 2925 2026 2235 2487 Length Query Match 100.0 100.0 92.4 92.4 84.8 80.0 80.0 19.4 119.4 117.8 116.8 116.8 Result õ 0 0 0 0 0 0 0 0

Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; ss; neuron; hormone; pepfide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; probe; hybridsation. Rat membrane metalloprotease NEPII gene probe #2.

(first entry)

01-FEB-2000

Synthetic.

Rattus rattus.

15-0CT-1999,

FR2777291-A1

08-APR-1998;

98FR-0004389 08-APR-1998; (INRM) INSERM INST NAT SANTE & RECH MEDICALE

Gros. C, Haret C, Bonhomme MC, Facchinetti P; Ouimet T, G Schwartz JC;

WPI; 1999-593429/51

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Sequences AA228811-228827 represent probes for detecting the rat membrane metalloprotease designated neprilysine II (NEPII) gene (AA228810). NEPII 1s involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and itssues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic
                                                                                                                                                                                                                                                                                           signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin, disturbances of the hypothalamic hypophyseal axis or endocrine
                       involved in proteolysis of
to screen for inhibitors,
                                                                  cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 3 A; 7 C; 6 G; 5 T; 0 other;
                   New membrane metalloprotease NEP II, neuronal and hormonal peptides, used potentially useful for treating e.g.
                                                                                                             Claim 3; Page 20; 29pp; French
                                                                                                                                                                                                                                                                                                                                                                     disorders.
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Score 21; DB 20; Le Pred. No. 1.1; 1 AGTICCCACTIGGGGCCCAIG 21 ; 0 100.0%; 100.0%; Local Similarity 100. les 21; Conservative Query Match Matches

1 AGTICCCACTIGGGGCCCATG 21

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Gaps

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Indels

Length 21;

AA228810 standard; cDNA; 2765 BP AAZ28810; AAZ28810/c RESULT 2

01:FEB-2000 (first entry)

Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds. Rat membrane metalloprotease NEPII gene.

Rattus rattus

FR2777291-A1. 15-0CT-1999 98FR-0004389 08-APR-1998; 98FR-0004389 08-APR-1998;

Bonhomme MC, Facchinetti P; Haret C, Gros C, Schwartz JC; Ľ Ouimet

(INRM) INSERM INST NAT SANTE & RECH MEDICALE

WPI; 1999-593429/51.

P-PSDB; AAY44177

involved in proteolysis of to screen for inhibitors, cardiovascular disease -New membrane metalloprotease NEP II, neuronal and hormonal peptides, used potentially useful for treating e.g.

Claim 2; Page 12-16; 29pp; French

This sequence represents the gene for the rat membrane metalloprotease designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of

as premature ejaculation, anorgasmia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is SEP consensus DNA sequence found in human, mouse and rat.

(e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such

also

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An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as
disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human. SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD)
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        enzyme; gynaecological; antisense-therapy; male erectile dysfunction;
MED; female sexual dysfunction; FSD; female sexual arousal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                       FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds
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                                                                                                      20; Length 2765;
                                                                                                                                  0; Indels
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                                                                        Sequence 2765 BP; 684 A; 735 C; 787 G; 559 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                           Soluble secreted endopeptidase (SEP) consensus DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "Encodes catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                           endopeptidase; SEP; endocrine;
                                                                                                    Score 21; DB 20
Pred. No. 1.4;
; Mismatches
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1664..2286
                                                                                                                                                                             741 AGTICCCACTIGGGGCCCAIG 721
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                                                                                                    100.0%;
100.0%;
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Best Local Similarity 100...
Best 21; Conservative
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                                           endocrine disorders.
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Gaps

Query Match

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Matches

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AAA63763;

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
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                 Length 2925;
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               21;
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                 DB
                                        8.3;
                                                               Mismatches
                 Score 19.4;
Pred. No. 8
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                                                                                                                                          936 AGTTCCCACTTGAGGCCCATG 916
92.4%; Scu.
95.2%; Pred
                                                                                                                1 AGTICCCACTIGGGGCCCATG 21
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                                                               Conservative
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                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;
NEP-like enzyme; protein production; protein secretion;
neurological disease; Alzheimer's disease; pain; psychiatric disorder;
fertility; bone disease; abnormal phosphate metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "neutral endopeptidase metallopeptidase-like enzyme NL-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-1.
                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
                                                                                      ); Score 19.4; DB 24; Length 2286; Pred. No. 8.2; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a murine neutral endopeptidase
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                                           Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
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332..2629
/*tag= a
/product= "neutral er
                                                                                                                                                                                                                 617 AGTTCCCACTTGAGGCCCATG 597
                                                                                                                                                                                          1 AGTICCCACTIGGGGCCCAIG 21
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ID AAA63763 standard; cDNA; 2925
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                                                                                      92.4%;
llarity 95.2%;
Conservative
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P-PSDB; AAB08130.
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tes 20; Conserv
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Length 520;
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Conservative 0; Mismatche
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                                                                                                                                                                                                                                                                                          9US-0142
                                                                                                                                                                                                                                                                                                                                       9US-0143
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Gaps

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proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis; rheumatold arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          having at least 90% identity to (I) or a biologically active or immunogenic fragment of (I) (I) is useful for screening a compound for specificativeness as n agonist or antagonist, for screening a compound that specifically binds (I) or modulates the activity of (I), and for preparing a polyclonal or monoclonal antibody by hybridoma technology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human disease detection and treatment polypeptide, useful in
diagnosis, prevention or treatment of cell proliferative disorders e.g.
arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 254 sequences (ABP51231-ABP51484) given in the specification, a naturally occurring polypeptide comprising a sequence
                                                                                                                                                                                                                                                                               Human; MDDT; disease detection and treatment molecule polynucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective; antirheumatic; antiarthritic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lincoln SE, Altus CM, Dufour GE, Ch
Yu JY, Wright RJ, Gletzen D, Liu TF,
G. Bradley DL, Rohatgi SD, Harris B,
Peralta CH, David Mi, Panzer SR, F
Chen AJ, Chang SC, Au AP, Inman RR;
                                                                                                                                                                                                                           Human MDDT encoding cDNA SEQ ID NO 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 361-362; 618pp; English.
                                                          BP.
                                                 AB072543 standard; cDNA; 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36-SEP-2001; 2001WO-US27628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC
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2000US-231167P
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                                                                                                                                                                   (first entry)
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Gerstin EH, Peralta
Marwaha R, Chen AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-527544/56.
P-PSDB; ABP51325.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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07-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. AIDS
                                                                                                            ABQ72543;
RESULT 6
ABQ72543/
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Nucleic acids (II) (ABD72449-ABD72700) encoding (I) are useful for screening a compound for effectiveness in altering expression of a target polynucleotide comprising. Oligonucleotides and antibodies are useful for detecting MDDT in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the expression of MDDT in a biological sample, for detecting (I) in a sample, and for purifying (I) from a sample, A composition comprising (I), an agnosist or antagonist is useful for treating a disease or condition associated with decreased or increased expression of functional MDDT. (I) or (II) are useful for diagnosing, treating or preventing disorders associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis, psoriasis, and cancer and an autonomenue/fine mantary disorder such as Alexanda Companion.
                                                                                                                                                                                                                                                                                                                                                                                                     germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuals and as hybridisation probes for mapping naturally occurring genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                   allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis crheumatoid arthritis. (II) are useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.8; DB 24; Length 2026;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2026 BP; 296 A; 631 C; 742 G; 357 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stomach cancer related gene sequence SEQ ID NO:2767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    789 AGTGCCCACTTGGAGCCCAT 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGTICCCACTIGGGGCCCAI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL64430 standard; DNA; 2235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%;
90.0%;
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20000S-234052P.
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2000US-233617P
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20000S-234923P
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2000US-235077P
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es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200194629-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-SEP-2000;
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22-SEP-2000;
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2000US-235637P

Human, secreted protein, immunosuppressive, antiarthritic, antirheumatic, antiproliferative, cytostatic, cardiant, vasotropic, cerebroprotective, nootropic, neuroprotective, antibacterial, virucide, fungicide, neoplasm;

Human secreted protein gene 27 SEQ ID NO:37.

(first entry)

02-FEB-2001

AAC74249;

opthalmalogical; autoimmune disease; rheumatoid arthritis; angiogenesis; hyperproliferative disorder; cardiovascular disorder; infection; cerebrovascular disorder; nervous system disorder; ocular disorder; wound healing; chemotaxis; ss.

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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%; Score 16.8; DB 24; Length 2235; 90.0%; Pred. No. 1.4e+02; 1ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2235 BP; 524 A; 632 C; 693 G; 386 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 2767; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-188264/24.
                                                                      8-SEP-2000;
                                                 -SEP-2000
                                                                                                                     8-SEP-2000
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Soppet DR,
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                       7-SEP-2
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7-SEP-
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Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition

Komatsoulis G;

Rosen GA, Ruben SM, NPI; 2000-579483/54. P-PSDB; AAB39205

(HUMA-) HUMAN GENOME SCI INC

99US-0125362. 99US-0169980.

19-MAR-1999; 10-DEC-1999;

16-MAR-2000; 2000WO-US06792

WO200056754-A1. Homo sapiens.

28-SEP-2000.

Claim 1; Page 354-355; 434pp; English.

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The polynucleotide sequences given in AAC74223-C74279 encode the human secreted proteins represented in AAB39179-B39226. Sequences
AAB3927-B39308 are alternative proteins encoded by the genes, and also protein sequences with which they share homology. The proteins have activities based on the tissues and cells in which they are expressed. Examples of activities include: immunosuppressive; antiarthritic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The human secreted proteins, oplynucleotides, antagonists and agonists of the invention may be useful in the treatment, prevention, and/or diagnosis of various disease, disorders and conditions such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. fungi and ocular disorders e.g. corneal infections caused by bacteria, viruses and conditions and conditions caused by bacteria, viruses and thought and docular disorders e.g. corneal infection; the polypeppides condition and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and conditions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to regenerate tissues, maintain organs before transplantation, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemotaxis and as a food additive or preservative e.g. to increase storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used during the isolation and characterisation of the genes of the invention
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Pred. No. 1.4e+02;
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Best Local Similarity 90.0%;
Matches 18; Conservative
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Gaps

1390 GTTCCCCTTGGGGCCTATG 1371

2 GTTCCCACTTGGGGCCCATG 21

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18; Conservative

Local Similarity

Best Loca Matches

AAC74249 standard; cDNA; 2304 BP

RESULT 8
AAC74249/c
ID AAC7424

RESULT 9 AAI58283/c

leukaemia; ss domo sapiens

22-OCT-2001

Human;

AAI58283;

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hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging;
                                                                                                                                                                                                                                                                                                  Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    food additive; food preservative; gene therapy; gene; ss
                                                                                                                                                                                                                                            DNA encoding novel central nervous system protein #156.
                                                                            ABK43576 standard; cDNA; 2745 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001; 2001WO-US01332
                                                                                                                                                                                         05-JUN-2002 (first entry)
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.8-APR-2000;
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                            RESULT 10
                                                           ABK43576,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and sytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                        gene therapy; cancer;
                                                                                                                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzbaner's; Parkinson's disease; haemostatic; amyotrophic; lateral sclercsis; Shy-Drager Syndrome; chemotactic; chemoticit; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.8; DB 22; Length 2487;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels 0;
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Yang Y,
                                                                                                                                                                                                                           cytostatic;
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Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 486; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asundi V, Chen R,
                                                                                                                                                                                                                           nootropic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu C,
                                                                                                                                                                  Human polynucleotide SEQ ID NO 486.
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     BP
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AAI58283 standard; cDNA; 2487
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90.0%;
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2000US-0693036
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                                                                                                            (first entry)
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P-PSDB; AAM39127.
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Wang Z, W
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29-NOV-2000;

Tang YT, Wang J, V Zhao QA,

-AUG-2000; 9-OCT-2000;

21-JAN-2000;

25-APR-2000 39-JUL-2000

26-JUL-2001.

1624 GITCCCCTTGGGGCCTATG 1605

Query Match

Matches

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novel central nervous system protein. (1) and polypeptides (111) encoded by (1), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autolimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver cardiovascular disorders c.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders c.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses c.g. corneal infection, gastrointestinal disorders e.g. dysphagia, cadenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. clustemia, disorders involving neovascularisation e.g. malignancies, contex kidney failure and blood related disorders e.g. myocardial contextion. The polypeptides can also be used to aid wound healing and ceptihelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes an isolated nucleic acid molecule (I) encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       increase or decrease storage capabilities, fat content, lipid, protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maintain organs before transplantation, for supporting cell cultu
primary tissues, to regenerate tissues and in chemotaxis. The
polypeptides can also be used as a food additive or preservative
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Pred. No. 1.4e+02;
0; Mismatches 2;
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AA160069/c
ID AA160069 standard; cDNA; 3443 BP.
XX
AC AA160069;
                                                                                                                                                                                                                                                                                                                                                              Ruben SM
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Best Local Similarity 90.0%;
Matches 18; Conservative
                                              000US-0249299
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0000S-0249264
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P-PSDB; AAU87246.
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05-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
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01-DEC-2000;
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08-SEP-2000;
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Gaps

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22-OCT-2001

W0200153312-A1

26-JUL-2001

21-JAN-2000; -APR-2000; 9-JUL-2000;

Homo sapiens

Leukaemia; ss

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The specification describes a method for selecting or screening agents that modulate ABCA transporters. The method comprises using non-human recombinant mammals with an inactivated allele of the gene encoding the ABCA transporter, or cells with an inactivated allele of ABCA transporter, from any tissue of the recombinant mammal, preferably with an allele truncated in one or both exons corresponding to the first and/or second ATP-binding cassettes. (NBDI or 2). Compounds that stimulate ABCA transporters may be useful for increasing (normalizing) serum levels of high-density lipoprofein cholesterol. The present sequence represents the cDNA sequence of a murine ABCAX transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selecting agents that modulate ABCA transporters, useful e.g. for
normalizing serum cholesterol levels, comprises using transgenic
animals with an inactive ABCA gene allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5762 BP; 1135 A; 1690 C; 1692 G; 1245 T; 0 other;
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ABCAX transporter; ABCA7 transporter; ss.
                                                                                                                                   Nucleotide sequence of a murine ABCAX transporter
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                                                                                 (first entry)
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                                                                                                                                                                                                                     ABCAX transporter; ss.:
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                                                                                 15-MAY-2001
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                            AAF54792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and thrombolytic activity, cancer diagnosis and therapy, drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang D;
                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                      amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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Pred. No. 1.4e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 4058; 10078pp; English
                                                     Human polynucleotide SEQ ID NO 4058.
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AAFS4792/c
ID AAFS4792 standard; cDNA; 5762 BP.
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illarity 90.0%;
Conservative (
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Wang 2, W
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nes 18; Conserv
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P-PSDB; AAM40913

Wang J, W

lang YT,

:9-NOV-2000; -SEP-2000;

-AUG-2000; -OCT-2000; disorders

specification

Query Match

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08-FEB-2001

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Sequence 23024 BP; 5195 A; 6205 C; 6348 G; 5266 T; 10 other;
                Claim 12; Page 80-84; 113pp; French.
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nes 18; Conserv
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AAF25499/c
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                                                                                                                                                                 normalizing serum cholesterol levels, comprises using transgenic animals with an inactive ABCA gene allele
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6607;
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Pred. No. 1.5e+02;
); Mismatches 2;
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                                                                   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(CNRS ) CNRS CENT NAT RECH SCI.
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AAF54793 standard; DNA; 14044 BP.
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90.0%;
             28-JAN-2000; 2000WO-FR00209
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                                                                                                                                       WPI; 2001-182953/18.
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The specification describes a method for selecting or screening agents that modulate ABCA transporters. The method comprises using non-human recombinant mammals with an inactivated allele of the gene encoding the ABCA transporter, or cells with an inactivated allele of ABCA transporter, from any tissue of the recombinant mammal, preferably with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 16.8; DB 22;
90.0%; Pred. No. 1.5e+02;
No. Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. (CNRS ) CNRS CENT NAT RECH SCI:
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0; Gaps Query Match 80.0%; Score 16.8; DB 22; Length 23024; Best Local Similarity 90.0%; Pred. No. 1.6e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0;

Search completed: July 8, 2003, 02:18:50 Job time: 133.941 secs

Appli Appli

nucleic

Run on:

Sequence:

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FOR THE TREATMENT AND BODY WEIGHT DISORDERS, INCLUDING OBESITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                           US-08-959-382-1
US-08-765-662-13
PCT-US95-08745-13
US-09-042-785A-3
                                                                                                                                                                                                                                                                                                                                                   PCT-US94-14030A-14
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US-08-333-576C-14
                                                              US-08-392-367B-1
US-08-893-467A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/631,200
FILING DATE: 12-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: DIAGNOSIS OF INUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ANDRECEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08631200 Patent No. 5646040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TICCCACTIGGGGCCCAIG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kleyn, Patrick W. APPLICANY: Moore, Karen J. TITLE OF INVENTION: COMPOSIT. TITLE OF INVENTION: DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 437 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
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                                                                                                                                                                                                                                                         6405
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Matches 17; Conserv
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222.151 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-829-553-5
US-08-922-267A-3
US-08-922-267A-4
US-08-922-267A-4
US-08-936-707A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -08-936-706A-4
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                  using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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21
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Match Length
                                                                                                                     nucleic search,
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Perfect score:
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Minimum DB Maximum DB

Database

Result

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Searched:

Gaps

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APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/829,553 FILING DATE: 28-MAR-1997 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.8;
Pred. No. 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                         FILING DATE: 12-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/631,200
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION UNDBER: 7853-
REFERENCE/DOCKET NUMBER: 7853-
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence .3, Application US/08829553
Patent No: 5817762
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 TTCCCTCTTGTGGCCCATG 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 H: 437 base pairs
nucleic acid
DEDNESS: single
OGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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US-08-631-200-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                             GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: MOOSE, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
KUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/O8631200
Patent No. 5646040
GENERAL INFORMATION:
APPLICANT: ALEYN, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
RPDICATION NUMBER: US/08/631,200
FLLING DATE: 12-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.8;
Pred. No. 5
                                                                                                                                                                                                                                                           SEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: COTIZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERRENCE/DOCKET NUMBER: 7853-057
RELECOMMUNICATION INFORMATION:
                                                            Sequence 4, Application US/08631200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 790-9990
TELEX: (212) 869-9741/8864
TELEX: 66141 PENNER
TRECRMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 TTCCCTCTTGTGGCCCATG 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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nucleic acid
DEDNESS: unknown
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                       STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 10036-2711
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                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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STREET: STATE:

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RESULT 5

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COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                           COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.8;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                             SEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/631,200
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          IUMBER: US/08/829,553
28-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7853-057
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08922267A Patent No. 5861239 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 TICCCICTTGIGGCCCATG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J
TITLE OF INVENTION: COMPOSITIOI
TITLE OF INVENTION: DIAGNOSIS (NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TICCCACTIGGGGCCCAIG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A. 742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                              APPLICANT: Kleyn, Patrick W. APPLICANT: Moore, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 75.2
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
                                                                                      TITLE OF INVENTION: CO
TITLE OF INVENTION: DI
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
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: U.S.A.
                                                                                                                                                                                                                                  New York
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10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-829-553-5
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                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
KUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
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                                                                                                                                    DB 1; Length 437;
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                                                                                                                                  ; Score 15.8; Di
; Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,553
FILING DATE: 28 MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/631,200
FILING DATE: 12-APR:1996
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-08-829-553-5
; Sequence 5, Application US/08829553
                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08829553 Patent No. 5817762 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TTCCCACTTGGGGCCCATG 21
                                                                                                                                                                                                                                             343 TTCCCTCTTGTGGCCCATG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                      3 TTCCCACTTGGGGCCCATG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

US-08-829-553-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                  Query Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10036-271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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Gaps

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Length 437;

Gaps

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US-08-922-267A-5

Sequence 5, Application US/08922267A

Patent No. 5861239

GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 82
                                                                                                                                                                                                                                                                                                                                                                                             Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/922,267A
FILING DATE: 2-SEP-1997
CLASSIFICATION: 530
APPLICATION NUMBER: US 08/829,553
FILING DATE: 28-MAR-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Pennie & Edmonds LLP
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/631,200
FILING DATE: 12-APR-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COUZZI, LAURA
                                          NAME: COUUZZI, LEULRA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-C
TELECOMUNIOATION 100-0909
TELEPAR: (212) 790-999
TELERA: (614) PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 TTCCCTCTTGTGGCCCATG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TTCCCACTTGGGGCCCATG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212) 790-9090
(212) 869-9741/8864
                             ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 437 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-922-267A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kleyn, Patrick W.
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, CORRESPONDENCE ADDRESS:
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                          CLASSIFICATION: 2.52F-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/829,553
FILING DATE: 28-MAR-1997
CLASSIFICATION DATA:
PRICK APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/631,200
FILING DATE: 12-APR-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 38,742
RELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741/8864
TELEX: 66.441 previte
                                        APPLICATION NUMBER: US/08/922,267A
FILING DATE: 2-SEP-1997
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/922,267P
FILING DATE: 2-SEP-1997
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FILING DATE: 28-MAR-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION'NDMBER: US 08/631,200
FILING DATE: 12-APR-1996
CLASSIFICATION: 530
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Patent No. 5861239
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.2%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 437 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Conservative
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Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
TELEX: 6
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DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

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NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,747
                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-936-707A-4
                                                                                                        COUNTRY:
                                                                                                                                                                                                       SOFTWARE
                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                    COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 437;
                                                          Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08936707A
Patent No. 5871931
GENERAL INFORMATION:
APPLICANT: K1940, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/ABANA
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.8;
Pred. No. 50;
                                                                                             0; Mismatches
                                                             Score 15.8;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.5EP-1997
                                                                                                                                                                                                                                                                                                                                                                                        E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                       Sequence 3, Application US/08936707A Patent No. 5871931
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                                                                                                                                                            343 TICCCICITGIGGCCCAIG 361
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                                                                                                                              3 TTCCCACTTGGGGCCCATG 21
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NAME: COFUZZI, LEURA A.
REGISTRATION NUMBER: 30,742
REFERBNCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                       APPLICANT: Kleyn, Patrick W. APPLICANT: Moore, Karen J. TITLE OF INVENTION: COMPOSITITLE OF INVENTION: DIAGNOSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.2%;
ilarity 89.5%;
Conservative (
                                                           75.2%;
nilarity 89.5%;
Conservative 0
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nucleic acid
EDNESS: single
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
; TOPOLOGY: linear; MOLECULE TYPE: DNAUS-08-922-267A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 17; Conserv
                                                                Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                             Patent No. 5871931
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
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                                                                                                                                                                                                                                                                                                                                                                                                                        New York
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US-08-936-707A-3
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US-08-936-707A-4
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COMPOSITIONS FOR THE TREATMENT AND .
DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
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                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/936,707A FILING DATE: 24-SEP-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/936,707A FILING DATE: 24-SEP-1997 CLASSIFICATION: 514
                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08936707A Patent No. 5871931
                                     & Edmonds LLP
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                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kleyn, Patrick W. APPLICANT: MOORE, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 437 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New YORK
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE: CHARACTERISTICS:
NUMBER OF SEQUENCES: 6
                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Moore, K
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                   10036-271
                                                     1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                           MEDIUM TYPE:
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REFERENCE/DOCKET NUMBER: 78.

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COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
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1: COMPOSITIONS FOR THE TREATMENT AND
1: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,706A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.2%; Score 15.8; 189.5%; Pred. No. 50; tive 0; Mismatches
                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                     Sequence 4, Application US/08936706A
Patent No. 5876919
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         STAIL.
COUNTRY: U.S.A.
21P: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPATIBLE FORM:
PEDIUM TYPE: PLOPPY disk
PEDIUM TYPE: PLOPPY disk
PEDIUM TYPE: PLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08936706A Patent No. 5876919
GENERAL INFORMATION:
APPLICANT: Moore, Karen J.
                                                                                                                             APPLICANT: Kleyn, Patrick W.
APPLICANT: MOOTE, Karen J.
TITLE OF INVENTION: COMPOSITIT
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: COTUZZI, LAUTA N. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 785
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TTCCCACTTGGGGCCCATG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 437 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 89.5
Matches 17; Conservative
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TITLE OF INVENTION:
DI
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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US-08-936-706A-4
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                                RESULT 14
US-08-936-706A-4
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STREET: 11
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US-08-936-706A-5
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Patent No. 5876919
GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                      DB 2; Length 437;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/936,706A
FILING APPLICATION: 530
COMPUTER: SASSETCATION: 530
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Pred. No. 50;
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Pred. No. 5
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TELEPHONE: (212) 790-9090
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 Dasse pairs:
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                    3 TTCCCACTTGGGGCCCATG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 TTCCTCTTGTGGCCCATG 361
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TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 89.5%;
Matches 17; Conservative
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89.5%;
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 89.55
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-936-707A-5
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U.S.A.
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US-08-936-706A-3
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Gaps

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Query Match 75.2%; Score 15.8; DB 2; Length 437; Best Local Similarity 89.5%; Pred. No. 50; Matches 17; Conservative 0; Mismatches 2; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,706A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INVORMATION:
NAME: COLUZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-099
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090-
TELEFAX: (512) 869-9741/8864
FELEY A: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
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Gaps

Search completed: July 8, 2003, 09:31:00 Job time: 30.0402 secs

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Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 190, App Sequence 3270, App Sequence 3270, App Sequence 118, App Sequence 243, App Sequence 118, App Sequence 118, App Sequence 118, Appl Sequence 118, Appli Sequence 1, Appli Sequence 1646, A Sequence 1666, A Sequence 1666, A Sequence 376, Appl Sequence 376, Appli Sequence 376, Appli Sequence 376, Appli Sequence 376, Appli Sequence 376, Appli Sequence 376, Appli Sequence 376, Appli Sequence 376, Appli Sequence 376, Appli Sequence 376, Appli Sequence 98, Appli

Sequence 137, App Sequence 1380, App Sequence 28561, A Sequence 104, App Sequence 2463, Ap Sequence 27083, A Sequence 466, App Sequence 466, App

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HE SEEDS OF PLANTS
                                                    10 US-09-814-986-3

10 US-09-814-986-4

10 US-09-814-986-4

10 US-09-879-536-190

9 US-10-270-333-67

10 US-09-864-761-3270

10 US-09-871-161-118

10 US-09-871-161-118

10 US-09-871-161-118

10 US-10-156-761-6794

10 US-09-864-761-18646

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US-09-803-719-908

US-09-876-889-137

US-09-764-891-1580

US-09-918-995-28861
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US-09-974-300-4450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Famodu, Layo
APPLICANT: Rafalski, Jan A.
APPLICANT: Ramaker, Michael
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Thorpe, Catherine
TITLE OF INVENTION: PLANT METHIONINE SYNTHASE GEN
FILE REFERENCE: BB-1067-B
CURRENT APPLICATION WETHIONINE CONTENT OF THE SE
CURRENT APPLICATION WUMBER: COURSENT OF THE SE
CURRENT APPLICATION WUMBER: 2002-05-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09989339
Publication No. US20030088886A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Falco, Saverio Carl
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OTHER INFORMATION: n = A, C,
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ORGANISM: Triticum aestivum
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LOCATION: (344)
OTHER INFORMATION: n
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LOCATION: (367)
OTHER INFORMATION:
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LOCATION: (433)
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Sequence 1, Appli
Sequence 31713, A
Sequence 39, Appl
Sequence 160, App
Sequence 52, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 15243, A
Sequence 15243, A
Sequence 29, Appl
Sequence 29, Appl
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273.390 Million cell updates/sec.
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Sequence 17, Appl
Sequence 19, Appl
Sequence 23, Appl
Sequence 2362, Appl
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                                                                                           July 8, 2003, 19:09:54; Search time 121.288 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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0 US-09-995-542-1.
US-09-918-574-15243
US-09-918-995-30483
US-09-954-556-29
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US-10-198-846-10268
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US-10-037-270-160
US-10-084-817-52
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                                                    OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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AND METHODS FOR INCREASING THE

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Parent No.

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Soppet, Daniel

APPLICANT: Soppet, Daniel

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign

TITLE OF INVENTION: Sets

FILE REFERENCE: 689290-75

CURRENT APPLICATION NUMBER: US/09/962,436

CURRENT APPLICATION DATE: 2001-09-25

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FITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
FITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
FITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
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   Length 493
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DB 9;
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      Score 17.4; DE pred. No. 23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
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RIOR FILING DATE: NIMBER: US 60/298,155
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Patent No. US20020081301A1
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ublication No. US20030087270A1
ENERAL INFORMATION:
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                                                                                                                                  2 GTTCCCACTTGGGGCCCATG 21
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90.0%;
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1 Similarity 90.0%;
18; Conservative
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US-09-962-436-308
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Matches 18; Conserv
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LENGTH: 2235
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APPLICANT: Rafalski, Jan A.
APPLICANT: Ramaker, Michael
APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Thorpe, Catherine
TITLE OF INVENTION: PLANT METHIONINE SYNTHASE GENE AND METHODS FOR INCREASING THE
TITLE OF INVENTION: METHIONINE CONTENT OF THE SEEDS OF PLANTS
FILE REPERENCE: BB-1067-B
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SEQ ID NO 31713
                                                                                                                                                                 Length 475;
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                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                       Score 17.8;
Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31713, Application US/09918995 publication No. US20030073623A1 GENERAL INFORMATION:
                                           ; LOCATION: (473)...(474); OTHER INFORMATION: n = A, C, G, or T US-09-989-339-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: 08/703,829
PRIOR FILING DATE: 1996-08-27
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US-09-918-995-31713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09989339 Publication No. US20030088886A1 GENERAL INFORMATION:
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Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                       Query Match
Best Local Similarity 90.5%;
Matches 19; Conservative
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SOFTWARE: Microsoft Office 97
SEQ ID NO 1
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US-09-989-339-1
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DB 10)

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TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION: FILE REFERENCE: PA-0028 US CURRENT APPLICATION NUMBER: US/10/044,090

CURRENT FILING DATE: 2002-01-09

NUMBER OF SEQ ID NOS: 850

SEQ ID NO 448

LENGTH: 3690
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TITLE OF INVENTION: APP-Binding Cassette Transporter-Like Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-658-A
CURRENT APPLICATION NUMBER: US/09/995,542
                                                                                                                                                                                                                                                            DB 9; Length 3690;
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                                                                                                                                                                             NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID No. US20030119009A1 2314132CB1
                                                                                                                                                                                                                                                                                              Indels
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OTHER INFORMATION: Incyte ID No. US20020137081A1 2314132CB1
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                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 90:0%; Fred. No. 39;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                  0; Mismatches
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90.0%; Pred. No. 39;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                    1597 GITCCCCTIGGGCCTAIG 1578
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 448, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
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Sequence 1, Application US/09995542
Patent No. US20020127647A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/253,520
PRIOR FILING DATE: 2000-11-28
                                                                   PRIOR FILING DATE: 2001.
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PERL Program
SEQ ID NO 52
LENGTH: 3690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                      TYPE: DNA ORGANISM: HOMO Sapiens FEATURE:
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SOFTWARE: Patentin Ver: 2.0
LENGTH: 6633
                                  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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ORGANISM: Mus musculus
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                           Length 2235;
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                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               INVENTION: No. US20030104529Alel Nucleic Acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
                  Score 16.8;
Pred. No. 40;
                                           0; Mismatches
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Pred. No. 40;
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                                                                              1390 GTTCCCCCTTGGGGCCTATG 1371
                                                                                                                                                                Sequence 160, Application US/10037270
Publication No. US20030104529a1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/084,817
                                                            2 GTTCCCACTTGGGGCCCATG 21
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ATION NUMBER: 09/552,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/488,725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: Pt_FL_Genes Version 1.0
Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
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Publication No. US/20030119009A1
GENERAL INFORMATION:
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Ilarity 90.0%;
Conservative
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Liu, Chenghua
Asundi, Vinod
Zhang, Jie
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hen, Rui-hong
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Sharon E. Plon
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; LOCATION: (235) ·· (2469)
US-10-037-270-160
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Best Local Similarity
Matches 18; Conserv
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TLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                APPLICANT: Susan M. Freier
APPLICANT: Scott Cooper
APPLICANT: Scott Cooper
APPLICANT: SCOTT SCOTT RECEPTOR 2 EX
APPLICANT: SCOTT SCOTT RECEPTOR 2 EX
PILE REFERENCE: RIS-0250
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                                    0; Gaps
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 Length 500
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Score 16.4; DB 9;
Pred. No. 71;
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Pred. No. 52;
0; Mismatches
                                         0; Mismatches
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RRENT FILING DATE: 2001-05-23
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ING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/954,556 CURRENT FILING DATE: 2001-09-14 NUMBER OF SEQ ID NOS: 108 SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATION NUMBER: US 60/236,359
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US20020048763A1
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                                                                                                103 AGTTCCCACCTGGGGCCC 86
                                                                              18
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nilarity 94.4%;
Conservative (
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       ch 78.18;
1 Similarity 94.48;
17; Conservative
                                                                                1 AGTICCCACITGGGGCCC
                                                                                                                                                                                                                                                           APPLICANT: Brett P. Monia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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Matches 17; Conserva
            Query Match
Best Local Similarity
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                                                        Matches
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
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                                                                                                                                                       Length 6633;
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                       Indels
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                                                                                                                                                                                             0; Mismatches
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NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 20411-756.
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
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                                                                                                                                                        Score 16.8;
Pred. No. 37
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Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                       Course 15243, Application US/09878574 Patent No. US20020110548A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                2755 GITCCCGCTCGGGGCCCAIG 2736
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ilarity 94.4%;
Conservative
                                                                                                                                                                80.08;
90.08;
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Matches 18; Conservative
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US-09-918-995-30483
                                               NAME/KEY: sig_peptide
; LOCATION: (1)..(138)
; NAME/KEY: CDS
; LOCATION: (1)..(6504)
US-09-995-542-1
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Matches 17; Conserv
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US-09-878-574-15243
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LENGTH: 271
                                                                                                                                                                   Query Match
                                        FEATURE:
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PCT/US01/00665

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TITLE OF INTERVION: 29 Human Cancer Associated Proteins FILE REFERENCE: PA004P1
CURRENT APPLICATION NUMBER: US/10/023,896
CURRENT APPLICATION NUMBER: US/10/023,896
PRIOR APPLICATION NUMBER: US/00/023/94
PRIOR FILING DATE: 2001-12-21
PRIOR FILING DATE: 2000-08-30
PRIOR FILING DATE: 2000-08-30
PRIOR FILING DATE: 1999-09-03
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Pred. No. 83;
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227 AGTACCCATTGGGGCCTATG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/158,003
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                                                                                                                   5-10-023-896-19
Sequence 19, Application US/10023896
Publication No. US20030027776A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 85.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 19
LENGTH: 1298
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OTHER INFORMATION: MAP TO AC010872.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
US-09-864-761-14177
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR PELING DATE: 2001-07-18
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85.7%; Pred. No. 89;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10268
LENGTH: 485
                                              PCT/US01/00668
                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/00662 PRIOR FILING DATE: 2001-01-30
                                                                                             PCT/US01/00663
                                                                                                                                                                                                                                       ICATION NUMBER: PCT/US01/00670
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NAME/KEY: misc_feature

COCATION: 480, 481, 482, 483, 484, 485

COTHER INFORMATION: n = A,T,C or G

US-10-198-846-10268
                                                                                                                                                                                        LICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                    PPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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Publication No. US20030099974A1
GENERAL INFORMATION:
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                                                                                                                      ILING DATE: 2001-01-30
                                                                                                                                                                                                                                                             ILING DATE: 2001-01-30
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Best Local Similarity 85.78
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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Indels

0; Mismatches

1 AGTICCCACTIGGGGCCCAIG 21

Length 1298; Indels

DB 9;

BJ235482

OM nucleic

Run on:

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BG050044 FM1_65_G0
D41509 RICS4047A R
BG465041 EM1_35_D1
D40937 RICS3131A R
AV167513 AV167513
                                                                                                 D47961 RICS13778A
BF481816 FM1_20_F1
BE638127 WHE0995-0
C73949 C73949 Rice
ALS07110 ALS07110
                                                                                                                                                                                                                   BF481363 FM_18_B0
BF483281 WHEL791_A
C148 C27148 EXTER
BG050316 FM_53_E0
B1098822 IP1_33_E0
B1098823 IP1_33_E0
B1098823 IP1_33_E0
B1098823 IP1_33_E0
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BJ185439 BJ185439
BG050135 FM1_67_B0
BJ183732 BJ183732
AU096450 AU096450
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4044-75 Mouse E14.5 retina lambda ZAP II Library Mus musculus CDNA,
                                                                                                                                                                  BJ469066 BJ469066
BG050832 FM1_71_D0
BE500035 WHE0977_D
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AZ902604 RPCI-24-1
AJ433505 AJ433505
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AV940980 AV940980
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
Gene expression in the developing mouse retina by EST sequencing
                                                                                                                                                                                                                                                                                                                                                                                 BE414865 MWL001.C
BF481918 FM1_19_P
D40154 RICS1929A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Blochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA Tel: 713 792 3646
Fax: 713 790 0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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D40154
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BG050832
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BF483281
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BF656002 FM1_42_F1
BJ190226 BJ190926
R7454 ye96f09.s1
BF474621 WHE2L08_B
BJ280551 BJ280551
                                                                                                       (without alignments)
319.453 Million cell updates/sec
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                                                                                          8, 2003, 00:47:28 ; Search time 1064.65 Seconds
                                                                                                                                                                                                                                                               32308132
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                                                                                                                     16154066 seqs, 8097743376 residues
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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IP1_33_F0 BJ163201 946076A11

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                         /dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: pAMP10 (day 14.5 post-fertilization"
/note="Vector: pAMP10 (day 14.5 post-fertilization")
/note="Vector: pAMP10 (day 14.5 post-fertilization")
/note="Vector: pAMP10 (day 14.5 post-fertilization")
// Manniatis); Cloning rechindre: COR Cloning (CloneAmp, Life Technologies); Average insert size: 18 Rb;
// Insertion site: TACGTCCACTGAATTCTGAGTG--->. Other
/note: Arganation regarding entire library may be found at http://pga.swmed.edu/Data/Libraries/microarray_cdna_libraries.htm.
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PBLOSTIP II from Lambda Zap II; Site_1: XhoI; Site_2:
BCORI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorghum propinguum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
retina lambda 2AP II Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to be sequenced were prepared by
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         late April/early May, meristems were harvested The library was made from poly-A RNA in the cloning vect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF656002 204 bp mRNA linear EST 20. FM1_42_F12.bl_A003 Floral-Induced Meristem 1 (FM1) Sorghum propinguum cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                       92.4%; Score 19.4; DB 13; Length 600; 95.2%; Pred. No. 61; Live 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST database from Sorghum: floral-induced meristems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Floral-Induced Meristem 1 (FM1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: JEN REV
High quality sequence stop: 161
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mass excision."
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                                                                                                                                                                                                                                      . 157 g
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                                                                                                                                                                                                                                          182 c
                                                                                                                                                                                                                                                                                                                                                         20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                   Similarity .
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DB 12; Length 204;

Score 18.4;

87.68;

Query Match

ORIGIN

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Email: tshini@genes.nig.ac.jp
A backbone of the vector is pBluescript II, that was in vivo
excised from a modified IPS phage vector (Mo bi Tec. Germany). XhoI
digested-5' end of CDNA is ligated to Sall site of the vector, and
the BamHI digested-3' end including poly-A tail is ligated to BamHI
site of the vector. CDNA instert could be amplified with
conventional T7 and T3 primers. This normarized full-length cDNA
library was generated basically according to the method described
in Genome Research 10, 1617-1630 (2000), Carninci, P. et al.
Protonemata were blended by the POLYTRON, and then cultivated on
                                                                                                                                                                                                                                                                                                 EST 24-JAN-2002
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 545)
Jita,T., Shin-1,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.
Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R07454 407 bp mRNA linear EST 05-APR-1995 ye96f09.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:125609 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comparison of the moss Physcomitrella patens genome with flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Physcomitrella patens subsp. patens"
/db_xref="taxon:145481"
/clone="pphn11118"
/clone=lib="normalized full length cDNA library,
chloronemata, caulonemata and rhizoid-like protonemata"
/tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
/ in 154 c 140 g 127 t
                                                                                                                                                                                                                                                                                  BJ190926
BJ190926 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphn11118 5', mRNA sequence.
BJ190926
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Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                       Gaps
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                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: Tadasu Shin-1
Center For Genetic Resource Information
Institute of Genetics
1111 Yata Mishima, Shizuoka 411-8540, Japan
   Pred. No. 1.3e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.4; DB 13;
Pred. No. 1.8e+02;
0; Mismatches 1;
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                                                                                                                                          123 AGTICCCINTIGGGGCCCATG 103
                                                                                    1 AGTICCCACTIGGGGCCCAIG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                         BJ190926.1 GI:18358867
ilarity '90.5%;
Conservative
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95.0%;
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Matches 19; Conservative
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R07454
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Fax: 81-559-81-6855
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                                                                                                                                                                                Email:
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BJ280551/c
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae
                                                                                                                                                                                                                                                                                                                                 High gality sequence stops: 303 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1036 Std Error: 0.00
                                                                                             (Joses 1 to 407)
Hillier, L. (Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The Washquewerk Est Project
Conpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF474621 Hinear EST 04-DEC-200 WHE2108_B06_D12ZS Wheat salt-stressed crown cDNA library Triticum aestivum cDNA clone WHE2108_B06_D12, mRNA sequence.
                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 115)
Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Chol,D.W., Close,T.,
Dvorak,J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Klanian,P.
                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 407; 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -21ml3
High quality sequence stop: 303.
Location/Qualiflers
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:125609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="GDB:478154"
                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
Insert Size: 1036
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                                                                    Sukaryota; Metazoa;
Mammalia; Eutheria;
RO7454.1 GI:759377
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nes 18, Conservative
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                                                   Homo sapiens
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BF474621/c
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JOURNAL
COMMENT
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/Add_inst_E. Coll Sour.
/Add_inst_E. Coll Sour.
/Add_inst_E. Coll Sour.
/Add_inst_E. Coll Sour.
/Add_inst_E. Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA and poly(A) RNA were propared
from crown tissue, equal portions of RNA were propared
from crown tissue, a cDNA library was made, and the CDNA
clones were in vivo excised to give pBluescript phagemids
in the TJ Close lab at the University of California,
Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian,
Otto, Simons, Zhang). Plasanid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnollophyta; Lillopsida; Poaceae; Pooldeae; Triticeae; Triticum.

1 (bases 1 to 136)
Ogihara,Y. and Murai,K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRNA linear , EST 09-APR-2002 BJ280551 Y. Ogihara unpublished cDNA library, Wh_r Triticum aestivum cDNA clone whr8n23 5', mRNA sequence.
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                                                                                                                                                          US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773
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                  ,C.L., Simons,K., Tong,J.C. and Žhāng,D.
The structure and function of the expressed portion of the wheat genomes - Salt-stressed crown cDNA library
Otto, C., Nguyen, H.T., Rausch, C.J., Seaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                         sequence and low 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="WHE2108_B06_D12"
clone_lib="Wheat salt-stressed crown cDNA library"
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                                                                                                                                                                                                                                                                                                                                            Sequence have been trimmed to remove vector quality sequence with phred score less than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 84.8%; Score 17.8; DB 12; Best Local Similarity 90.5%; Pred. No. 2e+02; Matches 19; Conservative 0; Mismatches, 2;
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National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'dev_stage="Adult plant"
'lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="Crown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 g
                                                                                                                                                                                                                                                                                                                       oandersn@pw.usda.gov
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                                                                                                            Unpublished (2000)
Contact: Olin Anderson
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Tel: 81-559-81-6856
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of RNA
                              equal quantities
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                        42 AGCTCCCTCTTGGGGCCCATG 22
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Matches 19; Conservative
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AV939865/C
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BJ235482/c
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                                                                                                                                                                 / CLSSUR__LYPE=_ LOUG.
// Ade_stage=_ Neekes' scale 1."
// Inote=_ Neetor: Lambda Uni_SAP XR, excised phagemid;
// Site_1: ECORI; Site_2: XhoI; Plants were grown under
hydropoint conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
tissue, equal quantities of RNA were pooled from the two
library was made, and the CDNA clones were in vivo
excised to give pBluescript phagemids in the _TJ. Close lab
at the University of California, Riverside (Akhunov, Chin
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
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                                                                                                                                       clone_lib="Y. Ogihara unpublished cDNA library, Wh.r"
tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BJ280541 Y. Ogihara unpublished cDNA library, Wh.r.Triticum
aestivum cDNA clone whr8m17 5', mRNA sequence.
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tissue_type="root"
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National Institute of Genetics
1111 Yard, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                                                      organism="Triticum aestivum"
Cultivar="Chinese Spring"
(db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ogihara, Y. and Murai, K. ...
Expressed genes in Triticum aestivum
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db_xref="taxon:4565"
clone="whr8m17"
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Location/Qualifiers
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                                                                                                                      clone="whr8n23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.59
Matches 19; Conservative
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Email:
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samples; polyA was purified from the pooled from the two library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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BJ235482 Y. Ogihara unpublished cDNA library, Wh_e Triticum
aestrum cDNA clone whelfolf 5', mRNA sequence.
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AV939865 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah24f19 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                              Length 139;
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Barley EST sequencing project in NIG and Okayama Univ
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                      Score 17.8; DB 13;
Pred. No. 2.2e+02;
0; Mismatches 2;
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Pred. No. 2.2e+02;
); Mismatches 2;
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63 c 38 g 25 t
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Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta;
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National Institute of Genetics
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                                                                                                      Seq primer: JEN REV
Plant Sciences Buf
Tel: 706 542 1860
Fax: 706 583 0210
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Matches 19; Conserv
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D41509/c
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FML_65_G06.bl_A003 Floral-Induced Meristem 1 (FM1) Sorghum
propinguum cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Y. Ogihara unpublished cDNA library, Wh_e"
/tissue_type="seed DPA10"
/dev_stage="Feekes' scale 11.2"
/dev_stage="Feekes' scale 11.2"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid:
Site_1: ECORI; Site_2: XhOI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorzak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
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                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunoy, Chir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Otto, Simons, Zhang)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other authors).
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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 216;
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Tel: 81-559-81-6856
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                                                                                                                                           1 (bases 1 to 216)
Oglhara,Y. and Murai,K.
Expressed genes in Triticum aestivum
Onpublished (2002)
Contact: Tadau Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                               cultivar="Chinese Spring"
db_xref="taxon:4565"
clone="whe16n16"
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                                                                                                                                                                                                                                                                                                                                                      Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                              Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                               Tel: 81-559-81-6856
Fax: 81-559-81-6855
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ECORI; mature plants were placed in a growth chamber for 15 days with 16 hr darkness and 8 hr light (flowering is induced by short-day conditions); 16 days after being returned to the greenhouse under natural long days during late April, Carly May, meristems were harvested The library was made from poly A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 03-APR-2002
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RICS4047A Rice shoot Oryza sativa (japonica cultivar-group) cDNA,
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Oryza sativa (japonica cultivar-group)
Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                     Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
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Contact: Takuji Sasaki
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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Rm. 2502, Athens, GA 30602-7271, USA
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/clone_lib="Floral-Induced Meristem 1 (FM1)"
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/dev_stage="Etiolated shoot (8 days old)"
/note="Etiolated shoot (8 days old)"
73 c 65 g 51 t
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ilarity 90.5%; Pred. No. 2.6e+02;
Conservative 0; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Sorghum propinguum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'db_xref="taxon:39947
                                                                                                                                                                                                                                          High quality sequence start: 15
High quality sequence stop: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrhartoldeae; Oryzeae; Oryza.
1 (bases 1 to 238)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mass excision.
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Tracheophyta;

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AVIG7513 Mus musculus head C57BL/6J 13-day embryo Mus musculus CDNA AVIG7513 AVIG7513 AVIG7513 AVIG7513
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Transcriptional sequencing A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 270) a. Albata, K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fükuda,S., Fükunishi,Y., Funayama,T., Hara,A., Hayatsu,M., Havi,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shipamoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., T
                                                                                                                                                               Unpublished (1995)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondal 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                            Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)
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Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                              permatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Rice shoot"
/dev_stage="Etiolated shoot (8 days old)"
/note="Etiolated shoot (8 days old)"
83 c 73 g 54 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.8%; Score 17.8; DB 14; 90.5%; Pred. No. 2.7e+02; ive 0; Mismatches 2;
                                                                                                         Sasaki,T., Miyao,A. and Yamamoto,K.
Rice cDNA from callus 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar-"Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"taxon:39947"
                                                         hrhartoideae; Oryzeae; Oryza
(bases 1 to 265)
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; Viridiplantae;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Chie Owa
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19; Conserv
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AV167513/c
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AUTHORS
TITLE
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COMMENT
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72.c 75 g 56 t
                                                                                                                                                                                                                                                                                                                                                 EST 20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; Liliopsida; Poales, Poaceae, PACC clade, Panicoideae, Andropogoneae, Sorghum.
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RICS3131A Rice shoot Oryza sativa (japonica cultivar-group) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                        BG465041 263 bp mRNA linear EST 20-M2 EM1_35_D12.b1_A002 Embryo 1 (EM1) Sorghum bicolor CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon.4558"
/clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reid.S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H. Mn. BST database from Sorghum: developing embryos Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                              ö
                     Length 238;
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                     DB 14;
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Pred. No. 2.7e+02;
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Oryza sativa (japonica cultivar-group)
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                                                                           0; Mismatches
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                  Score 17.8;
Pred. No. 2.
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High quality sequence stop: 258
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BG465041.1 GI:13394129
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               84.8%;
90.5%;
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Best Local Similarity 90.5%;
Matches 19; Conservative
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                                                                        19; Conservative
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Fax: 706 583 0210
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D40937
               Query Match
Best Local Similarity
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D40937/c
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KEYWORDS
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KEYWORDS
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Gaps

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2; Indels

Length 265;

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/dev.stage="13-day embryo"
/dev.stage="13-day embryo"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                           EST 04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D47961
RICS13778A Rice green shoot Oryza sativa (japonica cultivar-group)
CDNA, mRNA sequence.
D47961
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantaa; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enhartoideae; Oryzae; Oryza, Liliopsida; Doales; Poaceae;
1 (bases 1 to 283)
Sasaki,T., Miyao,A. and Yamamoto,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki, T., Myao, A. and Yamamoto, K.
Rice cDNA from callus 1995
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
National Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7448
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                  clone_lib="Mus musculus head C57BL/6J 13-day embryo"
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/clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
89 c 73 g 60 t
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                  'organism="Mus musculus"
                                                 /db_xref="taxon:10090"
/clone="3110055G14"
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                                                                                                                       tissue_type="head"
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                                 strain="C57BL/6J
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115 AGCTCCCTCTTGGGGCCCATG 95
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2003, Search completed: July. 8, Job time: 1068.8 secs

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1 AGTICCCACTIGGGGCCCATG 21

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on:	July 8, 2003, 00:45:53 ; Search time 220.098 Seconds (without alignments) 2644.537 Million cell updates/sec	Seconds) 11 updates/sec
Title: Perfect score:	US-09-647-780A-7	
Sequence:	1 gctggaggattcctctgtcc 20	
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched:	2054640 segs, 14551402878 residues	
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	14707 Sequenc	1470	1182 Rattus n	95165 Rattus	22586	09505 Homo	95501	ഗയ	5847	AC004564 Drosophil	AC120994 Rattus no	107 Drosophi	AE103454 Drosophil AX164254 Sequence	126	928 Seque	Y00766 Rat mRNA fo AF225986 Homo sapi	235	286	560 Human 536 Homo	3463 Ношо	AC074009 Romo sapi	2452 Homo sa	ACIU5645 Rattus no BC012715 Mus muscu	917 · Homo	X06807 Hamster des X73524 R.norvegion	CBS29	G54304 CBS30 Human L17322 Mouse entac	28347 Mus	892 1			-	linear PAT 07-SEP-2000			, Bonhomme, M.C. and	its use for screening
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SOMMAKIES	ID	147	AX014701 AC094732	AC121182	AC095165	AC022586	AC009505	AL62/184 AC095501	AC095500 AY058691	AC095847	AC019884 AC004564	50.5	AC099307	AE003454 AX164254	F330116S11	AX401928	F 1 10			90	~		3 4 7	4 1	1	MADES5 RNDES		G54304 MUSENTO1	2834	MMU250633 MMDESMINP	ALIGNMENTS		•	20 bp t w09953077	0	·	C., Ouimet,T	e metalloprotease therapy
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553 GCTGGAGGATTCCTCTGTCC 572
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Weinstock, G. and Gibbs, R.
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Rattus norvegicus
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Patent: WO 9953077-A 7 21-OCT-1999;
INST NAT SANTE RECH MED (FR): SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR): OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHIMETTI PATRICIA (FR)

LOCATION/Qualifiers
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Patent: WO 9953077-A 1 21-0CT-1999;
Patent: WO 9953077-A 1 21-0CT-1999;
INST MAY SAMTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUTNET TANJA (FR); ROSE CHRISTIANE (FR); BONHOWME MARIE CHANTAL (FR); FACCHINETH PATRICIA (FR)
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Schwartz,J.C., Gros,C., Ouimet,T., Rose,C., Bonhomme,M.C. and
Facchinetti,P.
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/organism="synthetic construct"
/db_xref="taxon:33630"
/note="oligonuclectide" f
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'db_xref="taxon:10117"
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FEATURES

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AC094732 174953 bp DNA linear HTG 20-DEC-2001
Rattus norvegicus clone CH230-516, *** SEQUENCING IN PROGRESS ***,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K
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Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Depar Submitted (15-SEP-2001) Human Genetics, Baylor College of Medicine, of Molecular and Human Genetics, Baylor College of Medicine, Ravlor Plaza, Houston, TX 77030, USA
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Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwoke
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                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                          Consensus quality: 152255 bases at least Q40
Consensus quality: 158448 bases at least Q30
Consensus quality: 164461 bases at least Q30
Estimated insert size: 155965; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
          ------- Summary Statistics
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                                                                                                                                                                                                                                                                                           RS Muzny, D.W., Adams, C., Addo-Oduola, B., Ali-osman, F.R., Allen, C., Alabragoks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Blinge, K., Blankenburg, K., Bonnin, D., Barbaria, S., Birtera, M., Brown, B., Brown, B., Brown, B., Bonnin, D., Barbaria, S., Birtera, M., Brown, E., Brown, M., Bryant, N.P., Carron, T., Entera, M., Cavacos, S.R., Check, J., Chavez, D., Chen, G., Chen, R., Carter, M., Cavacos, S.R., Check, J., Chavez, D., Chen, G., Chen, R., Chowdiry, I., Christopoulos, C., Carron, T. E., Davis, C., Davy-Carroll, L., Dederich, D. David, R., Davis, C., Davy-Carroll, L., Dederich, D., Farniz, P., Douthwaite, R.J., Dapar, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edward, C.D., Carroul, J., Foster, P., Franiz, P., Goriell, J. H., Guevara, W., Gunzarhe, P., Hales, S., Hamilton, K.J., Barnhart, C., Hartis, K., Hart, M., Havlak, P., Hawes, A., Hernandez, D., Hodgson, A., Houyes, P., Hane, S., Hamilton, K.J., Hernandez, O., Hodgson, A., Houyes, P., Hawes, A., Harnandez, O., Hodgson, A., Houyes, P., Hale, S., Joudah, S., Krailsson, E., Kelly, S., Chan, U., Liu, Y., Johnson, R., Jar, Y., Johnson, R., Massey, C., Liu, J., Liu, Y., Liu, Y., Lu, X., Lucier, R., Luna, R., Massey, G., Mantin, R., Mantin, R., Massey, G., Miner, G., Miner, Z., Mitchell, T., Weiden, R., Massey, G., Scher, P., Sperks, A., Rapton, M., Nickerson, E., Medeo, R., Payton, B., Peters, L., Pickenson, R., Payton, B., Peters, L., Pickerson, E., Rubor, P., Ramerisa, A., Tamerisa, R., Rubor, P., Rubor, P., Schere, S., Scott, G., Shen, H., Shooshtari, N., Washun, G., Wallidanson, S., Warren, R., Sanke, T., Sparks, A., Rollow, R., Norleo, S., Warren, R., Stari, R., Walli, R., Walli, R., Walli, R., Walli, R., Walli, R., Walli, R., Wall
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                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Rattus norvegicus clone CH230-350Al3, *** SEQUENCING IN PROGRESS ***, 45 unordered pieces. AC121182
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On Jul 18, 2002 this sequence version replaced gi:20806209.
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Weinstock,G. and Gibbs,R.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pieces is a not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                 Chemistry: Dye-terminator Big bye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 115827 bases at least Q40 Consensus quality: 120596 bases at least Q30 Consensus quality: 124293 bases at least Q20
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Center clone name: CH230-350A13
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Kratcovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lil, J., Liul, W., Loulseged, H., Lozado, R.J., Lur, Z., Lucler, A., Luciar, R., Luna, R., Ma, J., Maheshwari, M., Mariello, Martindale, A., Martinez, E., Maheshwari, M., Mel, G., Mattinez, E., Machen, P., Martindale, A., Martinez, E., Marchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oriedo, R., Pace, A., Patton, B., Peery, J., Perez, L., Pickens, F., Parton, B., Peery, J., Perez, L., Pickens, R., Parton, B., Peery, J., Schers, F., Scher, F., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonakke, T., Sparks, A., Stanley, H., Stone, H., Stote, H., Stote, H., Stote, H., Stote, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tansey, J., Taylor, C., Vers, V., Villalon, D., Vinson, R., Wang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wailliams, G., Williams, G., Williams, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Verson, D., V
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Edgard, D., Edgards, C.C.; Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisla, A., Gaorda, Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Ganner, T., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homasi, F., Howard, S., Huber, J., Hully, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Keilly, S., Khan, U., King, L., Korvar, G., Karlsson, E.,
Kratovic, J., Kureshi, A., Landry, M., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 179992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 53 contigs. The true order of the pieces
is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: GCXQ
Center clone name: CH230-8D23
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieava, M., Brown, E., Brown, M., Bryant, N.P. Bunay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, M.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 2; Length 157126;
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Matches 19; Conservative 0; Mismatches
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Rattus norvegicus clone CH230-8D23,
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Rattus norvegicus
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Mus musculus 3-ketosteroid reductase (HSD3b5) mRNA, complete cds: L41519.1 GI:840649
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1592)
Abbaszade, I.G., Clarke, T.R., Park, C.H. and Payne, A.H.
The mouse 3 beta-hydroxysteroid dehydrogenase multigene family includes two functionally distinct groups of proteins Mol. Endocrinol. 9 (9), 1214-1222 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Direct Submission
Submitted (17-OCT-1997) Gyn/Ob, Stanford University Medical Center,
300 Pasteur Dr., Stanford, CA 94305, USA
Location/Qualifiers
1. 1592
/organism="Mus musculus"
/strain="BALB/C"

source

FEATURES

(bases 1 to 1592)

MEDLINE PUBMED REFERENCE AUTHORS TITLE

7491113 2 (base Payne, A.

JOURNAL

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MAEKAVLATNGRLLKNGGTLHTCALRLPFIYGEECQVTSTTVKTALKNNSIIKKNATF
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Homo sapiens chromosome 2 clone RP11-388J8 map 2, LOW-PASS SEQUENCE
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Norman,C.H., O'Connor,T., O'Donnell,P., Ollvar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 77333)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, N. Domino, Doyle, M., Fenestor, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                       note="3-beta-hydroxysteroid dehydrogenase;
-hydroxysteroid; ketosteroid; multigene family*
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Unpublished
                                                                                                                                                                                                                                                                                                                                                 product="3-ketosteroid reductase"
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/dev_stage="adult"
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                                                   tissue_type="liver"
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Submitted (06-FBB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6910752. All repeats were identified using RepeatMasker:
                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                       NOTE: This record contains 78 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                 Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                            will be sequenced to completion. In the event that
                                                                                                                            Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                           the record is updated, the accession number will be preserved.
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91 19790: gap of 100 bp
91 20676: contig of 886 bp in length
77 2076: gap of 100 bp
77 21659: contig of 883 bp in length
60 21659: contig of 896 bp in length
60 22655: contig of 896 bp in length
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15815: gap of 100 bp
16720: contig of 905 bp
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2755: gap of 100 bp
23657: contig of 902 bp in length
3757: gap of 100 bp
24633: contig of 876 bp in length
4733: gap of 100 bp
25699: contig of 876 bp in length
5709: gap of 100 bp
26614: contig of 905 bp in length
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: contig of 889 bp 1
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Submitted (27-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens BAC clone RP11-526D2 from 2, complete sequence.
AC009505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 64433; gap of 100 bp 14 65323; contig of 890 bp in length 465323; contig of 990 bp in length 66327; contig of 904 bp in length 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 b
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Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Pred. No. 23;
0; Mismatches
                                 59399; gap of 60286; contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24111 GCTGGAGGCTTCCTCTGTCC 24130
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65323: conf
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Sulston, J.E. and Water
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Waterston, R.H.
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   63439:
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COMMENT

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catenese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at the Roswell Park Cancer Institute (http://acpac.med.buffalo.edu)

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-363N21; the clone sequenced to the right is RP11-297N12. Actual start of this clone is at base position 1 of RP11-526D2; actual end is at base position 163880 of RP11-526D2.

, The sequence RP11-526D2 from base positions 68392 to 70834 is represented by sequence derived from PCR of clone DNA.

There are polymorphic base pair differences in the overlap between the clone RP11-526D2 and RP11-297N12. Location/Qualifiers

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organism-"Homo sapiens"
                                        db_xref-"taxon:9606
                                                                                  lone-"RP11-526D2"
                                                                                               clone_lib="RPCI-11
                                                                                                                                                                                                                                     pt_family="MaLR"
                                                                                                                                                                                                                                                                                                                   /rpt_family="MaLR"
11336. .11411
                                                                                                                                                                                                                                                       rpt_family="MIR"
                                                                                                                                                                                                                                                                                          .pt_family-"MIR"
                                                                                                                        pt_family-"MIR"
                                                                                                                                                   pt_family-"Alu"
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                                                      /chromosome="2"
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FEATURES
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repeat_region repeat_region repeat_region repeat_region misc_feature	/rpt_family="MIR" 1151. 11634 /rpt_family="L2" /rpt_family="MERI_type" /rpt_family="MERI_type" /rpt_family="CRI" 1341. 13753 /rpt_family="CRI" 1343. 14396	
1 1 1 1	20. 14389 20. 14389 20. 14389 20. 14389 20. 14586 20. 14586 20. 14586 20. 14586	0)" 5) mil6b0 =78)"
misc_feature misc_feature misc_feature misc_feature repeat_region	/note="similar to EST H11416 (NID:g8/6236) ym 14436. 14719 /note="similar to EST AW359793 (NID:g6864443) 14441. 14119 /note="similar to EST AW258675 (NID:g631656) /note="similar to EST AW481793 (NID:g7051899) /note="similar to EST AW481793 (NID:g7051899) /note="similar to EST AW653728 (NID:g719554) 18493. 18375) yml3g05.rl" 443)" 656) uq38h02.yl" 899)"
	fam. fam. fam. fam. fam.	467) zh27e06.s1"
c_featur c_featur eat_regi c_featur c_featur	24381 -"similar to EST N79496 (NID:g12421 .24515 Eamily="Alu" .24860 -"similar to EST W16691 (NID:g12910 .24877 family="Alu" .25156 -"similar to EST T54565 (NID:g65642 .2531 family="Alu"	97) zb07c11.s1" 72) zb07c11.r1" 6) yb40e12.r1"
misc_feature misc_feature misc_feature misc_feature misc_feature	619. 25831 ote="similar 652. 25857 ote="similar 652. 25842 ote="similar 652. 25839 ote="similar 652. 25839	724) ub27f12.rl" 899)" 554)" 656) uq38h02.yl"
	Cote-"similar to EST AW359793 (NID:g6) 694. 256028 ote-"similar to EST AW477500 (NID:g7) 616. 2623 ote-"similar to EST AW653728 (NID:g7) 616. 26407 EST AA249540 (NID:g5) 616. 26450 ote-"similar to EST AA249540 (NID:g5) 616. 26450 ote-"similar to EST AA249540 (NID:g5) 616. 26450 ote-"similar to EST AA4994 (NID:g5) 616. 26450 ote-"similar to EST AA404994 (NID:g5) 616. 265. 266. 266. 265. 266. 266. 266. 26	864443)" 047606)" 419554)" 545893) tz60b01.x1" 924051)"
misc_feature	2629426738 /note="similar to EST AW912988 (NID:98078622	622), uf47e08.y1'

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EST AW912919 (NID:98078549) uf46e08.yl"
                                                              EST AA722674 (NID:92740381) z990h06.s1"
                                                                                                       AA133513 (NID:91690500) zk96g02.rl"
                                                                                                                                               AA036848 (NID:g1509886) zk29f08.rl"
                                                                                                                                                                                      (NID:g5542929) wc17e11.x1"
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ne 4 clone RP23-125F21, *** SEQUENCING IN
                                                                                                                                                                                                                                                                 EST AA115694 (NID:91670786) zk96g02.s1"
                                                                                                                                                                                                                          EST AI934552 (NID:g5673349) wp09c10.x1"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 2, 2002 this sequence version replaced 91:21627911.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 214433; sum-of-contigs
Insert size: 200937; 13.8% error; agarose-fp
Quality coverage: 14.57x in Q20 bases; sum-of-contigs Quality
coverage: 15.70x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL627184.17 GI:21665928
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                      Length 163880;
                                                                                                                                                                                                                                                                                          %83/4. .zbo8>
/note="similar to EST AW371193 (NID:96875847)"
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Location/Qualifiers
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Sequencing vector: plasmid; LO8752; 100% of reads
Chemistry: Dye-terminator; 6% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nemistry: Dye-primer Big Dye; 0% of reads
hemistry: Dye-terminator Big Dye; 93% of reads
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Pred. No. 25;
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/organism="Mus musculus"

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AC095501 110491 bp DNA linear HTG 09-JUL-2002
Rattus norvegicus clone CH230-7P13, *** SEQUENCING IN PROGRESS ***,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
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finer, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.
foser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
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                                                                                    /clone_lib="RPCI-23"
                                            /clone="RP23-125F21"
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                                                 Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 110491)
Worley, K.C.
                                                                                                                                   Direct Submission
Submitted (09-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 9, 2002 this sequence version replaced g1:17942008.
Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                         (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                              Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GCME
                                                                                                                                                                                                                                                                                  Center clone name: CH230-7P13
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                                                                                                                                                                                                                                                                                                           Sequencing vector: Plasmid;
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Weinstock,G. and Glbbs,R.
Direct Submission
Unpublished
                                     (bases 1 to 110491)
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1 (Dases I to 158859)

MUZDA,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Buck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Christopoulos,C., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdiry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,R.R., Garcia,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Foxd,J., Foster,P., Frantz,P., Gorrell,J.H., Garcia,A., Garcia,A., Garner,T., Garza,N., Gall,R.R., Hartis,K., Hart,M., Halle,S., Hamilton,K., Hartis,C., Harris,K., Hart,M., Havlak,P., Hames,J., Jackson,L.E., Jackson,B., Jia,Y., Johnson,R., Holloway,C., Hollins,B., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Katovic,J., Kuretyic,J., Kuretyic,J., Lu,X., Lucier,R., Luna,R., Martinele,P., Martine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA linear HTG 10-JUL-2002
, *** SEQUENCING IN PROGRESS ***,
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Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
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                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                      DB 2; Length 110491;
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87452: contig of 2201 bp in length
87552: gap of unknown length
90136: contig of 2584 bp in length
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                                                                                                                                                                                                                 Score 18;
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Rattus norvegicus
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Matches 1
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AC095500/c
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ORGANISM
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                              Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 9, 2002 this sequence version replaced gi:17942007.

Center: Baylor College of Medicine
        Baylor College of Medicine, One USA
                                                                                                                                                                                                                                                                                                                               Center clone name: CR230-7P12
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 100849 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of unknown length
contig of 1202 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap; version 0.999329
Consensus quality: 88636 bases at least 040
Consensus quality: 95512 bases at least 030
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                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Molecular and Human Genetics,
lor Plaza, Houston, TX 77030,
                                                                                                                                                                                                                                                                                                              Center project name: GCMD
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                                          3 (bases 1 to 158869)
Worley, K.C.
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us-09-647-780a-7.rge

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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyh tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accuractly this particular CDNA clone. However, there artifacts associated with the generation of CDNA clones that may have not been detected in our initial analyses such as internal priming priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitily.perkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mprryQralnsakySaQVKTKTSDNESDSEDDLPPDQDAEDNNE
pdnlrSillenapHFSYPGLNTGMLGQLLYDHQDNPKQDLPNCSVTVPLPLFLAKDGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRVEACVQRPFRYDDWTRQLQLGKAIFDRRLKNWRQRVQKQEQGVHDASLFEMAEHIA
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                                                                                                        INV 17-0CT-2001
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                                                                                                                                                                                                           Eukaryota; Metazoa Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 27/7) Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J..
                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-0CT-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory

Berkeley, CA 94720
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db_xref="FLYBASE:FBgn0034631"
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Drosophila melanogaster LD41005 full length cDNA.
AY058691 ..
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="57E6-57E8"
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/db_xref="G1:16198211"
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              119728 GCTGGAGGATTCCTCTGT 119711
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1 GCTGGAGGATTCCTCTGT 18
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AUTHORS
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LANAVNERVQRENIRCTQYQSIPEIRDIFRDGAKRSKPEEKPLIVEEIEIDYGIEDTD
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LEQLPSGTVVPTFEDETTEGVPENPANYPGTSLPKIKGATTANYSVIPALNSDQDIGERLLS
PKKESPVEFGREYSILLPGQNTIIEDYPCAPPAKRPKVKHVKGF"
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Rattus norvegicus clone CH230-10D4, *** SEQUENCING IN PROGRESS ***,
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Sciurognathi; Muridae; Murinae;
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Weinstock,G. and Gibbs,R.
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Pred. No. 72;
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HTG; HTGS_PHASE1.
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Mammalia; Eutheria;
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                 Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 10, 2002 this sequence version replaced g1:17943453.
                                                                                        Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.990329
Consensus quality: 12551 bases at least Q40
Consensus quality: 13751 bases at least Q30
Consensus quality: 14782 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
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AUTHORS
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                                                      AUTHORS
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of 4372 bp in length.

Location/Qualifiers

FEATURES

Arcaina, T.T., Baxter, E., Blazej, R.G.

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Similarity
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Job time: 225.098 secs
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Drosophila melanogaster DNA sequence (Pl DS08012 (D224)), complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s sequence was identified as CDM:10211271 by the submitte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Geoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Pphydroidea; Drosophilidae; Drosophila.
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the accession number will be preserved.
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/db_xref="taxon:7227"
15390 a 10935 c 11441 g 16420 t
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                  /organism="Rattus norvegicus"
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                                                                   7702 t
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                                /db_xref-"taxon:10116"
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This sequence will be replaced
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.29937
                                                                6807 c
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Submitted (17-APR-1998) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On or Defore May 2, 1998 this sequence version replaced gi:2708064, gi:2708064, gi:2708066, gi:2708059, gi:2708054, gi:3056946. Sequence submitted by:

Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory, MS 64-121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Punch, E.,
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Library location: 44_84.
Location/Qualifiers
Chew,M., Doyle,C.M., Farfan,D.E., Flandgan,J., Houston,K.A.,
Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B.,
Lomotan,M.A., Mazda,P., Mok,M.S., Moshrefi,A.R., Moshrefi,M.
Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,D., Snir,E.,
Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R., Zleran,L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)

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94.7%; Pred. No. 90;
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SUMMARIES

Result Š

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Drosophila melanog Drosophila melanog Human SCN3A genomi Rat sequence diffe Human adult form o Rat membrane metal Rat membrane metal Description Match Length DB

Bonhomme MC, Facchinetti P;

(INRM) INSERM INST NAT SANTE & RECH MEDICALE. Haret C,

WPI; 1999-593429/51 Ouimet T, Gros C, Schwartz JC;

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88 88 84 0 66 88 88 84 0 67 88 88 8 0 68 88 0 69 88 0 60 0 6	7777		. a .	Rat; membrane metallopro neuron; hormone; peptide neuron; hormone; peptide nyrothalamic-hypophyseal Synthetic. Rattus rattus. 15-OCT-1999. 08-APR-1998; 98FR-0004
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                                                                                       Sequences AA228811-228827 represent probes for detecting the rat membrane metalloprotease designated neprilysine II (NEPII) gene (AA228810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic- hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds.
               involved in proteolysis of
to screen for inhibitors,
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                                                                                                                                                                                                                                                                            Length 20;
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Pred. No. 3.5;
Wismatches 0;
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           New membrane metalloprotease NEP II, neuronal and hormonal peptides, used potentially useful for treating e.g.
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                                                                                                                                                                                                                                                                                                                                          1 GCTGGAGGATTCCTCTGTCC 20
                                                                  Claim 3; Page 20; 29pp; French.
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es 20; Conserv
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to peptidergic signalling in which NEPII in involved ar or neurodegenerative diseases; growth disorders of disturbances of the hypothalamic-hypophyseal axis or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABLi30311), expressed DNA sequences (ABLi61787-ABB72072).
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ID ABL16565 standard; DNA; 2639 BP.
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2000US-0614150
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                   e.g. cardiovascular cendocrine origin; disendocrine disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
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                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 1165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 4716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1165; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4716 BP; 1298 A; 1022 C; 1009 G; 1387 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human SCN3A genomic DNA fragment SEQ ID NO:84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.4; Di
Pred. No. 84;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2846 GCTGGAGGATTCCTCTATC 2864
                                                             DNA; 4716 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGGAGGATTCCTCTGTC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 87.0%;
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH55840 standard; DNA; 566
                                                                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                2000US-191637P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                           (first entry)
                                                                                                                                                                                                         pharmaceutical; gene; ds
                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4PI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB57737-ABB72072)
                                                            ABL16564 standard;
                                                                                                                                                                                                                                                                   WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2001
                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH55840;
                                                                                            ABL16564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH55840
                                           RESULT
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Rat sequence differentially expressed in response to a hepatotoxin #1604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               individual's predisposition to epilepsy and/or development of epilepsy, as well as predicting the individual's response to medication. The mathod comprises determining the genotype of at least one gene selected from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium channel genes located on chromosome 2. The idiopathic generalised epilepsy (IGE) gene is more specifically localised on chromosome 2923-931. Compounds identified as modulators of the biological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy or other neurological disorders. They have anticonvulsant and neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAS, gene fragments, PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primers, oligonucleotides and proteins given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ragsdale D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST; drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining a predisposition to epilepsy and/or development of epcomprises determining the genotype of SCN1A, SCN2A and/or SCN3A, DNA variant, equivalent, or mutation which shows a linkage disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention describes a method (MI) of determining an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed sequence tag; EST; drug scr
m; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cossette P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 566 BP; 174 A; 93 C; 111 G; 187 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 22; 1 Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rochefort D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 179; 268pp; English.
neuroprotective; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK63697 standard; cDNA; 6822 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; P. Warches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 GCTGGAGGATTCCTCTG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGGAGGATTCCTCTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-2001; 2001WO-US23872
                                                                                                                                                                                                                                                    24-NOV-2000; 2000WO-CA01404.
                                                                                                                                                                                                                                                                                                               99US-0167623.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rouleau GA, LaFreniere RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; ss; hepatotoxin; exp
differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention.
                                                                                                                                                                                                                                                                                                                                                                             (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-355945/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
                                                                                                                     WO200138564-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200210453-A2
                                                                                                                                                                                                                                                                                                               26-NOV-1999;
                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2002
                                                                                                                                                                                      31-MAY-2001
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The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the compounds or the progression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic ceffect of a compound or progression of a toxic effect, preferably the expression in a tissue or cell sample exposed to the compound of two or cell sample exposed to the compound of two or ceression in a tissue or cell sample exposed to the compound of two or more genes is indicative of at least one toxic effect or progression of the method can also be used to identify an agent which modulates the method can also be used to identify an agent which modulates the coxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid specifically hybridises to a gene listed in the specification, a computer system comprising at least two genes listed in the specification, computed and atabase containing information identifying the expression level in a tissue or cell sample exposed to present information identifying the expression level in a tissue or cell sample expression economic confidenting global confidence in the specification. The method is useful for elucidating global confidence in the specification. The method is useful for elucidating global confidence in the markers in the proposed to a known toxii. The genes may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         issues or cell exposed to a known toxin. The genes may be used as coxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell
                                                                                                                                                                                                                                                                                                                                                Predicting toxic effects of compounds or the progression of these tox effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells -
                                                                                                                                                                                                                                                                   Johnson KR, Castle AL, Elashoff MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq ID No 1604; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterised by centrilobular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which is differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is an expressed sequence
                                                                                                               01US-295798P
                                                                                                                                                                               2001US-303459P
                                                                                                                                                                                                                                                                   Porter MW,
                                                                                                                                                                                                                 (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                       WPI; 2002-241625/29
                                                                                                                                                                          09-JUL-2001:
                                                                                                      06-JUN-2001;
                                                                                                                               13-JUN-2001;
                                                                                                                                                                                                                                                              Mendrick D,
                                                                    L5-MAY-2001
                                                                                    22-MAY-2001
                                           11-MAY-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17
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in response to a hepatotoxic agent. has been exposed to a compound or agent. Hepatotoxicity necrosis and steatosis. The tag (EST) or cDNA derived fr Sequence 6822 BP; 1861 A; 1525 C; 1650 G; 1786 T; 0 other;

ö Length 6822; Indels . 85.0%; Score 17; DB 24; I Mismatches 85.v., 100.0%; Pr 0; Ouery Match
Best Local Similarity 100.0
Matches 17; Conservative

ò g

AAH55823 standard; cDNA; 9112 BP. AAH55823; AAH55823 HXXXXXXXXXXXX

RESULT 7

(first entry) 04-SEP-2001

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Determining a predisposition to epilepsy and/or development of epileps comprises determining the genotype of SCNIA, SCN2A and/or SCN3A, or a DNA variant, equivalent, or mutation which shows a linkage disequilibrium
                                                              diagnosis; mutation; chromosome 2q23-q31; neurological disorder; anticonvulsant; neuroprotective; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rochefort D, Cossette P, Ragsdale D;
Human adult form of SCN3A nucleotide sequence SEQ ID NO:65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 150-154; 268pp; English.
                                                           chromosome 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rouleau GA, LaFreniere RG,
                                                                                                                                                                                                                                                                                                              24-NOV-2000; 2000WO-CA01404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-355945/37.
P-PSDB; AAB99678.
                                                                                                                                                                                                                                                                                                                                                                                                                     UYMC-) UNIV MCGILL
                                                      epilepsý;
                                                                                                                                                                                                          WO200138564-A2.
                                                                                                                                                                                                                                                                                                                                                                     26-NOV-1999;
                                                                                                                                                                                                                                                              31-MAY-2001
                                                      Human;
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these toxic

The present invention describes a method (M1) of determining an individual's predisposition to epilepsy and/or development of epilepsy, as well as predicting the individual's response to medication. The method comprises determining the genotype of at least one gene selected from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation sodium channel genes located on chromosome 2. The idiopathic generalised 2923-931. Compounds identified as modulators of the biological activity of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy or other neurological disorders. They have anticonvulsant and epilepsy or other neurological disorders. They have anticonvulsant and neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAS, gene fragments, PCR primers, oligonucleotides and proteins given in the exemplification of the present invention.

Length 9112; Sequence 9112 BP; 2769 A; 1695 C; 1861 G; 2785 T; 2 other;

0; Indels 85.0%; Score 17; DB 22; I 100.0%; Pred. No. 1.4e+02; 1ve 0; Mismatches 0; 2570 GCTGGAGGATTCCTCTG 2586 1 GCTGGAGGATTCCTCTG 17 Conservative Ouery Match
Best Local Similarity . QQ

Gaps

ö

04-SEP-2001 (first entry) AAH55824;

AAH55824 standard; cDNA; 9112 BP

RESULT 8 AAH55824 Human neonatal form of SCN3A nucleotide sequence SEQ ID NO:66.

diagnosis; mutation; chromosome 2; SCNIA; SCN2A; SCN3A; identification; anticonvulsant; neuroprotective; ss. Human; epilepsy; chromosome 2; SCN1A;

Homo sapiens

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Human sodium channels SCNIA and SCNIA and encoded genes, useful in
studying physiological mechanism in which excitant cells participate
and causes of diseases and developing drugs for motor endplate disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes human sodium channels SCNIA and SCNIA. The present sequence encodes the human sodium channel SCNIA. SCNIA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCN3A have been located to the human chromosome 2 long arm, positions 2924 and 2924-31 respectively. The sodium channel proteins are useful in studying the physiological mechanism in which excitant cells participate and cause human diseases, and in developing remedies for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEP; endocrine; vasotropic; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enzyme; gynaecological; antisense-therapy; male erectile dysfunction;
MED; female sexual dysfunction; FSD; female sexual arousal disorder;
FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypercalcaemic periodic paralysis of extremities and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB 24; Length 9123;
Pred. No. 1.4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9123 BP; 2770 A; 1700 C; 1870 G; 2783 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soluble secreted endopeptidase (SEP) consensus DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "Encodes catalytic domain"
                                                                                                                                     (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 50-71; 88pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD28130 standard; DNA; 2286 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2556 GCTGGAGGATTCCTCTG 2572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCTGGAGGATTCCTCTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .85.0%;
12-JUN-2001; 2001WO-JP04956.
                                                       13-JUN-2000; 2000JP-0177540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUL-2001; 2001WO-IB01263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUL-2000; 2000GB-0017387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1664..2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   motor endplate disease.
                                                                                                                                                                                             Goto J,
                                                                                                                                                                                                                                               WPI; 2002-098066/13.
P-PSDB; ABB06027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200206492-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            familial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAY-2002
                                                                                                                                                                                             Kanazawa I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD28130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (MI) of determining an individual's predisposition to epilepsy and/or development of epilepsy, as well as predicting the individual's response to medication. The method comprises determining the genotype of at least one gene selected from SCNIA, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which shows a linkage disequilibrium. SCNIA, SCN2A and SCN3A-are all sodium channel genes located on chromosome 2. The idiopathic generalised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epilepsy (IGE) gene is more specifically localised on chromosome 2q23-q31. Compounds identified as modulators of the biological activity of SCNIA, SCNZA or SCN3A proteins or genes, are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                 epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epilepsy or other neurological disorders. They have anticonvulsant and neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679 represent SCNIA, SCN2A, and SCN3A cDNAS, gene fragments, PCR primers, oligonucleotides and proteins given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; sodium channel; SCN3A; chromosome 2q24-31; gene; ss;
familial hypercalcaemic periodic paralysis; motor endplate disease.
                                                                                                                                                                                                                                                                              Cossette P, Ragsdale D;
                                                                                                                                                                                                                                                                                                                                                                                                Determining a predisposition to epilepsy and/or development of epcomprises determining the genotype of SCNIA, SCNIA and/or SCNIA, DNA variant, equivalent, or mutation which shows a linkage disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9112 BP; 2769 A; 1695 C; 1857 G; 2789 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human sodium channel SCN3A encoding cDNA SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB 22;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "sodium channel SCN3A'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                              Rochefort D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 154-157; 268pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
472..6474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL39690 standard; cDNA; 9123 BP
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                                                                                                            2000WO-CA01404.
                                                                                                                                                                                                                                                                              LaFreniere RG,
                                                                                                                                                              99US-0167623
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/product=
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Les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention
                                                                                                                                                                                                                                                                                                                             WPI; 2001-355945/37..
P-PSDB; AAB99679.
                                                                                                                                                                                                                      (UYMC-) UNIV MCGILL
  WO200138564-A2
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                                                                                                         24 - NOV - 2000;
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                                                                                                                                                              26-NOV-1999;
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                                                                                                                                                                                                                                                                              Rouleau GA,
                                                       31-MAY-2001
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Best Local
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Key

RESULT 9 ABL39690

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"Conserved region 3; this region shows a high degree of conservation between the murine and human desmin gene 5' flanking sequences"
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degree of conservation between the murine and
human desmin gene 5' flanking sequences"
                                            human desmin gene 5' flanking sequences'
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standard_name= "Spl binding motif"
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                                                                                                                                                                                        "Bicoid binding element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                e= "MyoD1 binding element"
..1897
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note= "MyoD1 binding element"
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note= "Krox 20/24 motif"
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note= "Krox 20/24 motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Krox 20/24 motif"
                                                                                                           "CArG motif 1"
                                                                                                                                                    "C/EBP motif"
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/note= "MEF-2 motif"
                                                                                                                                                                                                                                 "PEA3 motif"
                                                                                                                                                                                                                                                                                                                                                                                   note= ."Mt motif"
805..1811
                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Mt motif"
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'note= "M5 motif"
969..1977
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                              1209.:1210
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                             misc_feature
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                                                                   FT
                                                                                                                                                         The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD) also useful for treating the above disorders and other disorders such also useful for treating the above disorders and other disorders such hypoactive sexual desire disorder. The present sequence is SEP consensus DNA sequence found in human, mouse and rat.
                                                                An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as
                      Phillips SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desmin gene; 5' flanking sequence; CArG motif; arterial smooth muscle;
tissue specific promoter; murine; expression construct;
cardiovascular disease; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine desmin gene 5' flanking region, including the promoter region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Conserved region 1; this region shows a high degree of conservation between the murine and human desmin gene 5' flanking sequences"
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Conserved region 2; this region shows a high degree of conservation between the murine and
                                                                                                                                                                                                                                                                                                                                                         Score 16.8; DB 24; Length 2286;
Pred. No. 1.6e+02;
); Mismatches 2; Indels 0:
                      CP,
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                       Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
                      Wayman
                   Wayman CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "CArG motif 2" 973..1209
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223..520
/*tag= a
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note= "HNF-5 motif"
                                                                                                                                Disclosure; Fig 6; lé7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= c
note= "AP-1 motif"
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'note= "NFT motif"
                                                                                                                                                                                                                                                                                                                                                                                                                        431 GCTGGAGGATTCCACTGCCC 450
                  Walsh RT,
                                                                                                                                                                                                                                                                                                                                                                                                          1 GCTGGAGGATTCCTCTGTCC 20
                                                                                                          female sexual arousal disorder -
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ID AAA38443 standard; DNA; 2729 BP.
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                                                                                                                                                                                                                                                                                                                                                         84.0%;
90.0%;
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                Stacey P,
                                        WPI; 2002-155042/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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               Harrow ID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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"N corresponds to a 522 base pair sequence
not reproduced in specification"
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note= "Putative consensus binding site for
transcription factor"
                                                                                                                                                                                                                                                                                                                                                                  '*tag* g
'note* "Putative consensus binding site for
transcription factor"
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note= "Putative consensus binding site for
                                                                                                                                                                                                         'tag= e
abel= Consensus binding site for HNF-5
                                                                                                                           *tag= d
label= Consensus binding site for AP-1
                                                                        label- Consensus binding site for NFI
Consensus binding site for NFI
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sl= Myotube enhancer Mt site
..1826
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label= Krox 20/24 binding site
144..1955
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                                                                                                                                                                                                                                                                                                     abel = CArG-2 box motif
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/label= MyoDl
2612..2618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enhancer
                                                                                                                                                                                                                                                                                                                                                        initiation site. This sequence contains regulatory elements specific to smooth, cardiac and skeletal muscle cells, and includes CArC-like sequences. CArG motifs are elements known to regulate many musclesspecially the alpha actin gene in cardiac and specific genes, especially the alpha actin gene in cardiac and cardiac and cardiac and skeletal muscle. Sequence comparison between the murine and human desmin gene 5' flanking sequences (AAA38443, AAA38444) shows four conserved regions between the two species, one of which is located in the arterial smooth muscle-specific region. Murine desmin 5' flanking region sequences may be used to construct expression cassettes for tissue-specific expression of a gene of interest. The sequence of at least part of 10000 to 4600 (preferably 4006 to 4603) of the mouse cander the expression of a gene of the human desmin gene) is used to target the expression of a gene to cardiac, skeletal, or smooth muscle, and at least part of 5000 gene for the cardiac, skeletal, or smooth muscle, and at least part of 5000 for 6000 (preferably 4006 to 2495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and at least part or -boud to -2400 (preserved)

(AAA38442) of the mouse desmin gene is used to target the expression of a gene to a minimal promoter in an arterial smooth muscle. The expression cassettes, and vectors and eukaryotic cells comprising the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ischaemia, intimal hyperplasia, hypercholestesterolaemia, atherosclerosis and smooth muscle proliferation.
                                                                                                                                                                                                                                                                                                             sequence represents the murine desmin gene promoter, comprising the between nucleotides -3168 to +83 relative to the transcription
                                                                                                                                                                              Novel nucleic acids comprising the 5' flanking region of a desmin gene located useful producing drugs and targeting gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desmin gene; 5' flanking region; promoter; cardiovascular disease; smooth muscle cells; restenosis; ischemia; intimal hyperplasia; atherosclerosis; hypercholesterolemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic animal; gene expression; artery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.8; DB 21; Length 2729;
Pred. No. 1.6e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular diseases. The cardiovascular diseases include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "putative consensus binding site for
transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       smooth muscle cell proliferation; cancer; viral hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2729 BP; 639 A; 708 C; 720 G; 659 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
223..521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aorta; pulmonary artery; mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2571 GCTGCAGGATCCCTCTGTCC 2552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCTGGAGGATTCCTCTGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ93780 standard; DNA; 2730 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse desmin promoter sequence.
                                                                        Li Z, Mericskay M;
                                                                                                                                                                                                                                                          Claim 6; Fig 1; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338..340 /*tag= b
                     (UYPA-) UNIV PARIS VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense; ribozyme;
                                                                                                                           WPI; 2000-306012/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
misc_binding
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                                                                        Paulin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ93780;
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AAZ93780/c
ID AAZ9378
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The desmin gene encodes a cytoskeletal protein constitutive of intermediate filaments which occur in the cytoplasm of most muscular cells. Studies have revealed a complex regulatory mechanism to promote the temporal and tissue-specific expression of the desmin control sequences have been described in the first 1000 bp of the 5' flanking region of the cessin gene. It is thought therefore that the desmin gene promoter cells and this might be beneficial to avoid the potential side effects inherent to a widespread gene expression. The desmin gene 5' flanking region can be used to prepare expression. The desmin gene 5' containing a selected gene for the controllable expression of that gene: Such methods could be used for gene therapy, of cardiovascular atheroscherosis, hypercholesterolemia and smooth muscle cell proliferation), for expression of a therapeutic polypeptide, antisense molecule or ribozyme, e.g. in cases of genetic disorders, antisense molecule or ribozyme, e.g. in cases of genetic disorders, used to produce transgenic animals, useful as models for studying effects of the desmin gene 5' flanking region and heterologous genes the desmin gene 5' flanking region and heterologous expression of effects of the desmin gene 5' flanking region and heterologous genes the desmin gene 5' flanking region and heterologous genes cope expression such avergence of the using attached genes to cardiac, skeletal and smooth muscle cells, cespecially arterial smooth muscle cells, cespecially arterial smooth muscle cells and pulmonary artery.
                                                                                                                                                                                                                                                                                    in gene therapy,
                                                                                                                                                                                                                                                                    New regulatory region from the desmin gene, useful in gene operticularly of cardiovascular disease, provides expression specifically in arterial smooth muscle cells
                                                                                                                                                                                                                                                                                                                                                           Claim 1; Figure 1; 37pp; English
                                                                                                                                                                              Li Z, Mericskay M;
                                                98AU-0087889.
                                                                                       98AU-0087889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            norta and pulmonary artery
                                                                                                                                (UYPA-) UNIV PARIS 7.
                                                                                                                                                                                                                        WPI; 2000-318229/28.
                                           02-OCT-1998;
                                                                                       02-OCT-1998;
  06-APR-2000
                                                                                                                                                                            Paulin D,
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Score 16.8; DB 21; Length 2730; pred. No. 1.6e+02; 0; Mismatches 2; Indels 0; Indels Sequence 2730 BP; 639 A; 715 C; 714 G; 661 T; 1 other; Query Match 84.0%; Best Local Similarity 90.0%; Matches 18; Conservative

ò d

AAZ01425 standard; DNA; 1038602 BP. AAZ01425; RESULT 13 AAZ01425

Complete genome sequence of Chlamydia trachomatis. (first entry) 07-0CT-1999

Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; vehereal lymphogranulomatosis; ss.

Chlamydia trachomatis

WO9928475-A2

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trachonatis. Open reading frames (ORFS) of the genome encode polypeptides AAX36754-Y37949. The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microoraganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion epidymitis, genital diseases such as nongonococcal uretritis, penumpathy in breast feeding infants; and venereal premumpathy in breast feeding infants; and venereal lymphogramical control of the invention may be of use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1038602 BP; 304265 A; 214645 C; 214259 G; 305001 T; 432 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.4; DB 20; Length 1038602;
Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents the complete genome of Chlamydia
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                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 373-656; 1755pp; English.
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                                                                                                       98US-0107077.
97FR-0015041.
97FR-0016034.
                                                       98WO-IB01939.
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94.4%;
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                                                                                                                                                                                                                                                                                                                            WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                    (GEST ) GENSET
                                                     27-NOV-1998;
                                                                                                                                28-NOV-1997;
17-DEC-1997;
                                                                                                          04-NOV-1998;
10-JUN-1999
                                                                                                                                                                                                                                                                         Griffals R;
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RESULT 14 AAC16982/c ID AAC16982 standard; cDNA; 245 BP. AAC16982;

Gaps

; 0

Human secreted protein 5' EST, SEQ ID NO: 21057. 06-OCT-2000 (first entry)

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss. Human; 5' EST; expressed Homo sapiens

3P1033401-A2, 06-SEP-2000.

21-FEB-2000; 2000EP-0200610. 99US-0122487 26-FEB-1999;

Duclert A, Dumas Milne Edwards J, (GEST) GENSET

Giordano

WPI; 2000-500381/45.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for

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990S-0134219.
990S-0134219.
990S-0134370.
990S-0134768.
990S-0135124.
                                                                                                                                                                           99US-0135353.
99US-0135629.
99US-0136021.
99US-0132487.
99US-0132863.
99US-0134256.
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99US-01367
99US-01372
99US-01375
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99US-01377
99US-01385
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99US-01394
99US-01394
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99US-0139
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99US-01
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                                                                                                          4-MAY-1
                                                                                                                                            9-MAY-1
                                                                                                                                                                                                                                 - MAY -
                                                                                                                                                                                                4 - MAY -
                                                                                  The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oilgo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
     obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 21; Length 245;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 23888.
                                                                                                                                                                                                                                                                                                                                                      Sequence 245 BP; 61 A; 67 C; 52 G; 65 T; 0 other;
                                                       Claim 1; SEQ ID 21057; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                     expression and secretion vectors,
                                                                                                                                                                                                                                                                                                                                                                                           80.0
100.08; Pi
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99US-0126264.
99US-0126785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GGAGGATTCCTCTGTC 19
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99US-0123548
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                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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05-MAY-1999;
06-MAY-1999;
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29-MAR-1999
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AAC39240
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PR 22-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 27-JUL-1999; 99US-0145218.
PR 27-JUL-1999; 99US-0145218.
PR 27-JUL-1999; 99US-0145318.
PR 02-MG-1999; 99US-0145318.
PR 02-MG-1999; 99US-0145318.
PR 02-MG-1999; 99US-0147302.
PR 02-MG-1999; 99US-0147302.
PR 03-MG-1999; 99US-0147302.
PR 13-MG-1999; 99US-0147302.
PR 13-MG-1999; 99US-014972.
PR 13-MG-1999; 99US-014972.
PR 13-MG-1999; 99US-014972.
PR 13-MG-1999; 99US-014972.
PR 23-MG-1999; 99US-015972.
PR 23-MG
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					,									Length 1537;	Indels
•									•					DB 21; 3.7e+02;	es 0;
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99US-0160815.	990S-0160980	9US-01609R1	99US-0160989	99US-0161404	99US-0161405	99US-0161406	99US-0161359.	161360	161361.	9US-0161920.	9US-0161992	9US-0161993	9US-0162142.	08; .08;	ive. 0;
99US-)-Sn66	-Sn66	3-SD66	0-S066	0-SD66	0-SD66	0-SD66	99US-0161360	99us-016136	0-S066	0-S066	0-SD66	0-S066		Conservative
21-OCT-1999;	22-OCT-1999;	2-OCT-1999;	2-OCT-1999;	5-OCT-1999;	-OCT-1999;	-OCT-1999;	-OCT-1999;	-OCT-1999;	26-OCT-1999;	28-OCT-1999;	-OCT-1999;	8-OCT-1999;	-OCT-1999;	atch cal Simi	16;
PR 21	PR 22	PR 22	. PR 22	PR 25	PR 25	. PR 25	PR 26	PR 26	PR 26	PR 28	PR 28	PR. 28	PR 29-C	Query Best	Matches
			•												

Search completed: July 8, 2003, 02:18:53 Job time: 128.659 secs

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0; Gaps

us-09-647-780a-7.rni

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 01:24:03; Search time 27.6098 Seconds

(without alignments)
222.151 Million cell updates/sec

Title: US-09-647-780A-7

Perfect score: 20
Sequence: 1 gctggaggattcctctgtcc 20
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724
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Database: Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4496 75996 75996 7610 7610 7610 7610 7610 7610 7610 761		ns/	ethong Pamela METHODS PROTEIN-	5-006 WUMBER: US/09/149 : 1998-09-09 NUMBER: 60/064,05 : 1997-11-03		a, c,	imilarity 89.5%; conservative GCTGGAGGATTCCTCTGT GCTGGAGGATTCCTCTGT GCTGGAGGATTGCTCTGT	
23,23,000		ication 74 ION:	Welhong t, Pamela N: METHOI	, z, z,	chia	base n=a, base	y rvat ATT(cation US 5 10N: 10N: 11ON: MU TION: MU ENCES: 5 ADDRESS: SUGHRUE,
000000000000000000		icat 74 ION:	f: Hsing, We f: Taggart, INVENTION: INVENTION:	PERENCE: 9366 APPLICATION FILING DATE: APPLICATION FILING DATE: FILING		modified_ 58 ORMATION: modified_ 105 ORMATION:	Similarity 7; Conser GCTGGAGGA	115-1 1, Applicatio 5, 5958685 INFORMATION: ANT: Ebina, OF SEQUENCES PONDENCE ADDR
722777777777777777777777777777777777777		5 Applica 265174 RMATION Menzel	HSING, W Taggart, INVENTION:	CATIO CATIO CATIO CATIO IG DAT	acentin 33 Escheri	EE: TEX: modified TON: 58 INFORMATION: EE: TEX: modified CON: 105 ON: 105 1NFORMATION:	tila Co TIGG	PD11 8868 WAT ED TVEN SEQU
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	•	T 1 -149. uence ent PERAL	EECC	FILE RECORRENT CURRENT CURRENT EARLIER EARLIER NUMBER	SOFTWARE: EQ ID NO 5 LENGTH: 2 TYPE: DNA ORGANISM:	FEATURE: NAME/KEY: LOCATION: OTHER INF(FEATURE: NAME/KEY: LOCATION: OTHER INF(y M. Loc hes.	ULT 2 08-737-715-1 acquence 1, Applicati atent No. 5958685 GENERAL INFORMATION: APPLICANT: EDina, APPLICANT: EDina, TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD ADDRESSEE: SUGH
2000 000 000 000 000 000 000 000 000 00		SULT 1 -09-149-922-5 Sequence 5, Applicat Patent No. 6265174 GENERAL INFORMATION: APPLICANT: MADELICANT: MADELICANT:	APPLICANT: APPLICANT: TITLE OF I	FILE RE CURRENT CURRENT EARLIER EARLIER NUMBER	SEQ ID LENGT TYPE:	0	Ouery Match Best Local Matches 1	SSULT 2 7:08-737-715 Sequence 1, Patent No. GENERAL IN APPLICAN UUMBER O CORRESPO ADDRES
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GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001158
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Eastman; Alan R.
APPLICANT: Krieser, Ronald J.
TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND CDNAS
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        DB 4; Length 36741;
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                                              Indels
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Pred. No. 1.2e+02;
0; Mismatches 3;
        Score 15.8; Di
Pred. No. 80;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/800,960
CURRENT FILING DATE: 2001-02-00
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.8;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/574,942
CURRENT FILLING DATE: 2000-05-10
PRIOR ADDITOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/541,840
                                                                                                        10280 GCTGGAGTCTTCCTCTGTC 10298
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                                                                                                                                                                                                                  Sequence 3, Application US/09800960
Patent No. 6387677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09574942
Patent No. 6358723
                                                                                  1 GCTGGAGGATTCCTCTGTC 19
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    y Match 79.0%;
Local Similarity 89.5%;
hes 17; Conservative
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89.5%;
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Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserva
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SOFTWARE: Patentin V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 62804
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        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                            Matches
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APPLICANT: KELLEMS, RODNEY E.
APPLICANT: DATTA, SURJIT K.
APPLICANT: BLACKBURN, MICHAEL R.
TITLE OF INVENTION: ADENOSINE DEAMINASE DEFICIENT TRANSGENIC MICE AND
TITLE OF INVENTION: METHODS FOR THE USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4149;
                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
2100 Pennsylvania Avenue, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.8;
Pred: No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/301,665
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 134827/1995
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              APPLICATION NUMBER: US/08/737,715
FILING DATE: 12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 60/083,408
EARLIER FILING DATE: 1998-04-29
EARLIER APPLICATION NUMBER: 60/083,370
EARLIER FILING DATE: 1998-04-28
                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09301665 Patent No. 6207876
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                              NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4149 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                            (202)293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                            OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-301-665-3
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                  Washington
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USA
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RESULT

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TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Ave., NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U1-08/08/007,999B
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
FILING DATE: 20-APR-1992
FILING DATE: 20-APR-1992
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: U5 07/930,022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.2; DB 2;
Pred. No. 1.2e+02;
0; Mismatches 3
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06-AUG-1996
                                                                                                                                                                                                                                                                                                                                                            NUMBER: US 07/930,022
17-AUG-1992
                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1630 GCTGGAGGCTACCTTTGTCC 1611
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Tanzi, Rudolph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202)371-2571
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202)371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2358 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Solomon, Frank
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Best Local Similarity 85.0%
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Bupp, Keith
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APPLICATION NUMBER:
   COMPUTER READABLE FORM:
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APPLICANT: Wasco,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-689-276A-2/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-007-999B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                APPLICANT: Tanzi, Rudolph E. APPLICANT: Kovacs, Doza M. TITLE OF INVENTION: Methods For Modulating Transcription TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMYLOID PRECURSOR-LIKE PROTEIN AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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00 New York Ave., NW
                                                                                                                                                                                                                                                                                      SEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.: 1100 New York Ave., NW, Suite 600 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.2; DE
Pred. No. 1.2e<sup>4</sup>
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/339,152A FILING DATE: 10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1630 GCTGGAGGCTACCTTTGTCC 1611
Sequence 15, Application US/08339152A Patent No. 5643726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08007999B Patent No. 5851787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wasco, Wilma
APPLICANT: Bupp, Keith
MapplicANT: Margaret
APPLICANT: Tanzi, Rudolph
APPLICANT: Solomon, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCTGGAGGATTCCTCTGTCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 2358 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 88..2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-339-152A-15
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                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                STATE:
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Gaps

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PAJUSOLA, KALTI
ENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
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APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                  ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
SITX: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         venson, McKeown, Edwards & Lenahan, P.L.L.C.
G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%; Score 14.8; DB 2; 11arity 88.9%; Pred. No. 1.9e+02; Conservative 0; Mismatches 2.
                                                                                                                              DNA CODING THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: EVANS, Joseph D
REGISTRATION UNDBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR SPELICATION 233.
PRIOR APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08851896
Patent No. 6331301
GENERAL INFORMATION:
                                 Ulf
Birgitta
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERIKSSON, Ulf
OLOFSSON, Birgitta
ALITALO, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCTGGAGGATTCCTCTGT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: DNA (genomic)
US-08-609-443B-17
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO:
                                                                                                          TITLE OF INVENTION: VARY TITLE OF INVENTION: DAY NUMBER OF SEQUENCES: 57 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                  COUNTRY: US
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                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                            APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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Batent No. 637625

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCO
FILE REFERENCE: CLOO1063

CURRENT APPLICATION NUMBER: US/09/754,250

CURRENT APPLICATION NUMBER: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.2; DB 2;
Pred. No. 1.2e+02;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.2; DB 4;
Pred. No. 1.6e+02;
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
RAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 29,021
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32099 GCTGGGGGAGTCTTCTGTCC 32118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCTGGAGGATTCCTCTGTCC 20
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; OTHER INFORMATION: n = A,T,C or US-09-754-250-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                         TELEPHONE: (202)371-2571
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                             LENGTH: 2358 base pairs
                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88..2046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA FEATURE:
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NAME/KEY: ; LOCATION: US-08-689-276A-2

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Gaps ö

ORGANISM: Human

SEQ ID NO 3 TYPE: DNA LENGTH:

US-08-609-443B-17/C

RESULT 10

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E: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CD3 Specific Recombinant Antibody NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/116,247
                                                                                                                                                                                                                                                                                                                                                                                                                 , DB 2;
1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08116247
Patent No. 5929212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jolliffe, Linda K.
Zivin, Robert A.
Adair, John R.
Athwal, Diljeet S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 GCTGGAGGATTTGTCTGT 311
                                                                REFERENCE DOCKET NUMBER: CATELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (215) 568-310(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-OCT-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           1570 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.95
Matches 16; Conservative
                                   NAME: Trujillo, Doreen
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEOUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 0
                                                                                                                                                                                              nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: One Liberuy
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                         41..1444
                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                  TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                         LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-303-569B-6
                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%; Score 14.8; DB 4; 88.9%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Entage, John S.
ITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                  SUSPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,896
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, URRENT APPLICATION DATA:
                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08303569B Patent No. 5859205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            920 GCTGAAGGATGCCTCTGT 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTGGAGGATTCCTCTGT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       26,269
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: EVANS, Joseph D
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 88.9
Matches 16; Conservative
                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
             COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
STATE:
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APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS: ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 GURRENT APPLICATION DATA: US/08/272,255 FILING DATE: 08-JUJ-1994 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: July 8, 2003, 09:31:02 Job time : 29.6598 secs
                                                                                                                                                Cashmore, Anthony R. Ahmad, Margaret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2025 GCTGGAAGATTCCGCTGT 2008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTGGAGGATTCCTCTGT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
NFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                               19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-272-255-5
                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Improved methods for transforming Phaffia and recombinant DNA for use therein
                                                                                                                                                DB 2; Length 1570; 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.8; DB 4; Length 1882; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,725
FILING DATE: 23-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                Score 14,8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Morrison & Foerster 11p
: 2000 Pennsylvania Avenue, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 82.1212
; OTHER INFORMATION: /product= "PRCITE"
US-09-091-725-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 95203620.0 FILING DATE: 22-DEC-1995
APPLICATION NUMBER: EP 96200943.7 FILING DATE: 11-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         US-09-091-725-14

; Sequence 14, Application US/09091725

; Patent No. 6329141

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                              328 GCTGGAGGATTTGTCTGT 311
                                                                                                                                                                                                                       1 GCTGGAGGATTCCTCTGT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Phaffia rhodozyma
                                                                                                                                          74.0%;
ilarity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1882 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: E. Victor Donahue
REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.99
Matches 16; Conservative
SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIOR APPLICATION DATA:
                                                              CDS
41..1444
                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20006-1888
  STRANDEDNESS:
TOPOLOGY: lin
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                , LOCATION:
US-08-116-247-6
                                                              NAME/KEY:
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Length 2458;

Score 14.8; DB 1; Pred. No. 1.9e+02; 0; Mismatches 2

74.0%; 88.9%;

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July 8, 2003, 19:09:54; Search time 115.512 Seconds (without alignments) 273.390 Million cell updates/sec
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5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                           1105431 seqs, 789497651 residues
 GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                        Title:
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Sequence:
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./cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq na/US08_NEW_PUB.seq na/US07_PUBCOMB.seq pna/US10_NEW_PUB pna/US10_PUBCOMB pubpna/US60_NEW_PUB 1a/US09_NEW_PUB ptodata/2

Published_Applications_NA:

Database :

/cgn2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Sequence 46, Appl	Sequence 1604, Ap	Sequence 581, App	Sequence 473, App	Sequence 670, App	Sequence 796, App	Sequence 13156, A	Sequence 3834, Ap	Sequence 6439, Ap	Sequence 21, Appl	Sequence 22, Appl	Sequence 1246, Ap	Sequence 3668, Ap	Sequence 367, App	Sequence 12, Appl	Sequence 3, Appl1	Sequence 3, Appli	Sequence 20, Appl	Sequence 7, Appli
	QI	US-10-108-605-46	US-09-917-800A-1604	US-09-815-242-581	US-09-815-242-473	US-09-815-242-670	US-09-815-242-796	US-09-864-761-13156	US-09-815-242-3834	US-09-815-242-6439	US-09-798-889-21	US-09-874-132-22	US-09-954-456-1246	US-09-880-107-3668	US-09-070-927A-367	US-09-782-378A-12	US-10-096-960-3	US-09-822-871-3	US-09-771-208-20	US-10-138-505-7
	BB	σ	70	10	10	10	10	10	10	10	σ	10	10	10	10	10	12	6	σ	6
	Query Match Length DB	1323	6822	306	311	311	311	533	639	969	1727	1901	5180	5180	14557	36741	62804	254366	659158	409
æP	Query	87.0	85.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	77.0
	Score	17.4	17	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.4
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Sequence 29, Appl	Sequence 8, Appli	Sequence 25, Appl	Sequence 12621, A	Sequence 531, App	Sequence 7795, Ap	Sequence 5313, Ap	Seguence 2561, Ap	Sequence 141, App	Sequence 1164, Ap	Sequence 1, Appli	Sequence 23, Appl	Sequence 23, Appl	Seguence 21, Appl	Seguence 21, Appl	Seguence 1448, Ap	Sequence 75, Appl	Sequence 63, Appl	Sequence 659, App	Sequence 1, Appli	Sequence 182, App	Sequence 15, Appl	Sequence 79, Appl	Sequence 67, Appl.	Sequence 3, Appl1	Sequence 3, Appli
US-10-138-505-29	US-10-207-655-8	US-10-138-505-25	US-10-198-846-12621	US-10-044-090-531	US-09-960-352-7795	US-09-983-965-5313	US-09-974-300-2561	US-10-023-282-141	US-10-156-761-1164	US-09-949-434-1	US-09-991-053-23	US-09-957-187-23	US-09-991-053-21	US-09-957-187-21	US-09-917-800A-1448	US-09-808-602-75	US-09-800-198-63	US-09-938-842A-659	US-08-915-048A-1	US-09-925-302-182	US-09-798-889-15	US-09-808-602-79	US-09-800-198-67	US-10-094-989-3	US-09-822-246-3
6	6	6	6	12	10	10	10	9	σ	10	6	6	σ	δ	10	σ	σ	ڼ	œ	10	σ	σ	6	12	10
819	825	828	2473	6633	428	429	550	721	789	1224	1952	1952	2010	2010	2226	.2496	2496	2589	3363	3517	3692	8409	8409	111282	197997
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77	77	77	77	77	76	76	76	76	76	76	76	76	76	76	7	76	7	76	7	7	7	7	76	7	76
15.4	15.4	15.4	15.4	15.4	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15:2	15.2
20	21	22	23	24	25	56	27	28	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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                                                                                                             VLICANT: Kamdar, Kim
TLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DRC
TLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.4;
                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/108,605
                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/761,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1604, Application US/09917800A
Patent No. US20020119462A1
Application US/10108605
                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-108-605-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              686 GCTGGAGGATTCCTCTATC 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTGGAGGATTCCTCTGTC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.0%;
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                             2001-01-16
                                                                           Stam, Lynn
Bachmann, Jane
                                                         PPLICANT: Broadus, Julie
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver.
                                                                                                                                                                      FILE REFERENCE: 31133B
                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-917-800A-1604
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 46
LENGTH: 1323
                                                                                               PPLICANT:
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us-09-647-780a-7.rnpb

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Gaps
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                                                                                                                                                                                                                                                             Length 306;
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                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION: Identification of Essential Genes in ITLE OF INVENTION: Prokaryotes
ILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                             Score 15.8; DB 10;
Pred. No. 1.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
..2e+02;
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Pred. No. 1.2e
0; Mismatches
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DAME: 2000-12-22
PRIOR PELLING DAME: 2001-02-9,308
PRIOR FILING DAME: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASESEQ for Windows Version 4.0
LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR FILING DATE: 2000-05-23
DR APPLICATION NUMBER: 60/207,727
DR FILING DATE: 2000-05-26
DR APPLICATION NUMBER: 60/242,578
DR FILING DATE: 2000-10-23
DR APPLICATION NUMBER: 60/253,625
DR FILING DATE: 2000-11-27
DR FILING DATE: 2000-11-27
DR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 473, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-815-242-670/c
; Sequence 670, Application US/09815242
                                                                                                                                                                                                                                                                                                                                                     1 GCTGGAGGATTCCTCTGTC 19
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                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-581
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Zyskind, Judith W.
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ilarity 89.5%;
Conservative
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Trawick, John D.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels
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LE OF INVENTION: Prokaryotes
                                                        PPLICANT: Gene Logic, Inc.
ITLE OF INVENTION: Molecular Toxicology Modeling
                                                                                               FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-01-21
                                                                                                                                                                  : US 60/222,040
                                                                                                                                                                                     FILING DATE: 2000-07-31
APPLICATION NUMBER: US 60/222,880
                                                                                                                                                                                                                           FILING DATE: 2000-11-02
APPLICATION NUMBER: US 60/290,029
                                                                                                                                                                                                                                                                  FILING DATE: 2001-05-11
APPLICATION NUMBER: US 60/290,645
                                                                                                                                                                                                                                                                                                                      LING DATE: 2001-05-15
PLICATION NUMBER: US 60/292,336
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APPLICATION NUMBER: US 60/295,798
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-06-06
APPLICATION NUMBER: US 60/297,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-06-13
APPLICATION NUMBER: US 60/298,884
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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PPLICATION NUMBER: 60/242,578
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ILE REFERENCE: ELITRA.011A
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APPLICATION NUMBER: US 6
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ORGANISM: Rattus norvegicus
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                                                                                                                                                                     IOR APPLICATION NUMBER
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Gaps

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ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL.
ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
ILE REFERENCE: Acomica-X-1
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                                                                                                                                                                                                                                                                                                                   Length 311;
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.2e+02;
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Pred. No. 1.2e+
0; Mismatches
                 PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DAFE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 796
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URRENT APPLICATION NUMBER: US/09/864,761
WINTERNT FILING DATE: 2001-05-23
RIOR APPLICATION NUMBER: US 60/180,312
RIOR FILING DATE: 2000-02-04
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CLING DATE: 2001-01-30
PPLICATION NUMBER: PCT/USO1/00665
CLING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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PLICATION NUMBER: PCT/US01/00667
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PPLICATION NUMBER: PCT/US01/00664
LING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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PLICATION NUMBER: US 60/236;359
LING DATE: 2000-09-27
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PPLICATION NUMBER: US 09/632,366
LING DATE: 2000-08-03
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecalis US-09-815-242-796
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Pred. No: 1.2e+02;
0; Mismatches 2; Indels 0
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                                                                                                                                                                                                                                            ITLE OF INVENTION: Identification of Essential Genes in ITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/242,578
PRIOR PLICATION NUMBER: 60/242,578
PRIOR PLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 670
LENGTH: 311
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CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Enterococcus faecalis US-09-815-242-670
                                                                                                                                              Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Zyskind, Judith W.
Wall, Daniel
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US20020061569A1
                                                                                                                       Wall, Daniel
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CALUR APPLICATION NUMBER: 60/077,687

CALUR APPLICATION NUMBER: 60/077,687

PRIOR FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 185

SOFTWARE: Patentin Ver. 2.0

LENGTH.
                                                                                                                                                                                                                        TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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TITLE OF INVENTION: 31 Human secreted proteins
FILE REFERENCE: P2026P1
CURRENT APPLICATION NUMBER: US/09/798,889
CURRENT FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
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SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 6439
LENGTH: 696
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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Publication No. US20030004324A1
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                                                                                                                                    Trawick, John D.
Carr, Grant J.
Tamamoto, Robert T.
                                                                                           yskind, Judith W. all, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-05-26
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Matches 17; Conservative
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US-09-815-242-6439
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LENGTH: 1727
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels 0
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                                                                                                                                                                                                                                                                                                                Indels
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ITLE OF INVENTION: Identification of Essential Genes in
ITLE OF INVENTION: Prokaryotes
ILE REFERENCE: ELITRA.011A
                                                                                                                                        OTHER INFORMATION: MAP TO AC021401.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 0.45
US-09-864-761-13156
                                                                                                                                                                                                                                                                3; bc
1.2e+02;
2;
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13156
LENGTH: 533
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Pest Local Similarity 89.5%; Pred. No. 1.
Matches 17; Conservative 0; Mismatche
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CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3834, Application US/09815242
Satent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-815-242-6439; Sequence 6439, Application US/09815242; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRENT FILING DATE: 2001-03-21
TOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIOR APPLICATION NUMBER: 60/253,625
RIOR FILING DATE: 2000-11-27
RIOR APPLICATION NUMBER: 60/257,931
RIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIOR APPLICATION NUMBER: 60/269,308 RIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                            278 GCTGGAGGATTCCACAGTC 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rawick, John D.
arr, Grant J.
amamoto, Robert T.
                                                                                                                                                                                                                                                       Ouery Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLICANT: Haselbeck, Robert
                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-815-242-3834
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Gaps

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Length 696; Indels

Score 15.8; DB 10; Pred. No. 1.2e+02; 0; Mismatches 2;

79.0%; 89.5%;

DATE: 1999-09-09
APPLICATION NUMBER: 60/077,714
DATE: 1998-03-12
APPLICATION NUMBER: 60/077,686
DATE: 1998-03-12

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TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptic
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                                                                                                                                                                                                                                                                                                                                                                 Length 5180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gene Logic, Inc. FITLE OF INVENTION: Gene Expression Profiles in Liver Cancer. ILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 1.1e+02;
0; Mismatches 2;
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14
                                                         PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/237,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 367, Application US/09070927A
Setent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3668, Application US/09880107
Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .195 GCTGGAGAATTGCTCTGTC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 GCTGGAGAATTGCTCTGTC 213
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Scherf, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-10-02
                                     FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.
SEQ ID NO 3668
LENGTH: 5180
                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                         US-09-954-456-1246
                                                                                                                                                                                                                                    SEQ ID NO 1246
LENGTH: 5180
                                                                                                                                                                                                                SOFTWARE:
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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/09874132
Patent No. US20020037555A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHEN, HOMAN
TITLE OF INVENTION: HUMAN GLUCOSE-6-PHOSPHATASE MOLECULES AND USES THEREOF
FILE REFERENCE: 10147-3301
CURRENT APPLICATION NUMBER: US/09/874,132
CURRENT FILING DATE: 2001-06-04
PRIOR FILING DATE: 2000-06-02
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1.1e+02;
2;
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Pred. No. 1.1e+02;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URRENT APPLICATION NUMBER: US/09/954,456
URRENT FILING DATE: 2001-09-18
RIOR APPLICATION NUMBER: US/60/233,617
                                                                                                                                                                                                          ; OTHER INFORMATIÓN: n equals a,t,g, or c
US-09-798-889-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICATION NUMBER: US/60/234,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION NUMBER: US/60/234,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ION NUMBER: US/60/235,134
                                                                                                                            LOCATION: (1047)
OTHER INFORMATION: n equals a,t,g, or
                                                                                    OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1246, Application US/09954456 Patent No. US20020115057A1
                                                                                                                                                                                                                                                                                                                                                                                                           390 CTGGAGGATTTCTCTGGCC 408
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2:
                                                                                                                                                                                                                                                                            Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILE REFERENCE: 689290-76
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-874-132-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 22
                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                            LOCATION:
                                                                                                          NAME/KEY
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ADDRESSEE: Human Genome Sciences, Inc.
STREET: 94/0 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: UGSA
ZIP: 20850
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
OMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
COMPUTER: HP Vectra 1809/00/0, 927A
FILING DATE: 04-May-2000
CLASSIFICATION NUMBER: 60/046,655
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/046,009
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY-AGENT INFORMATION:
NAME: Kenley K. HOOSVET
REGISTRATION NUMBER: PB369
FELCOMMUNICATION INFORMATION:
TELEPENDER: (301) 309-812
INFORMATION FOR SEQ ID NO: 367:
SEQUENCE CHARACTERISTICS:
LENGTH: 14557 base pairs
TOPOLOGY: Innear
SEQUENCE CHRACTERISTICS:
LENGTH: 14557 base pairs
TOPOLOGY: Innear
SEQUENCE DESCRIPTION: SEQ ID NO: 367:
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Ouery Match

Query Match

Best Local Similarity 89.5%; Pred. No. 1e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gal

Oy 1 GCTGGAGGATTCCTCTGTC 19

Db 3202 GCTGGACGATTCATCTGTC 3184
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RESULT 15

US-09-782-378A-12

Sequence 12, Application US/09782378A

PAPLICAWT US20020102731A1

GENERAL INFORMATION:
APPLICAMT: Bahou, Wadie
APPLICAMT: Bahou, Wadie
APPLICAMT: Gnatenko, Dmitri
ITLE OF INVENTION: Adenoviral Vectors
FILE REPERENCE: STONYB-04970

CURRENT APPLICATION NUMBER: US/09/782,378A

CURRENT APPLICATION NUMBER: G0/237,747

PRIOR APPLICATION NUMBER: G0/237,747

PRIOR PILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Version 3.0

SEQ ID NO 1: SEQ ID NOS: 27

CORGANISM: Homo sapiens

US-09-782-378A-12
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Gaps

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Indels

DB 10; Length 36741;

Score 15.8; DB Pred. No. 95; 0; Mismatches

Query Match 79.0%; Best Local Similarity 89.5%; Matches 17; Conservative

Search completed: July 9, 2003, 02:21:52 Job time: 116:562 secs

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July 8, 2003, 00:47:28 ; Search time 1013.95 Seconds (without alignments) 319.453 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                        32308132
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                16154066 seqs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM nucleic - nucleic search, using sw model
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1 gctggaggattcctctgtcc 20
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

esuit No.	Score	Query Match	Query Match Length DB	DB	ΩI	Description
:						
-	18.4	92.0		14	BQ303884	BQ303884 PM1-BT075
7	18.4	92.0	793	17	BH486917	BH486917 BOGOC41TF
m	18	90.0		17	AZ379227	AZ379227 1M0134015
4	17.4	87.0		17	AZ567376	AZ567376 234PvA05
'n	17.4	87.0		17	AZ567427	AZ567427 234PvF01
9	17.4	87.0	448	17	AQ783671	AQ783671 HS 3098 B

7780 BOGNB38TT 3309 BOGTG10T1 1153 BOHBY07TT 1851 BOWMT65TT 1851 BOGKW15TT 1051 BOMEW59TT 5014 BOHEW59T 5014 BOHEW59T 5012 ROH-HT09 372 AV027372	BF840278 RC4-HT098 A1710426 UI-R-AG1- BF355285 RC0-HT085 A2499695 IM0337E10 A4437457 v004903.s AW238059 xp15h02.x BF929991 ILI-NT019 BF5831 CTT-HSP-200 AL630827 AL645117 ms88801.v	0 HS_200 vy05d10 8 UI-R-B 4 IMO056 ms88d01 77 231560 CIT-HSP-	4-NWG N0004
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BH537780 BH488309 BH524153 BH672363 BH501851 BH716051 BH466014 BF840282	BF840276 AI710426 AI710426 AZ49595 AA437457 AW238059 BF929991 BF929991 AL630827 AI645117	AQ224410 AA798032 BF406708 AZ330954 AA174981 BF080527 B64751	10222211021110222110222222222222222222
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ALIGNMENTS

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BQ303884	
LOCUS	BQ303884 273 bp mRNA linear EST 16-MAY-2002
DEFINITION	PM1-BT0759-200700-006-b07 BT0759 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BQ303884
VERSION	BQ303884.1 GI:20821027
KEYWORDS	EST
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 273)
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
	Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
	Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
	Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
	, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
	Simpson, A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed
	sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G.
	Laboratory of Cancer Genetics
	Ludwig Institute for Cancer Research
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
	Brazil
	Tel: +55-11-2704922

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Gaps

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Indels

Pred. No. 2.7e+02;

0; Mismatches

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349 GCTGGAGGATTCCTCTTTCC 368
                                                      1 GCTGGAGGATTCCTCTGTCC 20
   95.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                  19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                          house mouse.
   Similarity
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   Best Local
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                Matches
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                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                        VERSION
                        (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMI&t2=PMI-BT0759-200700-006-b07&t3=2000-07-20&t4=1).
Seq primer: puc 18 forward
High quality sequence start: 146
High quality sequence stop: 273.
                                                                                                                                                                                                                                                /note-"Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 776 - Ludwig Institute for Cancer, Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH486917 793 bp DNA linear GSS 13-DEC-2001
BOGGC41TF BOGO Brassica oleracea genomic clone BOGCC41, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots;
Rosidae, eurosids II, Brassicales, Brassicaceae, Brassica.
                  LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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g BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18.4; DB 14; \ Length 273; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other GSS: BOGGC41TR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medical Center Drive, Rockville, MD 20850, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP
Project. This entry can be seen in the fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="BOGO"
/note="Vector: pHOS1; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Brassica oleracea"
/strain="ro1000DH3"
/db_xref="taxon:3712"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                            1. .273
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0759"
                                                                                                                                                                                                                                                                                                                                                           stringency conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCTGGAGGATTCCTCTGTCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                   92.0%;
llarity 95.0%;
Conservative
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301-838-0208
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Matches 19; Conserv
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Class: shear
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ORIGIN
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AUTHORS
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BH486917
LOCUS
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 [gb]h2129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
The State of Utah
The State of Utah
The State of Utah
Weill? USA
   GSS 02-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and selected for ampicillin resistance. " 61 c 55 g 68 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA
A2379227
211 bp DNA linear GSS 02-OCT-200
1M0134015F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0134015 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 211)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0134 row: 0 column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 211.
Location/Qualifiers
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'clone="UUGC1M0134015"
                                                                                                                                           AZ379227.1 GI:10492927
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DB 17; Length 211;

Score 18;

90.08;

Query Match

Score 18.4; DB 17; Length 793;

92.08;

Query Match

tag projects

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/note="Vector: Landar 2AP II (Stratagene); individual /note="Vector: Landar 2AP II (Stratagene); individual clones excised into phagemid pbluescript; Site_1: EcoR I; Site_2: EcoR I; Genomic DNA was prepared from asynchronous blood stage forms of the Belem line of P. vivax grown in squirrel monkeys. Parasitized erythrocytes were purified from contaminating host leukocytes by filtration of ADP activated blood through acid-washed glass beads and Whatman CFII cellulose columns by gravity filtration. Purified DNA was digested with mung bean nuclease in the presence of 4.5.% formamide at 50cc as described (Galinski, M. et al. 1992. Cell 69.1213-1226; Vernick, K.D. et al. 1988. N.A.R. 16, 6883-6896). Eco RI linkers were added and the constructs ligated into Lambad ZAP II. P. vivax Belem was originally isolated from a patient in Belem, Brazil 1980 by Mercia de Arruda, adapted to Salmiri monkeys, by Jurg Gysin, and maintained since 1983 in
                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                     University of Florida
2015 SW 32rd Avenue, Bldg.1017, Gainesville, FL 32611, USA
eel: 352 392 9700.
Fax: 352 392 9700.
                                                                                                                                                                                      The Plasmodium vivax and P. berghei gene sequence tag Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000) Contact: Dame JB Dept. of Pathobiology, College of Veterinary Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:5855"
/clone_llb="Pv MBN #26/#27 (amplified once)"
/dev_stage="asexual blood forms"
/lab_host="Saimiri bollviensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Plasmodium.vivax"
                                                                                                                                                                                                                                                                                                                                                          Email: damej@mail.vetmed.ufl.edu
                                                                                                                                                1 (bases 1 to 137)
Carlton, J.M.-R. and Dame, J.B.
                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13(-20) forward
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                       malaria parasite P. vivax.
                                            AZ567427.1 GI:13975516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Belem
        sednence.
                                                                                                            Plasmodium vivax
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234PvF01 Pv MBN #26/#27 (amplified once) Plasmodium vivax genomic
                                                                                                                                                                                                             GSS 07-MAY-2001
                                                                                                                                                                                                         A2567376 137 bp DNA linear GSS 07-MAY-200
234PvA05 Pv MBN #26/#27 (amplified once) Plasmodium vivax genomic
                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 137) Carlton, Apricant indemosporing; Flasmodium. Carlton, J.M.-R. and Dame, J.B.
The Plasmodium vivax and P. berghei gene sequence tag projects Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
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                         Gaps
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monkeys by Jurg Gysin, and maintained since 1983 in
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Florida
2015 SW 232 4 Avenue, Bldg 1017, Gainesville, FL 32611, USA
721: 352 392 4704
Fax: 352 392 9704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Belem was originally isolated from a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dept. of Pathobiology; College of Veterinary Medicine
                         Indels
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                       Mismatches
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Seg primer: M13(-20) forward
Class: shotgun.
    Pred. No.
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                                                                                                   170 GCTGGAGGATTCCTCTGT 187
                     ö
                                                               GCTGGAGGATTCCTCTGT 18
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100.08;
Best Local Similarity 100.
Matches 18; Conservative
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A2567376
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Best Local Simi
Matches 18;
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1 (bases 1 to 448)
Mahalras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
                                                                                                                                                                                                                                                                                                   GSS 03-AUG-1999
                                                                                                                                                                                                                                                                                                                         HS_3098_B1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3098 Col=9 Row=H, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primates; Catarrhini; Hominidae; Homo.
Length 137;
                                                       Indels
                                                                                                                                                                                                                                                                                                   linear
ch 87.0%; Score 17.4; DB 17; Similarity 94.7%; Pred. No. 4.4e+02; 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                448 bp
                                                                                                                                          111 CTGGAGGGTTCCTCTGTCC 129
                                                                                                            2 CTGGAGGATTCCTCTGTCC 20
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Eukaryota; Metazoa;
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42 t

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Gaps

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Indels

Length 513;

17;

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BH488309 623 bp DNA linear GSS 13-DEC-2001
BOGTG10TF BOGT Brassica oleracea genomic clone BOGTG10, DNA
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BOHBY07TR BOHB Brassica oleracea genomic clone BOHBY07, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
pHOS1 using BstXI linkers"
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/note="Vector: pHOS1; Site_l: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
13 c 147 g 219 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 623)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.4; DB 17;
Pred. No. 7.4e+02;
                                                                                Score 17.4; DB 1
Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Brassica oleracea
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94.7%; Pred. No. ...
0; Mismatches
                                                                                                                        0; Mismatches
   genomic DNA inserted into
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Class: sheared ends.
Location/Qualifiers
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                                                                                th 87.0%;
| Similarity 94.7%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Chris Town
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Matches 18; Conservative
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Brassica oleracea
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Brassica oleracea
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Best Local Si
Matches 18;
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BH524153
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                           BASE COUNT
ORIGIN
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COMMENT
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BH488309
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BOGNB38TR BOGN Brassica oleracea genomic clone BOGNB38, DNA
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Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea unpublished (2001)
                                                                                                                                                                                         Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BaC end Web Server: http://www.htsc.washington.edu
Plate: 3098 row: H column: 9
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3098 Col=9 Row=H"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Col1 DH10B"
       Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                         scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
                                                                                            High Throughput Sequencing Center
University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.4; DB 17;
Pred. No. 6.6e+02;
                                                                                Contact: Mahairas GG, Wallace JC, Hood L
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/strain="TO1000DH3"
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                                                                                                                                                                                                                                                                                        Class: BAC ends
High quality sequence stop: 448
Location/Qualifiers
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/clone="BOGNB38"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.0%;
ilarity 94.7%;
Conservative
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301-838-0208
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Best Local Similarity
Matches 18; Conserv
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BH537780/c
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KEYWORDS
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AUTHORS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 760)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                       /clone_lib-"BOHB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
128 c 156 g 219 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Bo_2_3 KB"
/note="Vector: pHOS1, Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers" 198 c 173 g 142 t
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 630)
TOWN,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOHBY07TF
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 630;
                                                                                                                                                                                             DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TR
Class: sheared ends.
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Unpublished (2001)
Contact: Chris Town
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Pred. No. 7.5e+02;
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/strain="rol000bH3"
/db_xref="taxon:3712"
/clone="BOMMT65"
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1. 630
/organism="Brassica oleracea"
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/db_xref="taxon:3712"
/clone="BOHBY07"
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                                                                                                                                                                              Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cdtown@tigr.org
DNA is from a doubled
                                                                                                                                                                                                                                                                                                                                                                                                                                     87.0%;
94.7%;
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                                                                                                  Contact: Chris Town
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                                                                                                                                                             Fax: 301-838-0208
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KEYWORDS
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BH716051 804 bp DNA linear GSS 20-FEB-2002
BOMEW59TR BO_2_3_KB Brassica oleracea genomic clone BOMEW59, DNA
                                                                                                                                                                                                                                                   BH501851 GSS 13-DEC-2001
BOGKW15TR BOGK Brassica oleracea genomic clone BOGKW15, DNA
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Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae: eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 804)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                               Brassica oleracea
Sukaryota, Vitidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Bogk"
//octe="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
1 198 c 192 g 141 t
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Length 760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 771)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome Shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOGKW15TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tom Osborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
                                                 Indels
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DNA is from a doubled haploid provided by 'Seq primer: TR
Class: sheared ends.
Location/Qualifiers
Score 17.4; DB 17;
Pred. No. 8e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.4; DB 17;
Pred. No. 8e+02;
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                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGKW15"
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                                                                                                                                         431 GCTGGAGGATTCCTCTTTC 413
                                                                                            GCTGGAGGATTCCTCTGTC 19
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BH501851.1 GI:17709948
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  87.0%;
94.7%;
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94.7%;
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Best Local Similarity 94.77
Matches 18; Conservative
  Ouery Match 87.0
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Brassica oleracea.
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Gaps

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Indels

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 315)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Soldman,G.H., Carvalho,A.F., Matsukuma,A., Balá,G.S., Simpson,D.H., M.J., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Balá,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4st2=RC4-HT0986-291100-011-h02st2=2000-11-29st4=1)
Seq prime: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                     BF840282
RC4-HT0986-291100-011-h02 HT0986 Homo sapiens CDNA, mRNA sequence.
BF840282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
               ed. No. 8.4e+02;
Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 51
High quality sequence stop: 315.
Location/Qualifiers
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/clone_lib="HT0986"
               Pred.
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                              . .
                                                                                                               443 GCTGGAGGATTCCTCTTTC 425
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                                                                          1 GCTGGAGGATTCCTCTGTC 19
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             Similarity 94.7%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tags
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BOHRJ30TR BOHR Brassica oleracea genomic clone BOHRJ30, DNA
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/notes"vector: pHOSI, Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOSI using BstXI linkers"
194 c 179 g 153 t
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/clone_lib="BohR"
/clone_lib="BohR"
/note="Vector: pHOSI; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOSI; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOSI using BstXI linkers"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Traci
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoi
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.4; DB 17; Length 804; Pred. No. 8.1e+02;
                                                                                                                                                                   Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR.
Class: sheared ends.
  Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOMEW59TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
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Unpublished (2001)
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                                                                                                            20850, USA
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    804
    /organism="Brassica oleracea"

                                                                                                        9712 Medical Center Drive, Rockville,
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/clone="BOMEW59"
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/db_xref="taxon:3712"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 GCTGGAGGATTCCTCTTC 254.
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94.7%;
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                                                                 Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: sheared ends.
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                                                                                                                              Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Conservative
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301-838-0208
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BH466014/C
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/note=Torgan: head_neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute.for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                           84.0%; Score 16.8; DB 12;
llarity 90.0%; Pred. No. 1.1e+03;
Conservative .0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 bp
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AV027372/c
LOCUS
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Length 877;

DB 17;

Score 17.4;

87.0%;

Query Match

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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: mammary gland; Vector: pr773D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco Pir; 1st strand cDNA was primed with a Not I - oligo(dT) Primer [5.
                                                                                                                                                                                                                                                                                     Acardici, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kituchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S.; Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV027372 Mus musculus adult C57BL/6J liver Mus musculus cDNA clone 1300008D14, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                  Gukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Vammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 316)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trehalose and its application for the synthesis of full length cop (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="Mus musculus adult C57BL/6J liver"
tissue_type="liver"
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Location/Qualifiers
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                                                                                           AV027372.1 GI:4806982
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Fax: 81-298-36-9098
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Unpublished (1999)
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Ouery Match 84.0%; Score 16.8; DB 9; Length 316; Best Local Similarity 90.0%; Pred. No. 1.1e+03; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps

1 GCTGGAGGATTCCTCTGTCC 20

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Search completed: July 8, 2003, 09:21:21 Job time : 1019.1 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nu	OM nucleic – nucleic search, using sw model	
Run on:	July 8, 2003, 00:45:53.; Search time 209.093 Seconds (without alignments) 2644.537 Million cell updates/sec	
Title: Perfect score: Sequence:	US-09-647-780A-8 19 1 cggggatcacatggtgccg 19	· ·
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched:	2054640 seqs, 14551402878 residues	
Total number of	Total number of hits satisfying chosen parameters: 4109280	
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	AX014708 AX014708 Sequence	AX014701 AX014701 S	AC094732 AC0947	AC121922 AC121922 Mus mu	AC093028 AC093028 HOMO	AP001517 AP001517 Bacil	HSDJ989D7 AL121911 Human	ACUZ61/1 AR206865	AX136894 AX136894	BD006820 · BD006820	AKZU0804 AX136892	AX417395	AX42/614	A08292519 A7292519	AF153086 AF153086	AE0124// AE011745	AC097605 AC097605 Rattus	AC102958 . AC102958 Rattu	AC010241 AC010241	AL355811 . AL355811 Homo	AC069098 AL353671	AC109770 Rattus	AF000501 HOMO AF000501 HOMO AF105393 HOMO	AC084692 HOMO	AC093326 . AC093326 Homo	AC115037 AC115037 Mus m	AP003002 AP003002	0 BC024640 · BC024640	0 GPINCPIB2 D37972 Guinea	0 GPINCP1A1 D37971 av069786 av06978	AT00278 AF000298 AC108358		ALIGNMENTS			DNA linear PAT 07-SEP-	linear PAT 07-SEP
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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Patent: WO 9953077-A B 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
LOCATION/Qualifiers
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Patent: WO 9953077-A 10 21-0CT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS
CLAUDE (FR); OUIMET TANNA (FR); ROSE CHRISTIANE (FR); BONHOWME
MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
LOCATION/QUALIFIES
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Schwartz,J.C., Gros,C., Ouimet,T., Rose,C., Bonhomme,M.C. and
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Schwartz, J.C., Gros, C., Oulmet, T., Rose, C., Bonhomme, M.C.
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                                                                                              /organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligonucleotide"
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Pred. No. 5.7;
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Bank, J., Bouck, J., Benton, J., Brimege, K., Blankenburg, K., Bonnin, D., Bouck, J., Burkett, C., Burell, K. L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, Dav, Delaney, K.R., Delagado, O., Davy-Carroll, L., Dederich, Dav, Delaney, K.R., Delagado, O., Dugan, Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Falls, T., Ferraquto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Ganer, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
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Rattus norvegicus clone CH230-516, *** SEQUENCING IN PROGRESS ***, 56 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                            CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME
MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
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                                                                                                                                                                                                                                                                                                                                                                           /note="unnamed protein product"
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inhibitors useful in therapy
Patent: WO 9953077-A 1 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWART2
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NOTE: This is a "working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Contact: hgsc-help@bcm.tmc.edu
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
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in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 Contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins, a novel gene and the 3' part of the gene for a novel protein similar to API1 and API2 (apoptosis inhibitor 1 and 2 (MIHB, MIHC, IAPI, IAP2)). Contains ESTS, a GSS and six putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence from clone LA16-316G12 on chromosome 16 confor C2 domain protein KIAA0734, the gene for a novel unlar to predicted yeast, worm and archae-bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; API1; API2; CpG Island; IAP1; IAP2; KIAA0734; MIHB; MIHC
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              FATURES
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KPGDGVEFFAHMRLMLKKGEGRQGLPCLEVPLRSGSPAPPEPVDPSLGLRALAPEEVE
                                                                                                               Oxford
                             part of a clone contig from the tip of the short arm of chromosome 16 spanning 2Mb of pl3.3 (Higgs D.R., Flint J., Daniels R., MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxford (unpublished)), and 1s from the Los Alamos, flow sorted human Chromosome 16 libraries constructed by Norman Doggett (unpublished), VECTOR: SCOs.1

[IMPORTANT: This sequence is not the entire insert of clone LA16-116G12 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Em: R24790 Em: R85179 Em: AA293357 Em: AA078749 Em: A1666810 Em: A1086907 Em: H15802 Em: AA293357 Em: H46334 Em: D81844 Em: A1301780 Em: A65522 Em: AA28001 Em: R60906 Em: AA716721 Em: A130104 Em: AA716524 Em: A60906 Em: AA716721 Em: R01878 Em: A1111375 Em: AA481839 Em: W01878 Em: A1146703 Em: AA627545 Em: AA079823 Em: AA482458 Em: AA682952 Em: A1593336 Em: AA5837389 Em: AA682952 Em: A158964 Em: A1564977
                                                                                                                                                                                                                                                                                                                 sections only once, except for a 100 base overlap.
The true left end of clone LA16-316612 is at 1 in this sequence.
The true left end of clone LA16-399E4 is at 37377 in this sequence.
The true right end of clone LA16-358B7 is at 21289 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7667 .7674,8993 .9052,9200 .9266,9365 .9560,9893 .91

10057 .10134,10252 .10354,10598 .10705,10790 .10885,

10984 .11087 .11464 .11584,12098 .12217,12298 .13288,

12540 .12596,12672 .12769,12869 .12217,12298 .13388,

1320 .13443,13818 .13961,14057 .14149,14241 .14432,

4513 .14581,14676 .14755,14918 .15026,15369 .15440,

5616 .15696,15772 .15892,15965 .16088,16167 .16372,
LA16-316G12 is
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: ESTs: Em:T77480 Em:H18551 Em:F13300 Em:R61025
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1-"CAB56182.1"
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[4581,14676, .14755,14918, .15026,15369, .1
[5696,15772, .15892,15965, .16088,16167, .1
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loin(1727, 1820,6611, .67
1567, .7674,8993, .9052,92
10057, .10134,10252, .1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="LA16-316G12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="CpG island"
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187. .2805
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RSSASRVQGHCHLVLKLITTQRDTAMSQRGRSGFLSHLLLLSHLLRLEHSAEEPNSSS
                    WRGELSTPAATĮLCLHGAQSNLSPLQLAVLHWQVSSRHHQTCTLDYSYLLGLLEDMQA
                                          HWEEAPSLPQEÖEESLADSLSAFSEFGLQLLRQLRDYFPATNSTAVHRLELLLKCLGK
LQLFQPSFEICPFESELNMDIAAALKRGNREWYDRILNDKSPREQPGPQRLPGLVVLA
                                                                                     DAVYDDLQFCYSVYASLFHSILNVDVFTLTFRQLERLVAEEAWVLTEELSPKMTLEVA
                                                                                                                               AVDMDTLEPVDASSRHSSSAATAGLCLSHIQELWVRLAWPDPAQAQGLGTQLGQDVCE
                                                                                                                                                                        EGVLPRPLLSCTQALDDDLQREAHTVTAHLTSKMVGDIRKYVQHISLSPDSIQNDEAV
                                                                                                                                                                                              APLMKYLDEKLALLNASLVKGNLSRVLEALWELLLQAILQALGANRDVSADFYSRFHF
                                                                                                                                                                                                                !LEALVSFFHAEGQGLPLESLRDGSYKRLKEELRLHKCSTRECIEQFYLDKLKQRTLE
                                                                                                                                                                                                                                         ONRFGRLSVRCHYEAAEQRLAVEVLHAADLLPLDANGLSDPFVIVELGPPHLFPLVRS
                                                                                                                                                                                                                                                           QRTQVKTRTLHPVYDELFYFSVPAEACRRRAACVLFTVMDHDWLSTNDFAGEAALGLG
GVTGYARPQVGGGARAGQPVTLHLCRPRAQVRSALRRLEGRTSKEAQEFVKKLKELEK
                                                                                                         SGLFELYLTLADLQRFWDSIPGRDSRSLALAGIHAPFLPAVKLWFQVLRDQAKWRLQG
                                                                                                                                                    ATLFYTELLRKKVDTQPGAAGEAVSEALCVVLNNVELVRKAAGQALKGLAWPEGATGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(17311. 17679,17960. 18023,18129. 18305,
18878. 19071,19450. 19669,19764. 19875))
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18878. 19071,19450. 19669,19764. 19835))
/gene="c316G12.2"
                                                                                                                                                                                                                                                                                                                          /note="Tandem repeat. Forced join. Region of tandem repeat, Typical sequence of each element: GGTGCACACACACGCACCACGGTTGCA Restriction digest data (BAMHI) suggest approximately 100 base pairs are missing from this assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="c316G12.2 (novel protein similar to predicted yeast, worm and archae-bacterial proteins)" /note="match: cDNAs: Em:AF109401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="101 copies 2 mer gg 56% conserved" 215. 11313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="29 copies 31 mer 65% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uote="3 copies 27 mer 84% conserved" 657, .8700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mer 66% conserved
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.8474
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8617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "8 copies 29 mer 72% conserved" 7953
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8535
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8673
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.8397
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8690
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.note="8 con'
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gene

mRNA

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AC121922 173200 bp DNA linear HTG 21-MAY-2002 Mus musculus chromosome UNK clone RP24-198H19, WORKING DRAFT SEQUENCE, 11 unordered pieces.
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MCPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
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0
                                                                                                                                                                                                                                                                                                                   Length 37476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center
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Quality coverage: 12.12 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 168389 bases at least Q40
Consensus quality: 168767 bases at least Q30
Consensus quality: 169076 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC121922.1 GI:21040046
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus.
                                                                                                                                                                                                                                                                                                                   Score 16.4; DB 9;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
complement(1731)
/gene="c316G12.2"
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Crani
Mammalia, Eutheria, Rodentia, Sclur
1 (bases 1 to 173200)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 187000; agarose-fp
Insert size: 171546; sum-of-conf
                                                                                                                                                                                                                                                                                                                                                                                                                 22044 GGGGATCAGATGGTGCCG 22061
                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                            2 GGGGATCACATGGTGCCG 19
match: ESTS:
Em:A1143673
Em:A1143673
Em:AA167317
Em:AA716721
Em:AA716524
Em:AA716524
Em:AA482458
Em:AA482458
Em:AA293357
Em:AA293357
Em:AA293357
                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                  polyA_site
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
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JOURNAL
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REFERENCE
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AC121922
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HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weinstock, G. and Glbbs, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drafting Center Code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sonaike, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 214042)
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Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                      Miner, Z.,
                          Homo sapiens
                          ORGANISM
                                                               REFERENCE
AUTHORS
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AUTHORS
KEYWORDS
SOURCE
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Homo sapiens chromosome 12 clone RP11-604N13, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
AC093028 9 GI:21954880
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           runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                      contig of 25375 bp in length
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of 1226 bp in length
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Pred. No. 2.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                       of 24253 bp
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note-"assembly_name:Contig14"
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'note="assembly_name:Contig15"
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/note="assembly_name:Contig16"
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44056 c 43959 g 40962 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                             note="assembly_name:Cont1g12"
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                                                                                                                                                                                                                                                                                                                                                                                                                    clone-"RP24-198H19"
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Best Local Similarity 94.4%;
Matches 17; Conservative
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VERSION
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AC093028
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Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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Submitted (09-AUG-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mitchell,T., Mohabbat,K., Morgan,M., Morris,S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
aalis,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
abisi,A., Gao,J., Garda,A., Garder,T., Garza,N., Gill,N.,
forrell,J.H., Guevar,W., Gunartne,P., Hale,S., Hamilton,K.,
farris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
fernandez,O., Hodgson,A., Hogus,R., Holloway,C., Hollins,B.,
fomsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
facobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
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, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L.
1, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.
                                                                                                                          (bases 1 to 214042)
ny.D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
                                                                                                                                                                                                                                        Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowley, B., Brown, E., Brown, M., Bryant, N. P. Bouck, J., Bowley, C., Burch, P., Burwett, C., Burrell, K. L., Byrant, N. C., Carron, T. F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R., Davila, M. L., Davis, C., Davy-Carroll, L., Dederich, D. A., Douthwaite, K. J., Draper, H., Dugan-Roch, S., Durbin, H. H., Douthwaite, K. J., Draper, H., Dugan-Roch, S., Durbin, K. J., Draper, H., Dugan-Roch, S., Din, H., Draper, H., Dugan-Roch, S., Din, H., Draper, H., Dugan-Roch, S., Durbin, R. D., Draper, H., Dugan-Roch, S., Din, H., Draper, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.N., Ovledo,R., Pace,A., Payton,B., Peery,J., Perez,L.
L., Pickens,R., Primus,B., Pu,L.L., Qulles,M., Ren,Y.,
I., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
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On Jul 25, 2002 this sequence version replaced gi:21553148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye: 100% of reads
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Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hqsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Newtson, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine Center code: BCM
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note="MER5A; RepeatMasker predicted
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:839. .4637
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33/10/2000"
  /map="16p13.3"
1. .14033
/organism="Homo sapiens"
                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cosmid 316912"
39209. 78044
                                                                                                                                                                                                                                                                                          /organism="Homo sapiens'
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                     clone="cosmid 438f12"
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                                                                                                                                                                                                                                                  "cosmid 399e4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="cosmid 390e6"
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                                                                                     cosmid 358b7"
                                                                                                                                                                                                                                                                                                                                 clone="cosmid 312e8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "cosmid 315g5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref-"taxon:9606
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                                                                db_xref-"taxon:96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"HS316G12"
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                                                                                                                                                                                                                                                                       .110196
                                                                                                                                                                                                                                                                                                                                                           126950
                                                                                                                                                                                                                                                  clone.
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                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as Thus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Submitted (07-DEC-2000) MRC Molecular Haematology Unit, Weatherall
Institute of Molecular Medicine, John Radcliffe Hospital, Oxford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence, structure and pathology of the fully annotated terminal Mb of the short arm of human chromosome 16 Hum. Mol. Genet. 10 (4), 339-352 (2001)
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Tufarelli,C., Kearney,L., Buckle,V.J., Doggett,N.A., Flint,J. and
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Pufarelli, C., Kearney, L., Buckle, V.J., Doggett, N.A., Flint, J. and
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Assembly program: Phrap; version 0.990329
Consensus quality: 213137 bases at least Q40
Consensus quality: 213777 bases at least Q30
Consensus quality: 21377 bases at least Q30
Estimated insert size: 21386; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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1 (bases 1 to 279011)
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AE006467.1 GI:14336745
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2760: gap of unknown length
65406: contig of 62646 bp in length
65506: gap of unknown length
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Pred. No. 2.9e+02;
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53357 a 50252 c 51683 g 57749 t
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/db_xref="taxon:9606"
/chromosome="16"
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Takami, H., Nakasone, K., Hirama, C., Takaki, Y., Masui, N., Fuji, F., Nakamura, Y. and Inoue, A.
Nakamura, Y. and Inoue, A.
An improved physical and genetic map of the genome of alkaliphilic Bacillus sp. C-125
Extremophiles 3 (1), 21-28 (1999)
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Extremophiles 3 (1), 29-34 (1999)
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Pred. No. 2.9e+02;
0; Mismatches 1; Indels 0;
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/note="(CACG)n; RepeatMasker predicted
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23/10/2000"
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/note="(CA)n; RepeatMasker predicted
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/note="(CA)n; RepeatMasker E
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ilarity 94.4%;
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/note="GC_rich; RepeatMasker predicted
13/10/2000"
note="GC_rich; RepeatMasker predicted
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                                /rpt_family="Low_complexity"
3559, .19342
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23/10/2000"
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/note="MIR: RepeatMasker
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GAGAAVMGAVSEDRGILAYELGADGEGAMHINOKGEYIQMNGREVFKFAVRQMGESAL
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BCLLLHECEGLKGTIENKODALQFAREFFNHKQPL"
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LSTSDQDTMAVLKRFKSLLLKQYHTISQLQVPNSHQMSPYDPPGEPLKGFIIEEKG"
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/protein_id="BAB06602.1"
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/product="3-oxoacyl-(acyl-carrier protein) synthase"
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/db_xref="G1:10175503"
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/db_xref="GI:10175502"
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/protein_id="BaB06603.1"
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/gene="BH2882"
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/transl_table=11
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/gene="BH2881"
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/gene="BH2880"
955. .1605
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ORGSLYFYRYRKTATSPYVSFRQQTIVIGNHIFAK"
955. . 1605
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URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html,
Tel:81-468-67-3895, Fax:81-468-66-6364)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28 (21), 4317-4331 (2000)
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and separate of an alkaliphilic Bacillus strain from an
industrial point of view
sxtremophiles 4 (2), 99-108 (2000)
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Direct Submission
Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and
Technology Center, Deep-sea Microorganisms Research Group; 2-15
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
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.koshi,K.
                                                                                                                                                                                                                                                                                                                                                                                         Takami, H., Masul, N., Nakasone, K. and Horikoshi, K. Replication origin region of the chromosome of alkaliphilic Bacillus halodurans C-125
Bacillus halodurans C-125
Biosci Biotechnol Biochem. 63 (6), 1134-1137 (1999)
  Sasaki,R., Hirama,C., Fuji,F. and Masui,N. Genetic analysis of the chromosome of alkaliphilic Bacillus halodurans C-125
                                                                                                                                                                                                                                                                                       Extremophiles in deep-sea environments (Ed.);
IKOSHI, K. TSUJII;
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IMPORTANT: This sequence is not the entire insert of clone
RP5-98D7 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP5-989D7 is at 1 in this sequence. The
true left end of clone RP5-989D4 is at 19691 in this sequence. The
true right end of clone RP11-199014 is at 19977 in this sequence.
This sequence was finished as follows unless otherwise noted: all
'translation="MSNQEERDFFTDLMFGRPPESTDVAEENPQESTSGSTVEETKTE
                                                                                                                                                                                                                                                                                                                                          /translation="MNVYTHGPYYRQYIGTGERFYPAVLPFLAGLAVGPLLFGGKP" YGGYGPAYGPSYGPNFGPNYGPNFGPMYGPPSQPPFGYYK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORWPEP database can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI 10-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNA sequence from clone RP5-989D7 on chromosome 20. Contains the 3' end of a novel gene, STSs and GSSs, complete sequence. AL121911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Aug 22, 2000 this sequence version replaced g1:9714378.
During sequence assembly data is compared from overlapping clones.
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                           GETKQEETNAAPALPLTFEQMEHIFRLAQSLGPALKSLSPYVKTIQQLISQQKKD"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 119790)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-WAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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Pred. No. 3e+02;
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                                                                                                                                                                                                                                                      /transl_table=11
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/db_xref="G1:10175507"
                                                      complement(5903. .6157)
                                                                                                            complement(5903. .6157)
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                                                                                    /gene="BH2885
                                                                                                                                                                  /note="BH2885
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94.4%;
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                                                                                                                                                                                                   unknown"
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Best Local Similarity
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HSDJ989D7
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.6316 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6165 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6168 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                        .5865 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consensus,
Jong. For
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5705 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 271. .360 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MER8 repeat: matches 87. .239 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 1. .354 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .249 of consensus"
                                                                                                                                                                                                                                            match: cDNAs: Em:AY007089" /ey1denca=nc*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 2740. .6162 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5892 of
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constructed by the group of Pieter
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12150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      copies 2 mer tt 57% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .308 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 1. .345 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="LIMA10 repeat: matches 6174.
                                                                                                                                                                                                                                                                                                                                                                                                     1294. .4326
/note="LIMB8 repeat: matches 5834.
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                                                                                                                                                                                                                                                                                                                                        /45. .3332
/note="TIGGER1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     7201. ..8108
/note="LLM4 repeat: matches 4784.
complement(8165. .8633)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches -260.
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                                                                                                                                                                                                                                                                                                                                                                                    Em: AQ380734"
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                                //www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                           'evidence=not_experimental
                                                                                            /organism="Homo sapiens
/db_xref="taxon:9606"
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                                                              Location/Qualifiers
                                                                                                                                                            clone_lib="RPCI-5"
                                                                                                                                                                                                                                                                                                                                                                     130. .4386
note="match: GSS:
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                                                                                                                                           'clone="RP5-989D7"
                                                                                                                                                                                                                                                                                                                       gene="dJ989D7.1"
                                                                                                                                                                                           "dJ989D7.1"
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                                                                                                                            chromosome="20"
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.6317 of consensus"
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                                                                                      consensus
                                                                                                     complement(27586. .28074)

//octe="match: GSS: Em:AQ605230"
//octe="17816A repeat: matches 148. .378 of consensus"
28592. .28729
//octe="MIR repeat: matches 26...167 of consensus"
28416. .29585
//octe="MIRFSB repeat: matches 1..177 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .385 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .221 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .433 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .196 of consensus
                                                                                                                                                                                                                                                                                           0759. 31042
note="MER33 repeat: matches 47. 323 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2745 of consensus"
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hote-"MLT1A1 repeat: matches 4. .365 of consensus"
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               repeat: matches 1. .345 of consensus"
                                                                                                                                                                                                                                                      0385. 30489
note-"MIR repeat: matches 40. 153 of consensus"
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                                                                                       .6326 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ote="9 copies 6 mer tagata 75% conserved"
968. 36019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .617 of
                                                                                                                                                                                                                                                                                                                                            .225 of
                                24440. 24524

/note-"LiMnJO repeat: matches 6095.

25218. 27841

/note-"LiMcI repeat: matches 3550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ote-"LTR16C repeat: matches 221.
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5934. .36427
note-"match: GSS: Em:AQ429711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="LTR16C repeat: matches 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note "LTR16A repeat: matches 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MER51B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                        'note="MER77 repeat: matches 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              copies 4 mer agat 100%
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46523
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note="L2 repeat: matches 2410.
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5535. .45726
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                                                                                                                                                                                                                                                                                                                                                                                                           complement(31606. .32269)
/note="match: GSS: Em:AQ266996"
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ACO26171 160819 bp DNA linear HTG 29-MAY-2000 Homo sapiens chromosome 3 clone RP11-166F3 map 3p, WORKING DRAFT SEQUENCE, 38 unordered pieces.
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Bao, W., Sun, Y., Wu, Q., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y.,
21, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y.,
Li, C., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D.,
Huang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J.
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Ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(an,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H.,
(hang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y.,
(hang,Z., Zhu,B., Yu,J. and Yang,H.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,
Feng,X., Guan,Q., Gu,X., Guo,D., He,L., Hu,S.,
Kang,N., Li,C., Li,C., Li,G., Li,J., Li,J.,
Li,X., Liu,N., Liu,B., Liu,Y., Li,W., Li,W.,
Qi,Q., Qi,X., Song,S., Sun,M., Sun,W., Sun,Y.,
Wang,J., Wang,J., Wang,L., Wang,L., Wang,R.,
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.2266 of consensus"
                                                     consensus,
                                                                                             /note="MIR repeat: matches 97. .139 of consensus" 4731. .47479
/note="MIR repeat: matches 99. .256 of consensus" complement(47625. .48021)
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                                                                                                                                                                                                                                                       Score 16; DB 9; Length 119790;
Pred. No. 4.9e+02;
0; Mismatches 0; Indels 0;
                                                  .2710 of
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Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator: ET 55% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 127562 bases at least 0.40
Consensus quality: 136470 bases at least 0.30
Consensus quality: 1347433 bases at least 0.20
matches 2022.
                                                  matches 2541.
                                                                                                                                                                                                       'note-"match: GSS: Em:AQ818871"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Bao, W., Bian, X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F., Jin, Y., Kang, N., Li, C. Li, T., Liu, Y., Liu, N., Li
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HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens.
                                               /note="L2 repeat:
17299 ... 47342
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ilarity 100.0%; P.
Conservative 0;
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/note="assembly_name:Contig10"
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/note="assembly_name:Contig14"
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note="assembly_name:Contig16"
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13446. 35867
note-"assembly_name:Contig30"
15968. 38450
note-"assembly_name:Contig31"
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/note="assembly_name:Contig18"
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'note="assembly_name:Contig19"
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note="assembly_name:Contig23"
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note="assembly_name:Contig34"
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'note="assembly_name:Contig33"
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note="assembly_name:Contig35"
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8608. .62353
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71311. 75769
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    160819
    organism="Homo sapiens"
    db_xref="taxon:9606"
    /chromosome="3"

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                             NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
     size: 125850; sum-of-contigs
7 coverage: 3.22x in Q20 bases;sum-of-contigs
                                                                                                                                                                                               g of 1884 bp in length
f unknown length
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PAT 31-JAN-2002

RESULT 12

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FEATURES

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N-Acetyl amino acid racemase, gene encoding the same, plasmid, vector and microorganism having the gene, primer and probe for the BD006820
                                                                                                                                                                     artificial sequences.

1 (bases 1 to 504)

Ferzeck,S., Kula,M.R., Bommarious,A. and Dorautz,C.

N-Acetyl amino acid racemase, gene encoding the same, plasmid, vector and microorganism having the gene, primer and probe for the
                                                                                                                                                                                                                                                                                                                                                                                                         C12N15/09,C12N1/21,C12N9/90,C12P13/04//(C12N15/09,C12R1:04),(C12N1/21,C12R1:04);(C12N9/90,C12R1:04);
                                                                                                                                                                                                                                                                                              Artificial Sequence
JP 2001046088-A/2
20-TEB-2001
21-2000 JP 2000222928
27-JUL-1999 DE 19935268.2
STEPHEN FERZECK,MARIA REGINA KULA,ANDREAS BOMMARIOUS, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.2%; Score 15.8; DB 6; Length 1107; llarity 89.5%; Pred. No..5.1e+02; Conservative 0; Mismatches 2; Indels 0;
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Verseck, S., Kula, M. R., Bommarius, A. and Drauz, K.
N-acetyl amino acid racemase
Patent: US 6372459-A 1 16-APR-2002;
Location/Qualifiers
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Pred. No. 4.9e+02;
0; Mismatches 2;
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/db_xref="taxon:32630"
163 c 185 g 79 t
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/organism='Artificial Sequence'..
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Patent: JP 2001046088-A 2 20-FEB-2001;
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Sequence 1 from patent US 6372459.
AR206864
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Verseck,S., Kula,M.R., Bommarius,A. and
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Verseck, S., Kula,M.-R., Bommarius,A
N-acetyl amino acid racemase
Patent: US 6372459-A 3 16-APR-2002;
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Sequence 3 from patent US 6372459.
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July 8, 2003, 00:43:28; Search time 119.376 Seconds
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

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& Query Match	100.0	100.0	100.0	86.3	86.3	86.3	86.3	83.2	83.2	
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ALIGNMENTS

RESULT 1

cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; probe; hybridsation Bonhomme MC, Facchinetti P; Rat; membrane metalloprotease; neprilysine II; NEPII; inan neuron; hormone; peptide messenger; inhibitor; detection; cardiovascular disease; neurodegenerative disease; growth Rat membrane metalloprotease NEPII gene probe #4. (INRM) INSERM INST NAT SANTE & RECH MEDICALE AAZ28814 standard; DNA; 19 BP Haret C, 98FR-0004389. 98FR-0004389. (first entry) Ouimet T, Gros C, Schwartz JC; Synthetic. Rattus rattus. 08-APR-1998; 08-APR-1998; FR2777291-A1 01-FEB-2000 15-OCT-1999. AAZ28814;

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Claim 2; Page 12-16; 29pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; ss; neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardlovascular disease; neurodegenerative disease; growth disorder;
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               involved in proteolysis of
to screen for inhibitors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  involved in proteolysis of
to screen for inhibitors,
cardiovascular disease
                                                                                                                                                                                                                                                                                                                                     0
                            neuronal and hormonal peptides, used to screen for inhibitor potentially useful for treating e.g. cardiovascular disease
                                                                                                                                                                                                                                                                                                      DB 20; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Facchinetti P;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat membrane metalloprotease NEPII gene probe #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                   Sequence 19 BP; 3 A; 5 C; 8 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                 Score 19; DB pred. No. 2.2; Pred. No. 2.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonhomme MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New membrane metalloprotease NEP II,
neuronal and hormonal peptides, used
potentially useful for treating e.g.
              New membrane metalloprotease NEP II,
                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 20; 29pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 21; 29pp; French.
                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.0%;
Matches 19; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98FR-0004389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ28816 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FR2777291-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schwartz JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouimet T,
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used to detect NEPII or for treatment of disorders related to peptidergic signalling in Which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the gene for the rat membrane metalloprotease
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; neuros; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
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to screen for inhibitors,
cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; Length 2765;
                                                                                                                                                                                                                                                                                                    21;
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                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2765 BP; 684 A; 735 C; 787 G; 559 T; 0 other;
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                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                     Sequence 21 BP; 4 A; 8 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                            .0%; Score 19;
.0%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat membrane metalloprotease NEPII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New membrane metalloprotease NEP II, neuronal and hormonal peptides, used potentially useful for treating e.g.
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RESULT 4

AAI90923;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes: (I) is useful in gene therapy techniques (C) restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; dlagnostic; genetic dlsorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3939 BP; 933 A; 1072 C; 1040 G; 894 T; 0 other;
                                                                                                                                   ONA encoding novel human diagnostic protein #24800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 24800; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3807 GGGGATCACATTGTGCCG 3790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . AAS94171 standard; cDNA; 3939 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGATCACATGGTGCCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.3%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                              13-FEB-2002 (first entry)
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Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABG24809
                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001.
   AAS88996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS94171
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ID AAS941
XX
AC AAS941
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 10983; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; vaccine; peptide therapy; atem cell growth factor; haematc tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 10983.
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AAS88996 standard; cDNA; 3939 BP.
CGGGGATCACATGGTGCCG 467
                                                                                                                                                                                                     BP
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                                                                                                                                                                                              AAI90923 standard; cDNA; 410
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2000US-0577409
                                                                                                                                                                                                                                                                                                                                  (first entry)
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18-MAY-2000;
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Claim 1;

Gaps

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Indels

Length 3939;

23; DB

Score 16.4; DE Pred: No. 69; 0; Mismatches

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Query Match

Matches

g 8

RESULT 5
AAS88996/c
ID AAS86

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39178
                                                                                                                                                                                                                                                                   WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -MAR-2000;
                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (FCR) primers, aligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantificating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponable for genetic disorders or other traits to assess biodiversity
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3939;
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                                                                         DNA encoding novel human diagnostic protein #29975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23;
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Pred. No. 69;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
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23-AUG-2000; 2000US-0649167.
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Best Local Similarity 94.4%;
Matches 17; Conservative
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13-FEB-2002 (first entry)
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P-PSDB; ABG29984.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                                                                                               Homo sapiens.
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AAK84366;

AAK84366 ID AAK8 XX AC AAKE XX DT 07-1

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many solutions and polynucleotides may be used in the prevention. (1) proteins and polynucleotides may be used in the prevention. (1) to proteins and polynucleotides may be used in the prevention. (1) creatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expression in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the notice; caids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic concers and cancer invention. AAK87694 to AAK87694 and AAM82169 represent invention. AAK87692 ond AAM82169 represent invention. AAK87692 to AAK87695 and AAM82169 represent invention. AAK87694 to AAK87695 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-acetyl amino acid racemase, AAR; enantiomerically enriched amino acid; enzyme-membrane reactor; N-acetyl-D-methionine; N-acetyl-L-methionine; heavy metal dependency; ds.
                                                                                                                                                                                                                                                                             AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides useful for preventing, diagnosing and/or treating cancers and metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 39178; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 70;
0; Mismatches 1;
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                                                                                                       Ruben SM
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                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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                                                                                                       Rosen CA, Barash SC,
                                                                                                                                       WPI; 2001-483426/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1074628-A1.
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2000US-0251869
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08-DEC-2000;
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This invention describes a novel N-acetyl amino acid racemase (AAR) enzyme (I) derived from Amycolatopsis orientalis ssp. lurida (DSM 43134). The invention also describes (1) a gene coding for (I); (2) a vector containing the gene; (3) a microorganism containing the gene; (4) a primer for the gene; and (5) a probe for the gene. (I) is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid;
                                                                                                                                              enzyme (1) derived from Amycolatopsis orientalis ssp. lurida (DSM 43134). The invention also describes (1) a gene coding for (1); (2) a vector containing the gene; (3) a microorganism containing the gene; (4) a probe for the gene. (1) is useful for primer for the gene; and (5) a probe for the gene. (1) is useful for producing enantiomerically enriched amino acids in an enzyme-membrane reactor, e.g. by AAR-catalyzed conversion of N-acetyl-D-methionine to N-acetyl-L-methionine to L-methionine (1) exhibits reduced heavy metal dependency compared with
                               New N-acetyl amino acid racemase enzyme derived from Amycolatopsis orientalis ssp. lurida, useful for producing enantiomerically enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New N-acetyl amino acid racemase enzyme derived from Amycolatopsis
orientalis ssp. lutida, useful for producing enantiomerically enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-acetyl amino acid racemase; AAR; enantiomerically enriched amino acienzyme-membrane reactor; N-acetyl-D-methionine; N-acetyl-L-methionine; L-methionine; heavy metal dependency; ds.
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                                                                                                                                                                                                                                                                                     the AAR of Amycolatopsis sp. TS-1-60 (Appl. Microbiol. Biotechnol
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                                                                                                                                 This invention describes a novel N-acetyl amino acid racemase
                                                                                                                                                                                                                                                                                                                                                                       Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            orientalis subsp lurida N-acetyl amino acid racemase DNA.
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Pred. No. 1.2e+02;
); Mismatches 2;
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                                                                                              Disclosure; Page 13; 23pp; German.
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ID AAF61120 standard; DNA; 1107 BP
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89.5%;
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 WPI; 2001-161182/17
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P-PSDB; AAB70760.
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nes 17; Conserv
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                                                                amino acids
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                                                             compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to the preparation of enantiomer-enriched
producing enantiomerically enriched amino acids in an enzyme-membrane reactor, e.g. by AAR-catalyzed conversion of N-acetyl-D-methionine to N-acetyl-L-methionine followed by acylass-catalyzed conversion to L-methionine. (I) exhibits reduced heavy metal dependency compared the AAR of Amycolatopsis sp. TS-1-60 (Appl. Microbiol. Biotechnol., 42,
                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-protected amino acid with N-acetyl amino acid racemase enzyme and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enantiomer-enriched; N-protected;
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                                                                                                                                                                                    DB 22; Length 1107;
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                                                                                                                                   Sequence 1107 BP; 164 A; 369 C; 404 G; 170 T; 0 other;
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                                                                                                                                                                                Score 15.8; DB 22;
Pred. No. 1.3e+02;
0; Mismatches 2;
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89.5%;
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ilarity 89.5%;
Conservative
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                                                                                                                                                                                                     Local Similarity
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                                                                                                      853, 1995).
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Matches

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Key

RESULT 11

AAL45919,

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vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; Alzhelmer's disease; infection; coular disorder; corneal infection; wound healing; epithelial cell proliferation; skin agelng; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                              Drosophila melanogaster genomic polynucleotide SEQ ID NO 38038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 592;
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                                                                                                                                   Drosophila; developmental biology; cell signalling;
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Pred. No. 2e+02;
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Best Local Similarity 94.1%;
Matches 16; Conservative
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2000US-0614150.
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                                                                                                                                                            pharmaceutical; gene; ds
                                                                                                                                                                                                               Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 enantiomerically enriched amino acid; chemical synthesis; enzyme; parenteral nutrition; gene; ds.
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     Gaps
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Pred. No. 1.3e+02;
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Indels
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Mismatches
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Conservative
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P-PSDB; AAO17352.
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Homo sapiens
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us-09-647-780a-8.rng

16-JUL-2001; 2001WO-IB01263.

24-JAN-2002

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diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatchid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, carebrovascular disorders e.g. carebral ischaemia, anglogenesis, nervous system disorders e.g. carebral ischaemia, anglogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi
                                                                                                                                      461 human secreted proteins for ameliorating medical conditions and
                                                                                                                                                                                                                                                                                                          rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in
                                                                                                                                                                                                                                                                    encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted endopeptidase; SEP; endocrine; vasotropic; analgesic;
enzyme; gynaecological; antisense-therapy; male arectile dysfunction;
WED; female sexual dysfunction; FSD; female sexual arousal disorder;
FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to ald wound healing and epithelial cell proliferation, to transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present
                                                                                                                                                                                                                                                      invention relates to isolated nucleic acid molecules and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence encodes a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soluble secreted endopeptidase (SEP) consensus DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.4; DB 22;
Pred. No. 2.1e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/note= "Encodes catalytic domain"
                                                                                                                                New nucleic acid molecules encoding 461 diagnosing, preventing, treating or amelused as food additives or preservatives
                                                                                                                                                                                                                SEQ ID No 284; 980pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1664..2286
                                      Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD28130 standard; DNA; 2286 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            930 GGGGATCACATGGTGGC 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGGGATCACATGGTGCC 18
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.1%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 94.18;
hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                      Barash SC,
                                                                          2001-488783/53
                                                                                            P-PSDB; AAU16118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200206492-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-2002
                                      Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp
                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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AAD28130/c
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as premature ejaculation, anorgasmia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is SEP consensus DNA sequence found in human, mouse and rat.
                                                                                                                                                                                                                                             An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as female sexual arousal disorder -
                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (RED) (e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such
                                                                                                                                                                      Phillips SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 38035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2286;
                                                                                                                                                                      Wayman CP, Wayman CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.4; DB 24;
Pred. No. 2.2e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 6; 167pp; English
                                                                                                                                                                      Walsh RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
ABL28854/c
ID ABL28854 standard; DNA; 4183 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GGGATCACATGGTGCCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.18;
94.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUL-2000; 2000US-0614150
                                                                         14-JUL-2000; 2000GB-0017387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 GGGATCACGTGGTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                      Harrow ID, Stacey P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC, Adams M,
                                                                                                                                                                                                         WPI; 2002-155042/20.
                                                                                                            (PFIZ ) PFIZER LTD. (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL28854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Claim 1; SEQ ID NO 38035; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 4183 BP; 1201 A; 832 C; 886 G; 1264 T; 0 other;

ö Gaps ö Length 4183; Score 15.4; DB 23; Length Pred. No. 2.3e+02; 0; Mismatches 1; Indels Query Match 81.1%; Best Local Similarity 94.1%; Matches 16; Conservative

1090 GGGATCTCATGGTGCCG 1074 3 GGGATCACATGGTGCCG 19 δ

Search completed: July '8, 2003, 02:18:54 Job time : 120.376 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compu
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OM nucleic - nucleic search, using sw model

8, 2003, 01:24:03; Search time 26.2293 Seconds Run on:

US-09-647-780A-8 Title: Perfect score:

1 cggggatcacatggtgccg 19 Sequence:

IDENTITY_NUC Gapop 10.0', Gapext 1.0 Scoring table:

441362 seqs, 153338381 residues Searched:

882724 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution. Pred. No.

			de			SOMMANTES	
pe,	Result		Query		٠.		
	No.	Score	Match	Length	DB	ID	Description
	c T	15.8	83.2	504	4	US-09-624-390-3	Sections 3
	c 0	15.8	83.2	1107	4	US-09-624-390-1	· -
	m	14.8	77.9	1679	٣	US-08-676-882-1	
	4	14.8	77.9	1912	Н	US-08-270-013B-1	ì
	س	14.8	77.9	1912	-	US-08-838-418-1	ì
	ø	14.8	77.9	1977	-	US-08-272-255-17	17
	7	14.8	77.9	1977	ഗ	PCT-US95-08565-17	17
	∞.	14.8	77.9	152331	٣	US-09-128-155-16	16.
	6 0	14.8	77.9	176373	m.	US-09-128-155-17	17,
	c 10	14.2	74.7	32	Н	US-08-465-687A-7	7.7
	c 11	14.2	74.7	32	m	US-09-030-970-7	Sequence 7. Appli
	. 13	14.2	74.7	1847	4	US-09-149-476-287	287
	c 13	14.2	74.7	3366	-	US-08-469-802B-1	1. Ar
	c 14	14.2	74.7	3366	~	US-08-267-803B-1	ì
	15	14.2	74.7	4214	4	US-09-221-017B-293	29
	16	14.2	74.7	6830	~	US-08-822-445-1	-
	17	14.2	7.4.7	6830	4	US-09-396-540-1	-
	c 18	14.2	74.7	10660	~	US-08-267-803B-8	8
	c 13	14.2	. 74.7	10660	4	US-09-041-886-16	Sequence 16, Appl
	50	14.2	74.7	4403765	4	US-09-103-840A-2	2,
	21	14.2	74.7	4411529	4	US-09-103-840A-1	٦,
	c 22	13.8	72.6	649	4	US-09-470-191-5	δ,
	53	13.8	72.6	1432	4	US-09-183-861-73	73
	. 54	13.8	72.6	1432	4	US-09-022-765-73	73,
	52	13.8	72.6	1847	4	US-09-149-476-149	149,
	c 56	13.8	72.6	4550	4	US-09-103-663-35	35, 7
	27	13.8	72.6	28720	4	US-09-341-587-7	7, A

JRRENT APPLICATION NUMBER: US/09/624,390
JRRENT FILING DATE: ; TYPE: DNA ; ORGANISM: Amycolatopsis orientalis US-09-624-390-3 Sequence 3, Application US/09624390 BOMMARIUS, ANDREAS PRIOR APPLICATION NUMBER: NUMBER OF SEQ ID NOS: SOFTWARE: Patentin V LE OF INVENTION: SEQ ID NO 3 LENGTH: 504

DB 4; Length 504; Query Match 83.2%; Best Local Similarity 89.5%; Matches 17; Conservative

N-ACTEYL AMINO ACID RACEMASE VERSECK, STEFAN KULA, MARIA-REGINA BOMMARIUS, ANDREAS DRAUZ, KARLHEINZ JS-09-624-390-1/c

Patentin Ver. 2.1

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NAME/KEY: misc_feature
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                                                                                                                                                                    DB.4; Length 1107;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATICS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,882
FILING DATE: 03-UUL-1996
CLASSIFICATION: 514
ATORNEY/AGERT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Akzo No. 6100241el Patent Department
1300 Piccard Drive, Suite 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function= "Eimeria lactate dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kok, Jacobus Johannes
APPLICANT: van den Boogaart, Paul
APPLICANT: vermeulen, Arnoldus Nicolaas
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1..51
OTHER.INFORMATION: /label= pBluescriptII
                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                 Score 15.8;
Pred. No. 20
                                       ORGANISM: Amycolatopsis orientalis
                                                                                                                                                                                                                                                                               220 CGGGGATCAGATGGTTCCG 202
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08676882 Patent No. 6100241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: Schizont IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gormley, Mary E.
REGISTATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
TELEFAX: (301) 977-0847
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       1 CGGGGATCACATGGTGCCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                     Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 280..1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Eimeria
                                                                              ; NAME/KEY: CDS
; LOCATION: (1)..(1107)
US-09-624-390-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20850
LENGTH: 1107
                                                                                                                                                                                                                                                                                                                                                                             JS-08-676-882-1
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                                                                                                                                                                      Query Match
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Sequence 1, Application US/08270013B.

Sequence 1, Application US/08270013B.

Batcht No. 5686294

GENERAL INFORMATION:
APPLICANT: Sogabe et al.
TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY: USA

ZIF: 61601-6780

COMPUTER READABLE FORM:
MEDLUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,013B
FILING DATE: 01-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                       Score 14.8; DB
Pred. No. 68;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Leydig, Voit & Mayer, Ltd.
Two Prudential Plaza, Suite 4900
OTHER INFORMATION: /label-pBluescriptII
                                                                                                                                          NAME/KEY: misc_feature
; LOGATION: 1621..1630
; OTHER INFORMATION: /label- ECORI-linker
US-08-676-882-1
                                          NAME/KEY: misc_feature
LOCATION: 45.54
OTHER INFORMATION: /label= ECORI-linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Bacillus stearothermophilus ATCC12016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 164701/1993
FILING DATE: 02-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          1 CGGGGATCACATGGTGCC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: (312) 616-5600 TELEFAX: (312) 616-5700 TELEFAX: (25)3533 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Green, Robert F. REGISTRATION NUMBER: 275 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1912 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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DB 1; Length 1912;

77.9%; Score 14.8;

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STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                          APPLICANT: Cashmore, Anthony R.
APPLICANT: Ahmad Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application PC/TUS9508565
GENERAL INFORMATION:
APPLICANT: Cashmore, Anthony R.
APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25.
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.8;
                                                                                                                                                                                                                                                                                                                                                                         , Application US/08272255
5824859
                                                                                                                                              NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1304 CGAGGATCAGATGGTGCC 1321
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VITORNEY/AGENT INFORMATION:
NAME: Leary Ph.D.; Kathryn
REGISTRATION NUMBER: 35,317
REFRENCE/DOCKET NUMBER: UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.9%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy dish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1977 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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ADDRESSEE: Woodcock,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                             USA
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US-08-272-255-17
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                            19103
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                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                           STATE:
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                           Gaps
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                                                                                                                                                                           Sequence 1, Application US/08838418
Patent No. 5744342
GENERAL INFORMATION:
APPLICANT: Sogabe et al.
TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
TITLES OF INVENTION: DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,418
FILING DATE: 17-MAR-1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                         3: Leydig, Voit & Mayer, Ltd.
Two Prudential Plaza, Suite 4900
       Pred. No. 69;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: Bacillus stearothermophilus STRAIN: ATCC12016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.8;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,013
FILING DATE: 01-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: JP 164701/1993
FILING DATE: 02-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                        1223 GGCGATGACATGGTGCCG 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1223 GCCGATGACATGGTGCCG 1240
                                                        GGGGATCACATGGTGCCG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (312) 616-5600
(312) 616-5700
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ilarity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: (25)3533
NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoover, Allen E.
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                Illinois
                                                                                                                                                                                                                                                                                                                                                                                                               60601-6780
                                                                                                                                                                                                                                                                                                                                                          Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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US-08-272-255-17
                                                                                                                                            RESULT 5'
US-08-838-418-1
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Gaps

CURRENT APPLICATION DATA:

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INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 176373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LL, ET AL.
TITLE OF INVENTION: Human Endothelin Receptor NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: CARELLA, BYRNE, BAIN, GILFILLAN, E: CECCHI, STEWART & OLSTEIN 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                          CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER PPLICATION NUMBER: US 60/054,646
EARLIER PPLICATION NUMBER: US 60/054,646
SARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOGTWARE: FEASLEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.8;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US94/11843
FILING DATE: 17 OCT 1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/465,687A FILING DATE: 6 JUNE 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08465687A Patent No. 5750370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGGGGATCACATGGTGCC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.98;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTI
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROSELAND . NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -08-465-687A-7/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OP INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
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Pred: No. 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14.8;
                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,255
FILING DATE: 08-UL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTATION NUMBER: 18,317
REFERENCE/DOCKET NUMBER: UPN-1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3109
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
    APPLICATION NUMBER: PCT/US95/08565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09128155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or G
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88.9%;
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nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: CDNA PCT-US95-08565-17
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Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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US-09-128-155-17/c
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APPLICATION NUMBER: PCT/US98/04493
                                                                                  FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/038,621
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07
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RARLIER FILING DATE: 1997-04-11
RARLIER FILING DATE: 1997-04-11
ARLIER FILING DATE: 1997-04-11
ARLIER FILING DATE: 1997-04-11
                LILING DATE: 1998-03-06
PPLICATION NUMBER: 60/040,162
LING DATE: 1997-07
PPLICATION NUMBER: 60/040,333
                                                                                                                                                                                                               PLICATION NUMBER: 60/040,336
LING DATE: 1997-03-07
PLICATION NUMBER: 60/040,163
LING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE: 1997-05-43
ATION NUMBER: 60/047,617
nate: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
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3 DATE: 1997-05-23
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ION NUMBER: 60/047,581
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NATE: 1997-05-23
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LLING DATE: 1997-05-23
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ATE: 1997-05-23
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FILING DATE: 1997-05-23
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ATE: 1997-05-23
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LING DATE: 1997-04-11
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
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3 DATE: 1997-05-23
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DATE: 1997-05-23
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G DATE: 1997-05-23
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ATE: 1997-05-23
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             Length 32;
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                                                Indels
   Score 14.2; DB 1;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Endothelin Receptor
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                ADDRESSEE: CECCHI, STEWER & OLSTEIN
ADDRESSEE: CECCHI, STEWART & OLSTEIN
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Sequence 287, Application US/09149476
Sequence 287, Application US/09149476
Sequence 287, Application US/09149476
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ0022P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/09/030,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,687
FILING DATE:
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US-09-030-970-7/c
; Sequence 7, Application US/09030970
; Patent No. 6143319
                                                                               1 CGGGGATCACATGGTGCCG 19
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                                                                                                     26 CGGGCTCGCATGGTGGCG 8
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                                                                                                                                                                                                                                                                                                                                                                           6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSTEM: MS-DOS
WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
       Query Match 74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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ilarity 84.2%;
Conservative
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TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
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Best Local Similarity
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STATE: NEW JERSEY
COUNTRY: USA
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STREET: 6
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60/047,594

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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,669
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,313
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672
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CATION NUMBER: 60/056,903
                              ILING DATE: 1997-04-11
PPLICATION NUMBER: 60/043,312
                                                                                                                               TILING DATE: 1997-04-11
PPLICATION NUMBER: 60/043,315
                                                                                                                                                             ILING DATE: 1997-04-11
PPLICATION NUMBER: 60/048,974
ILING DATE: 1997-06-06
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PLICATION NUMBER: 60/056,893
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ING DATE: 1997-08-22
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ING DATE: 1997-05-23
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Length 1847;
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STREET: 119 No. 5741645th Fourth Street, Suite 203
CITY: Minneapolis
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Pred. No. 1.4e+02;
0; Mismatches 3;
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                                                                                                           FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,576
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EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                   FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,614
                                                                                            APPLICATION NUMBER: 60/043,578
                                                                                                                                                   APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,670
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                   APPLICATION NUMBER: 60/047,593
                                                                                                                                                                                                                                                                                                                                                           60/056,881
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1997-05-23
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Best Local Similarity 84.2%;
Matches 16; Conservative
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APPLICANT: Chung, Ming-y
APPLICANT: Zoghbi, Huda
TITLE OF INVENTION: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                          FILING DATE:
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TITLE OF INVENTION:
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INFORMATION FOR SEQ ID NO

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Gaps
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GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON: FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                 Length 3366;
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOHNTHARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/No ""
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                             Sequence 293, Application US/09221017B Patent No. 6444799
                                                                                                                                                                                                                                                                2628 CGGGGATCACCAGGTGCTG 2610
                                                                                                                                                                                                                              1 CGGGGATCACATGGTGCCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 27
ELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              circular
E: DNA (genomic)
                                                                                                                                               74.7%;
nilarity 84.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP29
FILING DATE: 09-APR-1998
          LENGTH: 3366 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4214 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .: NO
UNKNOWN
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16; Conserva
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ORIGINAL SOURCE:
                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                             US-09-221-017B-293
                                                                                                         US-08-267-803B-1
                                                                                                                                             Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                           RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zogibi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 74.7%; Score 14.2; DB 1; Length 3366; Best Local Similarity 84.2%; Pred. No. 1.5e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A. STREET: P.O. Box 581415
CITY: Minneapolis
                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
UNRRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JHN-1004
                                                                                                                                     APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2628 CGGGGATCACCAGGTGCTG. 2610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08267803B Patent No. 5834183
                                                            IBM PC compatible
                                                                                                                                                                                                             NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                             TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           3366 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCormack, Myra H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ranum, Laura P
Chung, Ming-yi
                                                                                                                                                                                                                                                                                                                TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                         FILING DATE: 06
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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55401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IS-08-267-803B-1/c
                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-469-802B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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RESULT 14

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; FEATURE: ; NAME/KEY: misc_feature ; LOCATION: 1...4214 US-09-221-0178-293

0; Gaps Score 14.2; DB 4; Length 4214; Pred. No. 1.5e+02; 0; Mismatches 3; Indels 0; Query Match 74.7%; Best Local Similarity 84.2%; Matches 16; Conservative

. М QQ

Search completed: July 8, 2003, 09:31:08 Job time: 32.2793 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 19:09:54 ; Search time 109.737 Seconds

(without alignments)

273.390 Million cell updates/sec
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	(Without alignments) 273.390 Million cell upd	l upd
Title:	US-09-647-780A-8	
Sequence:	1 cggggatcacatggtgccg 19	
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	,
Searched:	1105431 segs, 789497651 residues	

meters:	,	
Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
ĭ	W W	A.

2210862

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

DB ID Decreases Surgering									•	: •											
Ouery Score Match Length DB I I I S 8 83.2 1107 10 15.8 83.2 1107 10 14.8 77.9 240 10 14.8 77.9 831 9 0 14.8 77.9 24533 9 0 14.8 77.9 152331 9 0 14.4 75.8 14962 9 0 14.4 75.8 3122 9 0		Description			Seguence 284, App	Sequence 2432, Ap	Sequence 81, Appl	Sequence 10019, A	Sequence 6, Appli	Sequence 8727, Ap	Sequence 1349, Ap	Sequence 16, Appl	٠. ٦	Sequence 27728, A	Sequence 11096, A	Sequence 6527, Ap	Sequence 1325, Ap	Sequence 24, Appl	Sequence 6, Appli	Sequence 244, App	Sequence 244, App
Score Match Length DI Match Length DI S. 8 83.2 1107 15.8 83.2 1107 15.4 83.2 1107 14.8 77.9 2087 14.8 77.9 2087 14.8 77.9 15.231 14.8 77.9 15.231 14.4 75.8 251 14.4 75.8 14662 14.4 75.8 146	SUMMAKIES	ΠD	US-09-973-765-1	US-09-973-712-1	US-09-764-864-284	US-09-923-876-2432	US-10-079-623-81	US-09-867-701-10019	US-10-029-217A-6	US-09-764-891-8727	US-09-764-868-1349	US-10-095-407-16	US-10-095-407-17	US-09-864-761-27728	US-09-864-761-11096	US-09-815-242-6527	US-09-917-800A-1325	US-10-161-803-24	US-10-013-477-6	US-10-079-854-244	US-09-764-878-244
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Result No		- 7	15.8	15.8	15.4	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4
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Sequence 1, Application US/09973712 Patent No. US20020106752A1

Sequence 7, Appli	Sequence 10553, A	Sequence 25291, A		Sequence 20655, A	Sequence 31928, A	Sequence 6460, Ap	Sequence 365, App	Sequence 152, App	013,	Sequence 13, Appl	Sequence 996, App	Sequence 535, App	Sequence 13, Appl	Sequence 13, Appl	Sequence 1, Appli	Sequence 133, App	Sequence 7096, Ap		Sequence 290, App	Sequence 5479, Ap	Sequence 10206, A	Sequence 1005, Ap	Sequence 4, Appli	Sequence 1, Appli	Sequence 5, Appli
0S-10-292-525-7	10 US-09-867-701-10553	US-09-918-995-25291	US-09-918-995-22699	US-09-918-995-20655	US-09-918-995-31928	US-10-156-761-6460	10 US-09-910-943-365	10 US-09-910-943-152	9 US-10-156-761-2013	US-10-239-420-13	10 US-09-974-300-996	US-10-037-270-535	US-10-116-821-13	US-10-117-283-13	US-10-116-175-1	US-10-197-666A-133	US-10-156-761-7096	US-09-809-391-287	US-10-156-761-290	US-09-764-891-5479	US-09-764-891-10206	US-10-205-428-1005	US-10-017-273A-4	.0 US-09-905-846-1	3. US-10-017-273A-5
32 9	309	458	464	200	502	504 9	750 1	771. 1	915 . 5	1150 9	1203 1	1411 9	1518 9	1518 9	1620 9	1717 9	1725 9	1847 9	2118 9	2232 9	2232 9	2232 9	2893 9	2893 1	2975
74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7
14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2
c. 20	21	c 22	c . 23	c 24	. 25	. 56	c 27	28	c 29	30	c 31	c 32	33	34	. 35	c 36	c 37	38	c 39	40	41	42	c 43	C 44	c 45
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ALIGNMENTS

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Gaps
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                                                                                                             ITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8;
                                                                                                                                                                      CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: DE 100 50 123.0
PRIOR FILING DATE: 2000-10-11
                                                                                                                                                                                                                                                                                                                     ORGANISM: Amycolatopsis orientalis
, Application US/09973765
US20020090684A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 CGGGGATCAGATGGTTCCG 202
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                                                                                                                                                                                                                                                : PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 83.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                      BOMMARIUS, ANDREAS
DRAUZ, KARLHEINZ
VERSECK, STEFAN
                                                                                                                             FILE REFERENCE: 214381US-1075
CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2001-10
                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)..(1107)
; OTHER INFORMATION:
US-09-973-765-1
                                                                                                                                                                                                                                                                                                                                                  FEATURE: NAME/KEY: CDS
                                                                                                                                                                                                                                                                SEQ ID NO 1
LENGTH: 1107
                                                                                                                                                                                                                                                                                                       TYPE: DNA'
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Gaps
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                                                                                                                                                                                                                                                                                                                               Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 491;
                                                                                                                                                                                          OTHER INFORMATION: Incyte, ID No. US20020013958A1 700160596H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CON: mammary gland and methods for their use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: HATLOCKEY, SUSAN L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                          Score 14.8; 'DB 10;
Pred. No. 2.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14.8; DB 9;
Pred. No. 2.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/079,623 CURRENT FILING DATE: 2002-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
                                                                                                                                                                                                                      ; NAME/KEY: unsure
; LOCATION: 43, 174, 183-184, 197-198
: OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-2432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10019, Application US/09867701
Patent No. US20020132237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 81, Application US/10079623
Patent No. US20020169302A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1) ... (491)
; OTHER INFORMATION: n = A,T,C or G
US-10-079-623-81
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Havukkala, 11kka J. APPLICANT: Glenn, Matthew APPLICANT: Grigor, Murray R. APPLICANT: Molenar, Adrian J. TITLE OF INVENTION: Compositions TITLE OF INVENTION: mammary glar PILE REFERENCE: 11000.1044c3
                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGGATCACATGGTGCCG 19
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                                                                                                                                                                                                                                                                                                                          Ouery Match 77.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGRAM
SEQ ID NO 2432
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.9
Best Local Similarity 88.9
Matches 16, Conservative
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                                                                                                                                 ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-867-701-10019/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-079-623-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH:
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                                      TITLE OF INVENTION: ACETYL AMINO ACID RACEMASE FROM AMYCOLATOPSIS ORIENTALIS FOR RACE TITLE OF INVENTION: CARBAMOYL AMINO ACIDS
FILE REFERENCE: 2143820505
CURRENT APPLICATION NUMBER: US/09/973,712
CURRENT APPLICATION NUMBER: D01-10-11
PRIOR APPLICATION NUMBER: DE 10050124.9
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Sequence 2432, Application US/09923876

GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TILLE OF INVENTION: POLXVUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1107;
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
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Pred. No. 1.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.8;
Pred. No. 6
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CURRENT FILING DATE: 201-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equence 284, Application US/09764864 atent No. US20020132753A1
                                                                                                                                                                                                                                                                                                      ORGANISM: Amycolatopsis orientalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 CGGGGATCAGATGGTTCCG 202
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                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.2%;
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Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 89.5'
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-09-764-864-284
                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)..(1107)
; OTHER INFORMATION:
US-09-973-712-1
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LENGTH: 970
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TILE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY ITLE OF INVENTION: AND USES THEREOF
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    Length 20987

    refer to PALM or file wrapper

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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT232
                                            2; Indels
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      ; DB 9;
2.5e+02;
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  Score 14.8; DB
Pred. No. 2.5e+
0; Mismatches
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Best Local Similarity 88.9%; Pred. No. 2.7e
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
FILING DATE: removed - refer to NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/054,646.
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                               Sequence 1349, Application US/09764868 Patent No. US20020168711A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/10095407
Patent No: US20020164330A1
                                                                                                          ; LOCATION: (1)...(152331); ; OTHER INFORMATION: n = A,T,C or G US-10-095-407-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65525 Cressarcaccresrec 65542
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                                            Conservative
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LOCATION: (1)...(15233:
                       Similarity
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Best Local Similarity
Matches 16; Conserv
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LENGTH: 24533
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                                                                                                                                                                                           Gaps
                                                                                                                                            Length 831;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8727
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                       Indels
                                                                                                                                            Score 14.8; DB 10;
Pred. No. 2.2e+02;
                                                                                                                                                                                         0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10019
LENGTH: 831
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Publication No. US20030077808A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/257,761
PRIOR FILING DATE: 2000-12-21
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Matches 16; Conservative
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OLSON, ERIC N. APPLICANT: WANG, DA-ZHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
                                                                              ; ORGANISM: Homo sapien
US-09-867-701-10019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (1)..(1053)
US-10-029-217A-6
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US-09-764-891-8727
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                                                             TYPE: DNA
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Gaps

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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILLE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXPRESSED IN BONE MARROW, SIGNAL - 0.87
EXPRESSED IN ADULT LIVER, SIGNAL - 0.86
EXPRESSED IN LUNG, SIGNAL - 1.1
EXPRESSED IN FETAL LIVER, SIGNAL - 0.83
EST_HUMAN HIT: BE379328.1, EVALUE 7.60e-02
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MUMBER: PCT/US01/00662
2001-01-30
                                       PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
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                                                                                                                                                                                                      PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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DATE: 2000-09-27
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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Patent No. US20020048763A1
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Best Local Similarity
Matches 15; Conserv
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ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                               GENERAL INFORMATION:

SPPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CORRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR APPLICATION NUMBER: US 60/094,646
PRIOR PILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SSOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 2.7e+02;
0; Mismatches 2;
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CURRENT FILING DATE: 2001-05-23
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APPLICATION NUMBER: US 60/207,456
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APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
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Patent No. US20020048763A1
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                                  Sequence 17, Application US/10095407
Patent No. US20020164330A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 17
LENGTH: 176373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
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US-09-917-800A-1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2051;
                                                                                                                                                                                                                                Length 546;
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Pred. No..3.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                  DB 10;
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                                                                                                                                                                                                                                                    :5e+02;
                                                                                                                                                                                                                                  Score 14.4; D:
Pred. No. 3:5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/917,800A
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6527
LENGTH: 546
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APPLICATION NUMBER: US 60/222,880
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PRIOR APPLICATION NUMBER: US 60/290,645
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PRIOR APPLICATION NUMBER: US 60/292,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
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PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1325, Application US/09917800A Patent No. US20020119462A1 GENERAL INFORMATION:
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                                                                                 TYPE: DNA ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                          277 GGCTCACATGGTGCCG 292
                                                                                                                                                                                                                                                                                                                    4 GGATCACATGGTGCCG 19
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Best Local Similarity 93.8%;
Matches 15; Conservative
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                                                                                                                                                                                                                                Query Match 75.8%;
Best Local Similarity 93.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elashoff, Michael
Gene Logic, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Rattus norvegicus
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                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (1)...
US-09-815-242-6527
                                                                                                                             FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.87 INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.86 INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1 INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILE OF INVENTION: Identification of Essential Genes in ITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11096
LENGTH: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                           FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                              APPLICATION NUMBER: PCT/USO1/00670
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
  PCT/US01/00668
                                       PPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                              FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-06 30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR APPLICATION NUMBER: 60/191,078
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APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
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APPLICATION NUMBER: 60/253,625
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APPLICATION NUMBER: 60/257,931
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Zyskind, Judith W.
Wall, Daniel
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Carr, Grant J.
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATI
US-09-864-761-11096
               PRIOR A
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Job time : 109.787 secs

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BQ984595 515 bp mRNA linear EST 21-AUG-2002 QGE3005 yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that corrected incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                           T (bases 1 to 515)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project http://comgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                           Lactuca sativa
Makaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: akozikeatgc.org [michelmoreevegmail.ucdavis.edu]
belongs to contig QG_CA_Contig3484, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Alexander Kozik [R.W. Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Thel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="QG_EFGHJ lettuce serriola"
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Location/Qualifiers
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/clone="QGE3c05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_SEQ-GCTAGTCGGG"
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                                                                                                                                                                     BQ984595.1 GI:22402120
                                                                                              OGE3c05, mRNA sequence.
BQ984595
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RESULT 15
BQ984595
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DEFINITION
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ö Score 16.4; DB 14; Length 515; Pred. No. 1.1e+03; 0; Mismatches 1; Indels 0 Ouery Match
Best Local Similarity 94.4%;
Matches 17; Conservative (

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Search completed: July 8, 2003, 09:21:26 Job time : 968.404 secs

130 CAGGGATCACATGGTGCC 147

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WHILE SHAPP M.S3.3, NIH.BMAP M.S3.2, NIH.BMAP M.S3.1,
NIH.BMAP M.S2, NIH.BMAP M.S1. The subtracted library
NIH.BMAP M.S4) was constructed as follows: Portamplified
CDNA inserts from NIH.BMAP M.S3.3, NIH.BMAP M.S3.2, and
NIH.BMAP M.S3.1 clones from which 3' ESTS had been derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NIHE_BMAP_M.54"
/dev_stage="127-32 days"
/dev_stage="127-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
Polylinker; Site_l: Not I; Site_2: Eco RI; The
Polylinker; Site_l: Not I; Site_2: Eco RI; The
NIHE BMAPP_M.54 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
   EST 04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of CDNAs from which ESTS had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Sesarchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                   Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
BF468707
UI-M-BH3-atg-f-07-0-UI.I NIH_BMAP_M_S4 Mus musculus cDNA clone
UI-M-BH3-atg-f-07-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Chin, H
National Institute of Mental Health
National Institute of Mental Health
20801-8643, USA
Tel: 301 443 1766
Fax: 301 443 9890
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Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mEST@mail.nih.gov
                                                                                                                                    BF468707.1 GI:11537890
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                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                            discovery
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uf62b09.x1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1515929 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pr713D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo.
                                AW823984 467 bp mRNA linear EST 17-MAY-2000 uf62b09.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1515929 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 503)

NCI-CRAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                               1 (bases 1 to 467)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_11b-"Soares_mammary_gland_NMLMG"
/clone_11b-"Soares_mammary_gland_NMLMG"
/tissue_type-"mammary gland"
/lab_host-"bH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.3%; Score 16.4; DB 10; 94.4%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 455.
Location/Qualiflers
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                                                                                                                            AW823984.1 GI:7917061
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Matches 17; Conservative
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Unpublished (1997)
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AW823459/c
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RESULT 11
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Gaps

Length 457; Indels 0

Score 16.4; DB 12; Pred. No. 1e+03;); Mismatches 1;

86.3%; 94.4%;

Query Match Best Local Similarity Matches 17; Conserv ö

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Indels

Length 504;

10;

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with a Not I - oligo(dT) primer. Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                         Score 16.4; DB 1
Pred. No. 1e+03;
                                                                                                                                                                                                                   0, Mismatches
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Location/Qualifiers
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Conservative
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Best Local Similarity
Matches 17; Conserv
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ORIGIN
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KEYWORDS
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JOURNAL
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AA214179
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                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: 1st strand CDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - 01190(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library mas constructed by Bento Soares and M. Fatima Bonaldo."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 504)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contact the
                                                                                                              information.
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Other_ESTs: uf79903.yl
Contact: Robert Strausberg, Ph.D.
Emal: cgapbs-remail.nlh.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pT/T3D-Pac (Pharmacia) with a modified
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                                                            Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL
IMAGE Consortium (info@lmage.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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/sex="female (lactating)"
                                                                                                                                                                                                                                                                           /clone_lib="Soares_mammary_gland_NMLMG"
                                                                                                                                                                                                                                                                                                 /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="IMAGE:1528372"
                                                                                                                                                                                                              /organism-"Mus musculus"
                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                               High quality sequence stop: 421.
Location/Qualifiers
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Location/Qualifiers
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/clone="IMAGE:1515929"
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    Tumor Gene Index
Unpublished (1997)
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Best Local Similarity 94.4
Matches 17; Conservative
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TITLE
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AA214179
AA214179
AA20607.11 Stratagene hWT neuron (#9437223) Homo sapiens CDNA clone IMAGE:649284 5' similar to contains Alu repetitive element; contains element MER22 repetitive element; mRNA sequence.
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1 (bases 1 to 514)

### Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kuchan,T., Le,N., Le,N., Lennon,G., Marra,M., Martin,J., Mylle,T., Walterston,R., Steptoe,M., Tan,F., Theising,B., WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
MAGE Consortium (info@mage.llnl.gov) for further information.
Insert Length: 2292 Std Error: 0.00
Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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/dev_stage="hwT neurons"
/lab_host="SOLR (kanamycin resistant)"
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Pred. No. 1.1e+03;
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us-09-647-780a-8.rst

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The sequence containings an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized brain stems library CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAPP cDNA is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements POLNA-Yes.
                                                                                             6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                    Contact: Chin, H
National Institute of Mental Health
                                                                                                                                                                                                          Email: mEST@mail.nih.gov
                                                                                                                                                 Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                           20892-9643, USA
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Best Local 9
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BF468707
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/foct="pooled cell_lines" (cell_line=CRL-1751 WEHI 164),
(cell_line=CRL-2116 JG), (cell_line=RCB-0035 WEHI-3),
(cell_line=RCB-0464 Meth-A), (cell_line=RCB-0545 OHTA),
(cell_line=RCB-0559 K-1 F1), (cell_line=RCB-1283 B16
metalenoma), (cell_type=B cell_s, cell_line=RCL-170 WEHI 231
), (cell_type=B cell_s, cell_line=CRL-2055 MITC-1),
(cell_type=Nullipotent stem cell_cell_line=CRL-2070 NE),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell_line=CCL-142 RAG), (tissue_type=submandibular gland, cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C, cell_type=B cells, cell_line=CRL-1669 BCL1 Clone 13.20-3B3), (strain=C3H, tissue_type=brain, cell_line=CRL-1443
                                                                                                                                                                                                                                                                                        sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
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                                                                              prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
waqi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
arninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW492539
UI-M-BH3-atg-f-07-0-UI.S1 NIH_BMAP_M_S4 Mus musculus cDNA clone.
UI-M-BH3-atg-f-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 432)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="RIKEN full-length enriched, RCB-0035 WEHI-3
                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system--384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (tissue_type=bone marrow, cell_type=stroma cell
cell_line= CRL-2028 SR-4987), (tissue_type=col
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Pred. No. 9.9e+02;
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'organism="Mus musculus"
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'clone="G430142108"
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/ Jab_nost="Whole (Life Technologies) / Jab_nost="Wetcor: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NiH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygadala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, The subtracted library (NIH_BMAP_M_S3.1, The subtracted library (NIH_BMAP_M_S3.1, Ichones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, and NIH_BMAP_M_S3.1; libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
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                                                                                                                                                                      /clone="UI-M-BH3-atg-f-07-0-UI"
/clone_lib="NH-BMAP_M-S4"
/clone_lib="NH-BMAP_M-S4"
/lab_host="DH10B (Life Technologies)"
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Pred. No. 1e+03;
0; Mismatches 1;
                                                                   /organism-"Mus musculus"
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TAG_TISSUE-brain-stems
                                                                                                                                          /db_xref="taxon:10090"
Location/Qualifiers
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٠	zo: em_gss_pro:* 27: em_gss_rod:*				Eukaryota; Me	F. Me
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•		Description	BG055194 nad03e01.	BF992713 CM1-GN016	BQ990877 QGF21F15.	AW908567 uf79q03.v	BE448826 ut88c12.v	, BB751033 BB751033	
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		nRNA lens cDNA element; c	rarrhini gov/nci r Genome rownstei nto Soar ennon, P niversit
BQ980809 BB792684 AW492539 BF468707 AW823459 AW823459 AA214179 BQ984595 BQ984595 BQ118971 BU010846 BQ983268 BW557704 BW557704 BW557704 BW557704 BW557704 BW557704 BW557704 BW557704 BW6883268	BB0B9035 BB0B43003 BB0B43003 BBCB20119 BBCD119635 AQ607581 AQ607560 BG607260 BG607260 AQ356342 AQ36659 AQ356342 AQ36669 AQ356342 AQ3693825 BF203825 BF203825 BF203825 BF204340 CNSQ40MC CNSQ40MC	ALIGNM 325 b 128 Homo u repeti mRNA seq	lm.n Can Can Ov 1 J. M. Greg gton Greg
	671 14 372 9 372 9 414 17 414 17 462 17 651 17 651 17 651 17 651 17 651 17 657 17 957 17 1046 17 1046 17	NCI_CGAP contains element ; GI:12512	Mammalia: Futheria: Primates; 1 (bases 1 to 325) NCI-CGAP http://www.ncbi.nlm.n National Cancer Institute, Can Tumor Gene Index Tumor Gene Index Orpublished (1997) Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Michael J. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. CDNA Library Arrayed by: Greg DNA Sequencing by: Washington Clone distribution: NCI-CGAP found through the I.M.A.G.E. Canfelmage.llnl.gov.
	666 667 667 667 667 667 667 667	BG055194 nad03e01.x1 similar to c EG055194 BG055194.1 EST. human.	Mammalia: Butheria; 1 (bases 1 to 325) NCI-CGAP http://www NCI-CGAP ttp://www NCI-CGAP ttp://www Corbublished (1997) Contact: Robert Strammal: cgapbs-remail Tissue Procurement: Emmert-Buck, M.D., Emmert-Buck, M.D., Ennest-Buck, M.D., Coba Library Arraye DNA Library Arraye DNA Sequencing by: Clone distribution: found through the I. info@imaqe.ilni.gov
	नम - ननननननननननननननननननन	RESULT 1 BG055194 LOCUS DEFINITION ACCESSION WESTOON KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT

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/organism="Lactuca sativa"
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Fax: 1-(530)-752-9659
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ilarity 94.4%;
Conservative
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                                                                                                                                                   BASE COUNT
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KEYWORDS
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BQ990877
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                                                                                                                                                                                       /note="Organ: prostate; Vector: pr713D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_PIZ2 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
a 108 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 12.2)

1 blas Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balia, G.S., Singson, D.H., Parnstein, A., deoliveire, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMl&t2=CMl-GN0161-301000-517-h04&t3=2000-10-30&t4-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF992713 122 bp mRNA linear EST 23-JAN-2001 CM1-GN0161-301000-517-h04 GN0161 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 12;
Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                         /clone_lib="NCI_CGAP_Pr28"
                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens
/db_xref="taxon:9606"
                                                                                  /clone="IMAGE:3432289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence start: 9
High quality sequence stop: 122
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
                                                              xref="taxon:9606
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_11b="GN0161"
                                                                                                                                               /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.5%;
100.0%;
                                                                                                                             /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.5
Best Local Similarity 100.
Matches 17; Conservative
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BF992713
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ORIGIN

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TITLE

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242 bp mRNA linear EST 21-AUG-2002 QGF21F15.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone QGF21F15, mRNA sequence.
/note-"Organ: placenta_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison Damme, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Lettuce and Sunflower ESTs from the Compositae Genome Project Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Embryophyta; Tracheophyta;
                                                                                                     population No. 136,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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                                                                                                                                                                                                                                                                                                                                                                               Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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/lab_host="E.coli"
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                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 12;
Pred. No. 6.9e+02;
); Mismatches 1;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. bases 1 to 391)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                       Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3369526"
/clone_lib="Soares_mammary_gland_NMIMG"
                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                 Seq primer: -40RP from Gibco
High quality sequence stop: 3
Location/Qualifiers
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                                                                                                                                                                                              MGI:1079130
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Best Local Similarity
Matches 17; Conserv
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BB751033
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                                                                                                                                                                                                                                 AW908567 383 bp mRNA linear EST 25-WAY-2000 uf79903.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1528372 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI CGAP http://www.ncbl.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was constructed by Bento Soares and M. Fatima Bonaldo.
94 c 110 g 97 t 1 others
                                                           Gaps
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                Length 242;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/lasue_type="mammary gland".
/lab_host="DH10B"
              Score 16.4; DB 14;
Pred. No. 8.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="IMAGE:1528372"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGE: 3369526 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:944472
Seg primer: -40RP from Gibco.
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                                                                                                                107 GAGGATCACATGGTGCCG 124
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                                                                                            2 GGGGATCACATGGTGCCG 19
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              86.3%;
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                                                       17; Conservative
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                                  Best Local Similarity
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Matches 17; Conserv
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                Query Match
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ORIGIN
                                                     Matches.
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AW908567
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Jobest Wester: pt773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and clonned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Patima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishli
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Salto,R., Sakal,C., Sakal,K., Sakazume,N., Sasaki,D., Sato,K:, Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Waramatsu,M. and Hayashizaki,Y. RIKEN Encyclopedia of Mouse Full-length cDNAS (Akimura,T., et al.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 410)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB751033 RIKEN full-length enriched, pooled tissues, cerebellum, etc. Mus musculus cDNA clone G130203K05 3', mRNA sequence.
BB751033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.4; DB 10;
Pred. No. 9.7e+02;
0; Mismatches 1;
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
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ilarity 94.4%;
Conservative
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Asmundson Hall, UCD,
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BB792684
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,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison
P., Kolkman, J., Slabaudh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, R.
Lettuce and Sunflower ESTs from the Compositae Genome Project
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                                                                                          prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wag1,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahlki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                       Shibata, K., Itoh
                                                                                                                                                                                                                                                              sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo
ex=mixed);
                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                    encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . ii (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RIKEN full-length enriched, pooled tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=0 days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 9.8e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                  Computer-based methods for the mouse full-length cDNA
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Department of Vegetable Crops, R.W.Michelmore Lab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ∕organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Mammalia; Butheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 414) Arimura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Tito, M., Rawai, J., Kojina, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Ashira, S., Tanaka, T., Tomaru, A.; Toya, T., Watchiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Income "Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                  Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig3186, see http://cgpdb.ucdavis.edu/
for details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="QG_EFGHJ lettuce serriola"
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Pred. No. 9.9e+02;
California at Davis (UCD)
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URL:http://genome.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:4236"
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                                                       Tel: 1-(530)-742-1742
                                                                                           Fax: 1-(530)-752-9659
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ilarity 94.4%;
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Title: Perfect score:

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                                                                                                  Genomic sequence
Genomic sequence
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                                                                                                    AAS28364
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11009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouimet T, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FR2777291-A1
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      AAZ28815;
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Arabidopsis thalia
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Human ovarian anti
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Rat membrane metal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                             (without alignments)
358.431 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:
                                                                                                                          ; Search time 131.941 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/qcgdata/geneseq/geneseqn-embl/NA1992.DAT
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT
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/gogdata/geneseq/geneseqn-embl/NA1996.DAT
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/SIDS2/gcgdata/geneseg/genesegn-embl/NA2000.DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981
                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                            2185239 seqs; 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAC48434
AAC39055
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AAV58755
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                                                                                               nucleic search, using sw model
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                                                                                                                                                                                                                                                              IDENTITY_NUC Gapox 1.0
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length: 2000000000
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Match
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WPI; 1999-593429/51.

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Sequences AA228811-228827 represent probes for detecting the rat membrane metalloprotease designated neprilysine II (NEPII) gene (AA228810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic- hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the gene for the rat membrane metalloprotease
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds.
 involved in proteolysis of
to screen for inhibitors,
cardiovascular disease -
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to screen for inhibitors,
cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                          0.32;
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                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 5 A; 7 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                        Score 21; DB Pred. No. 0.3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat membrane metalloprotease NEPII gene
New membrane metalloprotease NEP II, neuronal and hormonal peptides, used potentially useful for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New membrane metalloprotease NEP II,
neuronal and hormonal peptides, used
potentially useful for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                              21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                              1 CTACCCCAAGCTGCGTGATAG
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98FR-0004389
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                                                                       Page 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAY44177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-0CT-1999
                                                                                                                                                                                                                                                                     disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ28810;
                                                                       Claim 3;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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male erectile dysfunction (MED) or female sevual dysfunction (FSD) (e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such as premature ejaculation, anorgasmia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is SEP consensus DNA sequence found in human, mouse and rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sexual dysfunction,
dysfunction such as
disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 င္ပွဲ
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits for selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endopeptidase; SEP; endocrine; vasotropic; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ne; gynaecological; antisense-therapy; male erectile dysfunction; female sexual dysfunction; FSD; female sexual arousal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wayman CP; Phillips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunctor e.g. male erectile dysfunction or female sexual dysfunction su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated and/or purified nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat;
                                                                                                                                                                 ö
                                                                                                                           Length 2765;
                                                                                         G; 559 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Soluble secreted endopeptidase (SEP) consensus DNA.
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"Encodes catalytic domain"
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                                                                                                                           100.0%; Score 21; DB 20; 100.0%; Pred. No. 0.55;
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                                                                                                                                                                   Mismatches
                                                                                           787
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1664..2286
                                                                                                                                                                                                                          363 CTACCCCAAGCTGCGTGATAG 383
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                                                                                           Sequence 2765 BP; 684 A; 735 C;
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                                                                                                        Query Match
Best Local Similarity
Local 21; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted
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                   99US-0138540.
99US-0138540.
99US-0138847.
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990S-0144814
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990S-0145086
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990S-0145192
990S-0145145
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990S-0145213
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99US-0144352
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990S-01394
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990S-01397
990S-01397
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990S-0140
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                                                                          -JUN-1999;
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                                                                                                         Gaps
                                                             Score 19.4; DB 24; Length 2286;
Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                      Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                   Indels
             Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO: 57464.
                                                                                               0; Mismatches
                                                                                                                                                 246 CCACCCCAAGCTGCGTGATAG 266
                                                                                                                                1 CTACCCCAAGCTGCGTGATAG 21
                                                                                                                                                                                                              RESULT 4
AAC48434/C
ID AAC48434;
XX
AC AAC48434;
XX
XX
XX
T 18-OCT-2000 (first entry)
XX
T 18-OcT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment
XX
Hybridisation assay; genetic man protein identification; signal metabolic pathway; promoter; te.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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1999; 990x-01394 1999; 990x-01394 1999; 990x-01394 1999; 990x-01394 11999; 990x-01394 11999; 990x-01394 11999; 990x-01394 11999; 990x-01394 11999; 990x-01397 11999; 990x-01397 11999; 990x-01397 11999; 990x-01398	JUN-1999; 99US-01403 JUN-1999; 99US-01403 JUN-1999; 99US-01408 JUN-1999; 99US-01409 JUN-1999; 99US-01418 JUL-1999; 99US-01418 JUL-1999; 99US-01418 JUL-1999; 99US-01421	JUL-1999; 990S-014239; 990S-014280; JUL-1999; 990S-014290; 990S-014297; JUL-1999; 990S-014362-JUL-1999; 990S-0144008; JUL-1999; 990S-0144008; 990S-014408; 990S-0144	-ULL-1999; 990S-014433. -ULL-1999; 990S-014433. -ULL-1999; 990S-014433. -ULL-1999; 990S-014433. -ULL-1999; 990S-014433. -ULL-1999; 990S-014488. -ULL-1999; 990S-014488. -ULL-1999; 990S-014488.	1999; 9905-014508 1999; 9905-014518 1999; 9905-014514 1999; 9905-014521 1999; 9905-014521 1999; 9905-014591 1999; 9905-014591 1999; 9905-014591 1999; 9905-014638 1999; 9905-014638 1999; 9905-014638	ANG-1999; 99US-014719 ANG-1999; 99US-014719 ANG-1999; 99US-014730 ANG-1999; 99US-014749 ANG-1999; 99US-014741 ANG-1999; 99US-014741 ANG-1999; 99US-014831 ANG-1999; 99US-014831 ANG-1999; 99US-014831 ANG-1999; 99US-014831 ANG-1999; 99US-014831

ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrol pCOS; ovarian cyst, dysmenorrhoea; endocrine disorder; infection; informed disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis;

ovarian antigen; ovary; ovarian; breast; cancer; tumour;

Human ovarian antigen HAOTX62 cDNA, SEQ ID NO:930.

(first entry)

neuroprotective;

antiinflammatory; gynaecological; reproductive; gene; antibody preparation; cytostatic; immunomodulatory;

07-JUN-2001; 2001WO-US18569.

40200200677-A1 Homo sapiens

33-JAN-2002.

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The present sequence encodes a murine neutral endopeptidase metallopeptidase-like enzyme, designated NL-1. The specification also describes NL-2 and NL-3. The NL enzymes are used to test for specific inhibitors. The NL-erminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimeric constructs containing the foreign protein downstream from and in phase with the N-terminal region. The NL enzymes are have been localised to the brain, and may be useful in the treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders. NL enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product- "neutral endopeptidase metallopeptidase-like enzyme NL-1"
                                                                                                                                                                                                                                                                                                                                         Neprilysin; neutral endopeptidase metallopeptidase-like enzyme; NBP-like enzyme; prodeln production; protein secretion; neurological disease; Alzheimer's disease; pain; psychiatric disorder; fertility; bone disease; abnormal phosphate metabolism; ss.
                                                                                                                                                                                                                                                             cDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2925 BP; 710 A; 797 C; 836 G; 582 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 332..2629 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 3; 59pp; English.
AAA63763 standard; cDNA; 2925 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and abnormal phosphate metabol
processing by the NL-3 enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desgroseillers L, Boileau G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-2000; 2000WO-CA00147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99CA-2260376
                                                                                                                                                                             (first entry)
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P-PSDB; AAB08130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-1999;
                                                                                                                                                                         04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-2000
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ABP43228) and to convaire numeral variation during also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodes against human ovarian antigen antigen polynucleotides and polypeptides in diagnosing treating, progracing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system of disorders (e.g., infertility, disorders of pregnancy, anovilation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and immunodeficiencies autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modulate ovarian antigen expression or activity. The polynucleotides may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in disease diagnosis, drug targeting and phenotyping. The present ce represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                       the invention relates to 2175 novel human ovarian antigens (ABP41054-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             solypeptides may be used as food additives or to prepare antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ynucleotides may also be used in screening for compounds which
                                                                                                                                                                                                                                                                evention, treatment and diagnosis of cancer (e.gimmune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            system disorders. Ovarian antigen polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or gene therapy, chromosome mapping, in
individuals and in forensic analysis,
                                                                                                                                                                                                                                          encoding novel ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1521 BP; 436 A; 321 C; 336 G; 421 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 930; 2922pp; English.
                                                                                                                                                                                                                                          solated nucleic acid molecules
                                                 (HUMA-) HUMAN GENOME SCI INC
07-JUN-2000; 2000US-209467P
                                                                                                                                                                                                                                                                     useful in the prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be used for gene
                                                                                                                                                                                                                                                                                                                       neurological diseases
                                                                                                                                                             WPI; 2002-147878/19.
P-PSDB; ABP41973.
                                                                                                           Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dentification of
                                                                                                                                                                                                                                                                                                    ovarian cancer)
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Gaps

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0; Mismatches Pred. No. 24; Score 17.8;

Conservative

Local Similarity es 19; Conserv

Query Match Best Local S: Matches 19

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84.8%; 90.5%;

1 CTACCCCAAGCTGCGTGATAG 21

ABQ55050 standard; cDNA; 1521 BP

RESULT 7 ABQ55050 ПX

ABQ55050;

Length 2925; Indels

DB 21;

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Gaps

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Indels

5.

Pred. No. 74; 0; Mismatches

90.08;

18; Conservative

Best Local Similarity Matches 18; Conserv

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The invention relates to 592 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins. The polynucleotides can be used as probes for the folynucleotides can be used as probes for the polynucleotides and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and altergic reactions and conditions (e.g. Alzheimer's disease, parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for tissue regeneration, for wound healing and in the treatment of burns, inclsions and ulcers. The proteins are also useful for regulating haematopolesis and for treating myeloid or lymphoid cell deficiencies. Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autolumune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer; coagulation disorder; inflammatory disorder; Crohn's disease; incision; tissue regeneration; wound healing; burn; haematopolesis; myeloid cell deficiency; lymphoid cell deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crohn's disease) and tumours.; They are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Five hundred and ninety two polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viral infection; bacterial infection; fungal infection; diabetes; asthrautoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agostino MJ, Howes SH, Resnick RJ;
                                                              ö
            Length 1521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nutritional supplement;
                                                              Indels
          DB 24;
                                                           0; Mismatches
          Score 16.8;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA encoding secreted protein #389.
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                                                                                                                                    361 CTACCCCAAGCTGTGTAATA 380
                                                                                                            CTACCCCAAGCTGCGTGATA 20
                                                                                                                                                                                                                                                                                       ABK35251 standard; cDNA; 2026 BP.
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          80.0%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2001; 2001WO-US10224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2000; 2000US-195582P
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
Ouery Match
Best Local Similarity 90.03
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark HF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-179321/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-2001
                                                                                                                                                                                                                                                                                                                                      ABK35251;
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                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                ABK35251
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Score 16.8; DB 24; Length 2026;

80.08;

Query Match

624 A; 426 C; 425 G; 551 T; 0 other;

Sequence 2026 BP;

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a secreted or transmembrane protein on the basis of computer analysis of the encoding protein. It includes alternative reading frames encoding bg140.1 protein (see AAW69424.25). Homology is shown to some database sequences. The invention provides isolated polynucleotides (see AAV58754.63) obtained from human adult testis, brain, retina or placenta, or from foetal kidney or brain cDNA libraries. These are all deposited as AFCC 99353. They encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotides and secreted proteins - useful as, e.g. nutritional additives, immunostimulators, haemotopoiesis regulators and as diagnostic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for cDNAs encoding secreted proteins, or was identified as encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            novel human secreted proteins (see AAW69423-33) that may have e.g nutritional activity, immune stimulating or suppressing activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune stimulating or suppressing activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemostatic and thrombolytic activity, receptor/ligand activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition or other activities. They may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19; Length 2835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemotactic/chemokinetic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haematopoiesis regulating activity, tissue growth activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2835 BP; 869 A; 590.C; 622 G; 753 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human adult brain cDNA library using methods which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCCON JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This full-length cDNA clone, designated bg140_1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LaVallie ER,
Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; human; bp140_1; ds
                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein bp140_1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 68-69; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualiflers
                          1501 CTACCCCAAGCTGTGTAATA 1520
                                                                                                                                                                                            AAV58755 standard; cDNA; 2835 BP
1 CTACCCCAAGCTGCGTGATA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity, tumour inhibition oused for diagnostic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US04601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0036321
97US-0815381
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641..1651
/*tag= b
                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activin/inhibin activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agostino MJ, Jacobs
Racie LA, Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-520802/44.
P-PSDB; AAW69424-25.
                                                                                                                                                                                                                                                                                                           18-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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11-MAR-1997;
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                                                                                                                                                                                                                                                      AAV58755;
                                                                                                                                        RESULT 9
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(GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulating GA; M3 is useful for screening an agent capable of modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subject to a pathogen or sterile infilammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chronic) in a tissue, an allergic response in a subject, exposure of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an allergic response in a subject, exposure of a subject to a pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (4) treating (M5) an inflammation (especially chronic) or in a tissue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting granulocyte activation by detecting differential expression
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or sterile inflammatory disease, by contacting a tissue having:
inflammation with an agent that modulates the expression of gene(s)
from Gs in the tissue. MI is useful for detecting GCA; M2 is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to detecting (MI) granulocyte (GC) activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                   Human cDNA differentially expressed in granulocytic cells #1005
                                                                                                                                                                                                                                                                                                                                                                                                                                     viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psorilasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                granulocytic cell; DNA chip; bacterial infection;
                       Indels
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                       Mismatches
No. 77;
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                                                                                                             1711 CTACCCCAAGCTGTGTAATA 1730
.90.08; Pred.
                                                                                                                                                                                                                              ABK84434 standard; cDNA; 3328 BP.
                                                                  1 CTACCCCAAGCTGCGTGATA 20
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                                                                                                                                                                                                                                                                                                                        (first entry)
                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-435328/46
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200228999-A2
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                       18:
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                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                    RESULT 10
ABK84434
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             inflammatory disease (e.g. pooriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, paraitic infection, protozoal infection, fungal infection and MS is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part
response in a subject, exposure of a subject to a pathogen or sterile
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
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                                                                                                                                                                                                                                                                                                     Length 3328;
                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                    Sequence 3328 BP; 1052 A; 676 C; 768 G; 832 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #20704.
                                                                                                                                                                                                                                                                                                       DB 24;
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                                                                                                                                                                                                                                                                                                     Score 16.8; DE
Pred. No. 78;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                           2940 CTACCCCAAGCTGTGATA 2959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 3610 BP.
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90.0%;
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                                                                                                                                                                                                                                                                                                                             Local Similarity 90.0 les 18; Conservative
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                                                                                                                                                                                                                Cormat directly
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                                                                                                                                                                                                                                                                                                             Query Match
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WO200155448-A1
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14 - AUG - 2000;
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                                                diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AsS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                generating antibodies against it, detecting or
imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity the polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 imaging of sites expressing (II): (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity
                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                              Length 3610;
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                                                                                                                                                                                                        Sequence 3610 BP; 1009 A; 842 C; 848 G; 909 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #20703.
                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                          Score 16.8; 1
Pred. No. 79;
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                                                                                                                                                                                                                                                                                                                                2500 CTACCCCAAGCTGTAATA 2519
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                                                                                                                                                                                                                                                                                                              1 CTACCCCAAGCTGCGTGATA 20
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                                                                                                                                                                                                                                          Match 80.0%;
Local Similarity 90.0%;
les 18; Conservative
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
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P-PSDB; ABG20712.
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23-AUG-2000;
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The polypeptide and polynucleotide sequences have applications in diagnostics, forgansics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                        Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory; espiratory active; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence #206 encoding for novel human respiratory antigen
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                                                                                                                                                                                                                                                                                                                                                                             Length 4424;
                                                                                                                       amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the
                                                                                                                                                                                                                                                                                                               Sequence 4424 BP; 1282 A; 1001 C; 1041 G; 1100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                             DB 23;
                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                             Score 16.8; |
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACCCCAAGCTGTGTATA 3333
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                                                                                                                                                                                                                                                                                                                                                                                                          llarity 90.0%;
Conservative
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Best Local Similarity
Matches 18; Conserva
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        respiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel the manner of the polymorteory antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection e.g. diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the isolation of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7606 BP; 2043 A; 1602 C; 1685 G; 2276 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SED ID No 800; 546pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Barash SC, 'Ruben SM
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                                                                                                                                                                    2000US-024924
2000US-024926
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08-DEC-2000;
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7-NOV-2000;
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-SEP-2000;
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Ouery Match 80.0%; Score 16.8; DB 22; Best Local Similarity 90.0%; Pred. No. 86; Matches 18; Conservative 0; Mismatches 2; 1 CTACCCCAAGCTGCGTGATA 20

Gaps

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Length 7606;

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21-SEP-2000; 20000S-02342; 25-SEP-2000; 20000S-02342; 25-SEP-2000; 20000S-02349; 25-SEP-2000; 20000S-02354; 27-SEP-2000; 20000S-02358; 29-SEP-2000; 20000S-02353; 20-SEP-2000; 02353; 20-SEP-2000; 20000S-02353; 20-SEP-2000; 20000S-02353; 20-SEP-2000; 20000S-02353; 20-SEP-2000; 20000S-02353; 20-SEP-2000S-02353;  20-SEP-2000S-02353; 20-SEP-2000S-02353; 20-SEP-2000S-02353; 2
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02-OCT-2000;
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                                                                                                                                                                                                                                   Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory; respiratory active; ds.
                                                                                                                                                                                     Genomic sequence #207 encoding for novel human respiratory antigen.
                                               AAS28367 standard; DNA; 7608 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US01333
                                                                                                                                             (first entry)
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01-DEC-2000; 01-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 08-DEC-2000;

08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000 05-JAN-2001;

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2001WO-US01338
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WO200155367-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection e.g. diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SED ID No 801; 546pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM;
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90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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:0000S-02

musculoskeletal system; ds

AAL37558;

RESULT 15

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Isolated polypeptide for treating, preventing and or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.

diagnosis

WPI; 2001-451937/48.

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SEP-2000;
                                             NOV-2000;
                                                                                                 DEC-2000
                                                                                                          08-DEC-2000
08-DEC-2000
                                         NOV-2
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Ruben SM

Barash SC,

CA,

Rosen

(HUMA-) HUMAN GENOME

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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human itsues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, liug, or urogenital; (b) immune other cancers of the adresse, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound the infectious diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                  Example 2; SEQ ID NO 3923; 781pp + Sequence Listing; English.
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Best Local Similarity 90.0
Matches 18; Conservative
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Job time: 132.941 secs
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July 8, 2003, 01:24:03 ; Search time 28.9902 Seconds (without alignments) 222.151 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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21
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*

Issued_Patents_NA:

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## SUMMARIES

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	Description	Sequence 3. Appli		2.7	ì	, ,	, ;		H	1	m	1	'n	16,	17.	2	Sequence 1, Appli	. 99	99	Sequence 66, Appl	,99	3, 4	m	7	4	4	4	1
. `	CI	US-08-698-805-3	US-09-134-001C-1551	US-09-103-840A-2	US-09-103-840A-1	US-08-667-023-1	US-09-233-989-1	US-08-452-262-1	US-08-734-550-1	PCT-US96-07528-1	US-08-909-954-3	US-08-523-855A-1	US-08-539-205A-5	US-09-128-155-16	US-09-128-155-17	US-09-103-840A-2	US-09-103-840A-1	US-08-441-971-66	US-08-221-653-66	$\sim$	41	-	US-09-248-335-3	US-09-231-227-1	US-08-351-149-4	US-08-384-828-4	US-08-895-474-4	US-07-971-819A-1
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ф	Query Match	78.1	75.2	73.3	73.3	70.5	70.5	70.5	70.5	70.5	70.5	69.5	69.5	69.5	69.5	9.89	9.89	67.6.	9.79	9. 29	9.79	67.6	67.6	9.79	9.79	9.19	9.79	9. /9
	Score	16.4	15.8	15.4	.15.4	14.8	14.8	14.8	14.8	14.8	14.8	14.6	14.6	14.6	14.6	14.4	14.4	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2
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CDS 2..547

; NAME/KEY: ; LOCATION: US-08-698-805-3

28 14.2 67.6 2682 1 US-07-977-434-3 Sequence 3, Appli 30 14.2 67.6 2682 1 US-08-475-231-1 Sequence 1, Appli 31 14.2 67.6 2682 1 US-08-475-231-1 Sequence 1, Appli 31 14.2 67.6 2682 1 US-08-458-19-3 Sequence 3, Appli 32 14.2 67.6 2682 5 PCT-US91-07035-3 Sequence 10, Appli 34 14.2 67.6 9997 1 US-08-245-982A-15 Sequence 15, Appli 35 14.2 67.6 9997 1 US-08-453-265-15 Sequence 15, Appli 36 14.2 67.6 10103 2 US-08-457-273B-7 Sequence 15, Appli 37 14.2 67.6 10103 2 US-08-457-273B-7 Sequence 1, Appli 5 Sequence 1, Appli 5 Sequence 1, Appli 5 Sequence 1, Appli 6 Soguence 243, Appli 13 8 65.7 424 4 US-09-641-638-244 Sequence 244, Appli 6 Soguence 245, Appli 13 8 65.7 424 4 US-09-641-638-245 Sequence 21, Appli 6 Soguence 241, Appli 6 Soguence 242, Appli	RESULT 1  12.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-13  15.04-08-08-08-13  15.04-08-08-08-08-13  15.04-08-08-08-08-08-13  16.04-08-08-08-08-08-08-08-08-08-08-08-08-08-	USYURYB98, 80 USYURYB98, 80 AT US 60/002, 51 G-1995 ATION: en B. 30,073 MBER: 494-203 ORMATION: 1200 120 NO: 3: ICS: alrs

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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: USENING DATE: JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-240007,00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR-nm23 AND COMPOSITIONS, METHODS OF MAKING AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4411529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Woodcock, Washburn, Kurtz, Mackiewicz & No.
: One Liberty Place, 46th floor
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.3%; Score 15.4; 94.1%; Pred. No. 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/000,427
FILING DATE: 22-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2449159 CTACCGCAAGCTGCGTG 2449175
                                                                             Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08667023
Patent No. 5817783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Martinez, Robert V TITLE OF INVENTION: DR-nm23 A TITLE OF INVENTION: METHODS O
                                                                                                                         GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Callabreta, Bruno
APPLICANT: Venturelli, Donate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22-JUN-1995
CLASSIFICATION: 435
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTACCCCAAGCTGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (215)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-103-840A-1
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US-08-667-023-1
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                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                           APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence
CTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
UNRENT FILING DATE: 1998-06-24
NUMBER OF SEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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  Length 629;
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                                             Indels
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    DB 2;
  Score 16.4; DE Pred. No. 14; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ed. No. 30;
Mismatches
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Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.8;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PELICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
TENOM: TENOM: TENOM: 1551
                                                                                                                                                                                                               Sequence 1551, Application US/09134001C Cartent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2446460 CTACCGCAAGCTGCGTG 2446476
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                                                                                                          417 ACCCCAAGCTGGGTGATA 434
                                                                                    3 ACCCCAAGCTGCGTGATA 20
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94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
Query Match 78.18;
Best Local Similarity 94.48;
Matches 17; Conservative
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Best Local Similarity 94...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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5817783r1s

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION:
US-08-452-262-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09233989
Fatent No. 6248527
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
TITLE OF INVENTION: Method of Detecting Risk of Type II Diabetes Based on
TITLE OF INVENTION: Mutations Found in Carboxypeptidase E
FILE REFERENCE: 5800-14, 035800/14130
CURRENT FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: 60/105,102
EARLIER PILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.1
LENGTH: 2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; DB 4; Length 2439;
1e+02;
ches 2; Indels 0
                                                                                                                                                                                                            DB 1; Length 849;
                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Naggert, Jurgen K.
APPLICANT: Leiter, Edward H.
TITLE OF INVENTION: CLINICAL DISORDERS ASSOCIATED WITH
TITLE OF INVENTION: CARBOXYPEPTIDASE E MUTATION
NUMBER OF SEQUENCES: 19
CORRESPEDIDENCE ADDRESS:
ADDRESSE: Kevin M. Farrell, P.C.
STREET: VO. Box 999
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14.8; DB
Pred. No. 1e+02
0; Mismatches
                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                              Score 14.8;
Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: carboxypeptidase E US-09-233-989-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08452262 Patent No. 5593837 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           222 CTACGCCGAGCTGCGTGA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTACCCCAAGCTGCGTGA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTACCCCAAGCTGCGTGA 18
                                                                                                                                                                                                            70.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                 : 849 base pairs
nucleic acid
EDNESS: both
                                                                                                                                                                                                                             Best Local Similarity 88.9
Matches 16, Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (287)..(1714)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                              ) NAME/KEY: CDS
; LOCATION: 19..525
US-08-667-023-1
                                                                                           MOLECULE TYPE: CDNA
                                                                           both
                                                       STRANDEDNESS:
                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-233-989-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-452-262-1
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                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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DB 1; Length 2443;
le+02;
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                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.8;
                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35.505
REFERENCE/DOCKET NUMBER: JL-9501
TELECOMMUNICATION INFORMATION:
TELEPAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Revin M. Farrell, P.C.
STREET: P.O. BOX 999
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08734550 Patent No. 5690932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           455 CTACCCGAGCTGCGCGA 472
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTACCCCAAGCTGCGTGA 18
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APPLICANT: Naggert, Jurgen K.
APPLICANT: Leiter, Edward H.
TITLE OF INVENTION: CLINICAL I
TITLE OF INVENTION: CARBOXYPEI
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: FATEALI, KEVID M.
REGISTRATION NUMBER: 35.05
REFERENCE/DOCKET NUMBER: JL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.5%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                              LENGTH: 2443 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                       CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414..1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ns
                                                                                                   FILING DATE:
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APPLICANT: Allen, Maxine J.
APPLICANT: Buckler, Alan J.
TITLE OF INVENTION: GAP12 Genes and their Uses
FILE REFERENCE: SEQ-11P
CURRENT APPLICATION NUMBER: US/08/909,954A
CURRENT FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                         Sequence 3, Application US/08909954A Patent No. 6100058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2820 ACCCCAAGCTGCTGGATA 2837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ACCCCAAGCTGCGTGATA 20
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: M. musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (0)...(0)
US-08-909-954-3
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                                                                                                                                                                                                                                                                                                              3117
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                                                                                                                                                                                     Score 14.8; DB 1; Length 2443;
Pred. No. 1e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.5%; Score 14.8; DB 5; Length 2443; Best Local Similarity 88.9%; Pred, No. 1e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application PC/TUS9607528
GENERAL INFORMATION:
APPLICANT: The Jackson Laboratory
TITLE OF INVENTION: CLINICAL DISORDERS ASSOCIATED WITH
TITLE OF INVENTION: CARBOXYPEPTIDASE E MUTATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
AND APPLICATION DATA:
APPLICATION NUMBER: US 08/452,262
FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Kevin M. Farrell, P.C.: P.O. Box 999
York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: JL-9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             455 CTACCCGAGCTGCGCGA 472
                                                                                                                                                                                     Query Match 70.5%; Best Local Similarity 88.9%; Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (207) 363-055
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2443 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
414.:1721
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414..1721
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                                              TOPOLOGY: linear MOLECULE TYPE: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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LOCATION:
PCT-US96-07528-1
                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-734-550-1
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Score 14.8; DB 3; Length 3117; Pred. No. 1e+02; 0; Mismatches 2; Indels 0

70.5%;

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COMPUTER: Apple Macintosu OPERATING SYSTEM: Macintosh 7.5
Sequence 1, Application US/08523855A Patent No. 5824538 GENERAL INFORMATION:
                                                                                                                                                                                                      : USA MRMC - MCMR-JA
FORT DETRICK, FREDERICK
                                                           APPLICANT: Arthur A. Branstrom
APPLICANT: Donata R. Sizemore
APPLICANT: Jerald C. Sadoff
TITLE OF INVENTION: Bacterial D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Moran, John
REGISTRATION NUMBER: 2
REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA
                                                                                                                                                                                     John Moran
                                                                                                                                           NUMBER OF SEQUENCES: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic aci
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STRANDEDNESS:
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Length 152331;

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GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 18
SOFTWARE FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
69.5%; Score 14.6; DB 3;
Best Local Similarity 81.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 69.5%; Score 14.6; DB 3; Best Local Similarity 81.0%; Pred. No. 1.8e+02; Matches 17; Conservative 0; Mismatches 4;
FILE REFERENCE: 09404/052001
CURRENT APPLICATION WUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION WUMBER: US 60/091,650
EARLIER APPLICATION WUMBER: US 60/094,646
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASLESQ for Windows Version 3.0
SOFTWARE: FASLESQ for Windows Version 3.0
EENGTH: 152331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103933 CTACCCCAGCCTGGGTGACAG 103953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/09128155 Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTACCCCAAGCTGCGTGATAG 21
                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1) ... (152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTACCCCAAGCTGCGTGATAG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WHITE, Owen R.
FRASER, Claire M.
VENTER, John C.
                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
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LENGTH: 176373
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US-09-103-840A-2/c
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US-09-128-155-17
                                                                                                                                                                                                                                             TYPE: DNA
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US-09-128-155-16
5 Sequence 16, Application US/09128155
5 Patent No. 6117654
5 GENERAL INFORMATION:
7 APPLICANT: Pan, Yang
7 TITLE OF INVENTION:
8 TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                 Score 14.6; DB 1; Length 1674;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1:30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/539,205A
FILING DATE: 04-OCT-1995
ATTOKNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.6; DB 3;
Pred. No. 1.3e+02;
0; Mismatches 4;
                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CSV-005.01
BLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1243 CTTCTGCAAGCTGCATGATAG 1223
                                                                                                                                                                            1 CTACCCCAAGCTGCGTGATAG 21
                                                                                                                                                                                                                                                                             US-08-539-205A-5/c
; Sequence 5, Application US/08539205A
; Patent No. 6001619
; GENERAL INFORMATION:
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                                                            69.5%;
ilarity 81.0%;
Conservative
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TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3226 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 69.5%;
Best Local Similarity 81.0%;
Matches 17; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400..2901
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  Linear
                                                          Query Match
Best Local Similarity
Matches 17; Conserv
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; TOPOLOGY:
US-08-523-855A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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Length 176373;

Indels

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TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM; TITLE OF INVENTION: TUBERCULOSIS; FILE REPERENCE: 24.366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 44.03765
FTYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE: Mycobacterium tuberculosis
FEATURE: OTHER INFORMATION: Top 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Search completed: July 8, 2003, 09:31:28 Job time: 49.0402 secs

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0; Gaps

Query Match 68.6%; Score 14.4; DB 4; Length 4403765; Best Local Similarity 93.8%; Pred. No. 69; Matches 15; Conservative 0; Mismatches 1; Indels 0; (

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Run

Searched:

Database

Sednence:

Title:

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Sequence 1862,
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               Sequence 2.
Sequence
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Sequence 3
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Durham, Margarita
APPLICANT: Durham, Margarita
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TITLE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                    US-10-063-547-133
US-10-174-590-385
US-10-063-616-133
US-10-063-616-133
US-10-175-737-385
US-10-173-706-385
US-10-175-728-385
US-10-175-728-385
US-10-176-482-385
US-10-176-757-385
US-10-176-757-385
US-10-176-757-385
US-10-176-757-385
US-10-176-757-385
US-10-176-757-385
US-10-176-757-385
                           US-09-893-737-9
US-09-796-858-27
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                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2884, Application US/10066543
Publication No. US20030087818A1
GENERAL INFORMATION:
APPLICANT: Janay Yuqiu
APPLICANT: Pyle, Ruth A.
APPLICANT: Pyle, Ruth A.
APPLICANT: Lodes, Michael J.
APPLICANT: Gorist, Heather
APPLICANT: Gererist, Heather
APPLICANT: Gererist, Barther
APPLICANT: Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 CTACCCCAAGCTGTGTATA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-2884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTACCCCAAGCTGCGTGATA 20
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Best Local Similarity 90.0%;
Matches 18; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: .338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Fast
SEQ ID NO 2884
LENGTH: 364
                                        FEATURE:
                           . q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 797, App
Sequence 797, App
Sequence 4, Appli
Sequence 1, Appli
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2884, Ap
Sequence 34494, A
                                                                                           8, 2003, 19:09:54 ; Search time 121.288 Seconds (without alignments) 273.390 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wo. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed derived by analysis of the total score distribution.
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Sequence 3, Ap
Sequence 1, ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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/pubpna/US60_NEW_PUB.seq:
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       5.1.6
Compugen Ltd
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US-10-918-995-34494
US-10-084-817-324
US-09-822-849A-389
US-09-764-860-800
US-10-074-095-801
US-10-074-095-801
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UG-09-764-877-3923

US-10-074-095-798

US-10-074-095-797

US-10-074-095-797
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US-09-905-846-5
US-10-037-182-3
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         GenCore version
Copyright (c) 1993 - 2003
                                                                  nucleic search, using sw model
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_NA:*
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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and is score

Result g US-09-845-583-

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APPLICANT: Generals Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
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Best Local Similarity 90.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches
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CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 09/764,860
PRIOR APPLICATION NUMBER: 06/179,065
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/18,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 800, Application US/10074095 Publication No. US20030077704A1
                                                                                                                                                                                                                                                                LING DATE: 2001-09-04
ICATION NUMBER: 60/195,582
NG DATE: 2000-04-06
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                                                                                                 Resnick, Richard J
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                                                 gostino, Michael
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                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 598
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 389
LENGTH: 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 401;
                                                                                       APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT FILIGH DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/215,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34494
LENGTH: 401
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OTHER INFORMATION: Incyte ID No. US20030119009A1 988665.10
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APPLICANT: Jed G. Nuchtern
APPLICANT: Sharon E. Plon
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
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CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR FILING DATE: 2001-02-23
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                   Sequence 34494, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 324, Application US/10084817
Publication No. US20030119009A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 CTACCCCAAGCTGTGTAATA 122
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Best Local Similarity 90.0%;
Matches 18; Conservative
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Best Local Similarity 90.0%;
Matches 18; Conservative
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; OTHER INFORMATION: a, t, c,
US-10-084-817-324
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SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-918-995-34494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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IS-09-918-995-34494
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PRIOR APPLICATION NUMBER: 60/241,787

PRIOR APPLICATION NUMBER: 60/246,532

PRIOR APPLICATION NUMBER: 60/246,474

PRIOR APPLICATION NUMBER: 60/246,474

PRIOR FILING DATE: 2000-1108

PRIOR PRICE ADMENSION 100-1108

PRIOR PRICE ADMENSION 100-1109

PRIOR PRICE ADMENSION 100-1109

PRIOR PRICE ADMENSION 100-1109

PRIOR PRICE ADMENSION 100-1109

PRIOR PRILING DATE: 2000-11-17

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PRIOR FILING DATE: 2000-08-14

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TLING DATE: 2000-09-23
APPLICATION NUMBER: 60/229,343
APPLICATION NUMBER: 2000-09-01
                          FILING DATE: 2000-07-26
APPLICATION UNDRER: 60/217,496
FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,447
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LICATION NUMBER: 60/224,519
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ION NUMBER: 60/220,964
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APPLICATION NUMBER: 60/229,287
                                                                                                                    FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/218,290
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PLICATION NUMBER: 60/235,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LICATION NUMBER: 60/234,274
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LICATION NUMBER: 60/234,223
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                                                                                                                                                                TLING DATE: 2000-07-14
PPLICATION NUMBER: 60/225,757
                                                                                                                                                                                                                                      PLICATION NUMBER: 60/226,868
                                                                                                                                                                                                                                                                                                     ING DATE: 2000-07-07
LICATION NUMBER: 60/225,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LICATION NUMBER: 60/251,869
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LICATION NUMBER: 60/2
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008C1
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Pred. No. 26;
0; Mismatches 2;
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80.0%; Score 16.8; DB 9;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2;
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CURRENT FILING DATE: 2002-02-14
R FILING DATE: 2000-09-14

R APPLICATION NUMBER: 60/241,808

R FILING DATE: 2000-10-20

R APPLICATION NUMBER: 60/241,826

R FILING DATE: 2000-10-20

R APPLICATION NUMBER: 60/241,786

R APPLICATION DATE: 2000-10-20
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PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
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APPLICATION NUMBER: 60/214,886
FILING DATE: 2000-06-28
                                                                                                                                                                                                                APPLICATION NUMBER: 60/246,475
FILING DATE: 2000-11-08
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Publication No. US20030077704A1
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FILING DATE: 2000-09-08
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                                                                                                                                                                  APPLICATION NUMBER: 60/241,221
FILING DATE: 2000-10-20
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Best Local Similarity 90.0%;
Matches 18; Conservative
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GORGANISM: Homo sapiens
US-09-764-860-800
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US-10-074-095-801
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LENGTH: 7606
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60/236,369

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FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/236,367
FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/237,039
                                                                                         FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/236,370
                                                                                                                                                                                               LICATION NUMBER: 60/237,040
                                                                                                                                                                                                                                                          ICATION NUMBER: 60/239,935
                                                                                                                                    60/236,802
                                                                                                                                                                  LICATION NUMBER: 60/237,037
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APPLICATION NUMBER: 60/249,245
FILING DATE: 2000-11-17
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LICATION NUMBER: 60/249,244
TAG DATE: 2000-11-17
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SOFTWARE: Patentin Ver. 2.0
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US-09-764-860-801
Sequence 801, Application US/09764860
Fatent No. US20020094953A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
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Pred. No. 26;
0; Mismatches
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Pred. No. 26;
0; Mismatches
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/232,081
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/232,080
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FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/233,064
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FILING DATE: 2000-09-08
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FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,397
FILING DATE: 2000-09-14
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PPLICATION NUMBER: 60/241,786
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Best Local Similarity 90.0%;
Matches 18; Conservative
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US-09-764-860-801
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Matches 18; Conserva
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LENGTH: 7608
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APPLICATION NUMBER: 60/237,038
FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/236,370
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APPLICATION NUMBER: 60/240,960
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APPLICATION NUMBER: 60/241,785
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APPLICATION NUMBER: 60/244,617
FILING DATE: 2000-11-01
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ING DATE: 2000:12-08
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ATE: 2000-09-05
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ATE: 2000-10-02
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APPLICATION NUMBER: 60/220,964
FILING DATE: 2000-07-26
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APPLICATION NUMBER: 60/236,327
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LING DATE: 2000-09-01
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PLICATION NUMBER: 60/234,997
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LICATION NUMBER: 60/229,287
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FILING DATE: 2000-10-20
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FILING DATE: 2000-08-30
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                                     GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INFORMATION:
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
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IIILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TIEL REPERENCE: PCOORCI
CURRENT APPLICATION NUMBER: US/10/074,095
CURRENT FILING DATE: 2002-02-14
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Pred. No. 27;
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PRIOR PAPLICATION NUMBER: 09/764,860

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-02-04

**RIOR FILING DATE: 2000-02-04

**RIOR FILING DATE: 2000-06-28

RIOR PRICATION NUMBER: 60/214,886

**RIOR PLICATION NUMBER: 60/214,486

**RIOR PLING DATE: 2000-06-28

RIOR APPLICATION NUMBER: 60/217,487

RIOR APPLICATION NUMBER: 60/217,487
Sequence 3923, Application US/09764877 Patent No. US20020147140A1
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APPLICATION NUMBER: 60/218,290
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APPLICATION NUMBER: 60/226,868
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APPLICATION NUMBER: 60/216,647
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APPLICATION NUMBER: 60/225,447
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APPLICATION NUMBER: 60/225,757
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90.0%;
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Best, Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3923
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FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/246,532
FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/249,216
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/226,681
FILING DATE: 2000-08-22
APPLICATION NUMBER: 60/225,759
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TMRPP
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'ILING DATE: 2000-08-14
'PPLICATION NUMBER: 60,249,218
'ILING DATE: 2000-11-17
'PPLICATION NUMBER: 60,249,208
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PPLICATION NUMBER: 60/215,135
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MBER: 60/249,213
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NG DATE: 2000-11-17
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ATION NUMBER: 60/249,217
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CATION NUMBER: 60/231,242
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NG DATE: 2000-11-17
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3 DATE: 2000-11-17
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TLING DATE: 2000-09-14
PPLICATION NUMBER: 60/233, 063
ILING DATE: 2000-09-14
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198
SOFTWARE: Patentin Ver. 2.0
ENGTH: 17498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC008
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008C1
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; Pred. No. 27;
0; Mismatches
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Pred. No. 27;
0; Mismatches
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CURRENT FILING DATE: 2002-02-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
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PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2000-01-31
PRIOR PLING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR RILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                              16395 CTACCCCAAGCTGTGTATA 16414
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Publication No. US20030077704A1
GENERAL INFORMATION:
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Best Local Similarity 90.0%;
Matches 18; Conservative .
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90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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ORGANISM: Homo sapiens
US-09-764-860-798
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US-09-764-860-798
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PRIOR PRIOR

496 447 290 757 868 868 868 6647 267 2757 280 290 7757 7757 7757 7757 7767 7767 7767 776	223 223 369 369 809 809 964 809 964 967 967 967 967 967 967 967 967
2000-07-26  MUMBER: 60/215, 2000-07-11  MUMBER: 60/215, 2000-07-14  MUMBER: 60/215, 2000-08-14  MUMBER: 60/225, 2000-09-27  MUMBER: 60/224  MUMBER: 60/224  MUMBER: 60/226, 2000-09-29  MUMBER: 60/226, 2000-10-20  MUMBER: 60/226, 2000-11-01  MUMBER: 60/226	NUMBER: 60/234 2000-09-21 2000-09-21 2000-08-30 2000-08-30 2000-08-30 2000-08-14 NUMBER: 60/224 2000-09-24 2000-09-24 2000-09-29 2000-11-17 NUMBER: 60/224 2000-10-20 2000-10-20 2000-11-17 2000-10-20 2000-11-17 2000-10-20 2000-11-17 2000-11-17 2000-11-17 2000-11-17 2000-11-17 2000-11-17 2000-11-17 2000-11-17 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10 2000-11-10
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ING DATE: 2000-11-17 LICATION NUMBER: 60/249,211 ING DATE: 2000-11-17 TON NUMBER: 60/249,215
ATE: 2000-11-17 JING DATE: 2000-11-17 PLICATION NUMBER: 60/249,214
LING DATE: 2000-11-17
PLICATION NUMBER: 60/249,297 60/225, 266 PLICATION NUMBER: 60/249,213 LING DATE: 2000-11-17 PLICATION NUMBER: 60/249, 212 LICATION NUMBER: 60/249,245 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/232,400 LICATION NUMBER: 60/249,218 LICATION NUMBER: 60/249,208 CATION NUMBER: 60/249, 207 LING DATE: 2000 11 1, PLICATION NUMBER: 60/249,244 PLICATION NUMBER: 60/249;217 60/235,836 60/230,438 60/215,135 60/249,210 60/225,759 60/225,213 60/227,182 60/225,214 CATION NUMBER: 60/239,935 60/249,216 60/226,681 LICATION NUMBER: 60/236,802 ICATION NUMBER: 60/237,040 60/240,960 NUMBER: 60/246,532 PPLICATION NUMBER: 60/237,037 NUMBER: 60/239,937 60/241,787 NUMBER: 60/246,474 000-10-0 -01-000

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'PLICANT: Roderick Thomas Walsh
TILE OF INVENTION: Compounds for the treatment of sexual dysfunction
LE REFERENCE: PCS10926APME
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                                                         PPLICANT: Naylor, Alasdair M.
PPLICANT: Wan Der Grad, Pleter H
PPLICANT: Wayman, Christopher P.
TILE OF INVENTION: Treatment of Male Sexual Dysfunction
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                                                                                                                                                            URRENT APPLICATION NUMBER: US/10/017,273A URRENT FILING DATE: 2001-12-12
                                                                                                                                                                             CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/265,358
PRIOR FILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-215
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-07-03
PRIOR PILING DATE: 2001-07-13
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STREBNT FILING DATE: 2001-07-13
RIOR APPLICATION NUMBER: 0017387.2
RIOR FILING DATE: 2000-07-14
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NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/895,367
PRIOR FILING DATE: 2001-06-29
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RIOR FILING DATE: 2000-07-26
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SOFTWARE: Patentin version 3.1
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Best Local Similarity 85.78;
Matches 18; Conservative
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APPLICANT: Ian Dennis Harrow
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ORGANISM: Homo sapiens
                                                                                                                                         LE REFERENCE: PC22013
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; ORGANISM: Homo sapiens
US-10-017-273A-4
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Best Local Similarity
Matches 18; Conserve
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LENGTH: 2893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
DATE: 2000-09-08
ATION NUMBER: 60/232,081
                                                                      LING DATE: 2000-09-08
PLICATION NUMBER: 60/231,414
                                                                                                                                                                                              LING DATE: 2000-09-14
PLICATION NUMBER: 60/233,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31043 CTACCCCAAGCTGTGTAATA 31062
                                                                                                                                                                                                                                                                                                                        ILING DATE: 2000-09-14
PPLICATION NUMBER: 60/232,401
                                                                                                                                                                                                                                                                                                                                                                                             PPLICATION NUMBER: 60/241,808
                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICATION NUMBER: 60/241,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'ILING DATE: 2000-10-20
PPLICATION NUMBER: 60/241,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231,243
FILING DATE: 2000-09-08
                                                                                                                                                                                 PPLICATION NUMBER: 60/233,064
                                                                                                                                                                                                                                                                     60/232,397
                                                                                                                                                                                                                                                                                                            ON NUMBER: 60/232,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICATION NUMBER: 60/241,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60/246,475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 797, Application US/09764860
Patent No. US20020094953A1
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Best Local Similarity 90.0%; Promatches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match ... 80.0%;
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                           LING DATE: 2000-09
PLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Homo sapiens
US-09-764-860-797
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US-09-764-860-797
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US-10-017-273A-4
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453 CCACCCTGGCTGCGTGATAG 473

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OM nucleic - nu	OM nucleic - nucleic search, using sw model	
Run on:	July 8, 2003, 00:45:53; Search time 231.102 Seconds (without alignments) 2644.537 Million cell updates/sec	٠.
Title: Perfect score:	US-09-647-780A-9	
sequence: Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched:	2054640 seqs, 14551402878 residues	
Total number of	Total number of hits satisfying chosen parameters: 4109280	
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 200000000	

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries GenEmbl: Database :

Pred. No. is the number of results predicted by chance to have a

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ALIGNMENTS

PAT 07-SEP-2000

metalloprotease and its use for screening J.C., Gros, C., Ouimet, T., Rose, C., Bonhomme, M.C. and linear DNA Sequence 9 from Patent W09953077 Novel nep ii membrane metall inhibitors useful in therapy GI:10040982 artificial sequences 1 (bases 1 to 21) synthetic construct synthetic construct AX014709.1 Facchinetti Schwartz, RESULT 1
AXO14709
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE

363 CTACCCCAAGCTGCGTGATAG 383

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus rattus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nep 11 membrane metalloprotease and its use for screening inhibitors useful in therapy
Patent: WO 9953077-A 1 21-0CT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS
CLAUDE (FR); OUTMET TANAM (FR); ROSE CHRISTIANE (FR); BONHOWME.
MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
    Patent: WO 9953077-A 9 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schwartz,J.C., Gros,C., Oulmet,T., Rose,C., Bonhomme,M.C. and Facchinetti,P.
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    21
    /organism="synthetic construct"

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/note="unnamed protein product"
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'db_xref="taxon:10117"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1 from Patent W09953077. AX014701
                                                                                                                                             /db_xref="taxon:32630"
/note="oligonucleotide"
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1 CTACCCCAAGCTGCGTGATAG 21

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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Auzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Buratunge, H.C., Brown, M., Bryant, N.P., Buhay, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Caver, M.D., Dathorne, S.R., David, R., David, M., Davis, C., Caveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M., Daris, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C., Harnis, C., Harris, R., Hart, M., Havlak, P., Hawes, A., Harnandez, J., Hernandez, J., Hernandez, J., Hernandez, J., Hernandez, J., Hernandez, J., Holloway, C., Jackson, L.E., Jacobson, B., Jak, Y., Johnson, R., Johlvet, S., Jud, M., Lid, J., Lid, J., Lid, J., Lid, J., Lud, J., Marthnez, E., Massey, B., Mandule, R., Marthnez, E., Massey, B., Mandule, R., Morle, N., Moule, N.
                                                                                                   AC094732 174953 bp DNA linear HTG 20-DEC-2001
Rattus norvegicus clone CH230-516, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced 91:15624568.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae;
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Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tameriss
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.
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Wall,R., Wang,S., Ward-Moore,S., Warren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine
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Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                56 unordered pieces
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Rattus norvegicus
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RESULT 3
AC094732/c
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KEYWORDS
SOURCE
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AUTHORS
TITLE
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Matches 21; Conservative
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                                             Consensus quality: 152255 bases at least Q40 Consensus quality: 158448 bases at least Q30 Consensus quality: 164461 bases at least Q30 Estimated insert size: 155965; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Center clone name: CH230-516
------ Summary Statistics
Assembly program: Phrap; version 0.990329First call
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                                                                                                                                                                                                                                                  Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most
                                                                                                                          Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalla; Eutherla; Rodentla; Sclurognathl; Muridae; Murinae; Mus
1 (bases 1 to 2583)
Mus musculus neprilysin-like peptidase alpha mRNA, complete cds.
AF302075
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Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi
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Pred. No. 1e+02;
0; Mismatches 2;
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Eukaryota; Metazoa; Chordata; Cranlata;
Ammanlaia; Eutherla; Rodentla; Sciurognat
1 (bases 1 to 2601)
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Shirotani, K. and Saido, T.C.
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AF157106.1 GI:6467400
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nilarity 90.5%;
Conservative 0
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AQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCR
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                    Yokoyama,M. and Matsuo,M.
Molecular identification and characterization of novel
Molecular identification actses, the soluble secreted form of which
hydrolyzes a variety of vascactive peptides
J. Biol. Chem. 274 (45), 32469-32477 (1999)
                                                                                                                                                                                                                                             Submitted (08-JUN-1999) International Center for Medical Research, Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
L. (bases 1 to 2652)
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Mus musculus neprilysin-like peptidase beta mRNA, complete cds.
AF302076
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Emoto, N., Raharjo, S.B., Nurhantari, Y., Saiki, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product-"soluble secreted endopeptidase delta"
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J. Biol. Chem. 276 (24), 21895-21901 (2001)
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                                                                                                                                                                                                                                                                                                                                   1. 2601
/organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                 Ikeda,K., Emoto,N. and Matsuo,M.
Direct Submission
                                                                                                                                                                                                                                                                                                              Socation/Qualifiers
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Shirotani, K. and Salo
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CMNQSVIEKRDSEPLLSVLKMVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVL
                                                                                                                                                                                                                                                                                                                                                                                                 IDLF IWNDDQNSSRHVIY IDQPTLGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRK
                                                                                                                                                                                                                                                                                                                                                                                                                   DQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQERFGLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEEYSSLTFYEDLYFENGLONLKNNAQRSLKKLREKVDQNLWIIGAAVVNAFYSPNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIVFPAGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNMLDWWSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF302077 2694 bp mRNA linear ROD 11-JUN-2001
Mus musculus neprilysin-like peptidase gamma mRNA, complete cds.
AF302077
                                 Brain
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Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saltama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus, I (bases I to 2094)
Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T., Iwatsubo, T. and Saido, T.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory,
Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 2652;
                                                                                                                                                                                                                                                                                                             /translation="MVERAGWCRKKSPGFVEYGLMVLLLLLLG
                                                                                                                                                                                                                                           'product="neprilysin-like peptidase beta"
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Pred. No. 1e+02
0; Mismatches
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1. .2694
/organism="Mus musculus"
                                                                                                                                                     'db_xref="taxon:10090"
                                                                                                                                                                                                  /note="endopept1dase"
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                                                                                          Location/Qualifiers
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                                                                                                                                   /organism="Mus
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ilarity 90.5%;
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GAAVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGNVIGHEITHGFDDNGR
NFDKNGNMLDFWRSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNG
GVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arls/105 25-NOV-1999 MRNA linear ROD 25-NOV-1999 Mus musculus soluble secreted endopeptidase mRNA, complete cds. Arls7105
                                                                      /translation-"MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIALRD
SSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNSRYSVF
DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKMVG
GWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPT
                                                                                                                                                                            LGMPSREYYEQEDNNHKVRKAYLEFMTSYATMLKKDONLSKESAAVREEWAEVLELET
HLANATVPQEKRHDVTALYHRMDLMELQERFGLKDRVSLCSPGCPGTHSYDQAGLELG
NPPASDSRVLGLKGFNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSA
                                                                                                                                                                                                                                                        RTMONYLVWRLVLDRIGSLSQRFKEARVDYRKALIGTTYBEVRWRECYSYNISMESA
VGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQI
                                                                                                                                                                                                                                                                                                           GYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 2892)
Ikeda,K., Emoto,N., Raharjo,S.B., Nurhantari,Y., Saiki,K.,
Yokoyama,M. and Matsuo,M.
Molecular identification and characterization of novel
membrane-bound metalloprotease, the soluble secreted form of which
hydrolyzes a variety of vasoactive peptides
J. Biol. Chem. 274 (45), 32469-32477 (1999)
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DQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRWDLMELQERFGLKG
FNWTLFIQNVLSSVEVELFPDEEVVYYGIPYLENLEDIIDSYSARTMQNYLVWRLVLD
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Ilkeda,K., Emoto,N. and Matsuo,M.
Direct Submission
Submitted (08-UDN-1999) International Center for Medical Research,
Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MYERAGWCRKKSPGFVEYGLMVLLLLLLGAIVTLGVFYSIGKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2694;
/product="neprilysin-like peptidase gamma"
/protein_id="AAG18448.1"
/db_xref="G1:10505364"
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                                                                                                                                                                                                                                                                                                                                                                                                                 HSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.8; DB 10;
Pred. No. 1e+02;
0; Mismatches 2;
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Best Local Similarity 90.5%;
Matches 19; Conservative
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2925 bp mRNA linear ROD 11-MAY-2000 neprilysin-11ke metallopeptidase 1 (N11) mRNA,

Chordata, Craniata, Vertebrata, Euteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

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)QNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQERFGLKG
                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2925)
Ghaddar,G., Ruchon,A.F., DesGroseillers,L. and Boileau,G.
Direct Submission
Submitted (09-AUG-1999) Biochemistry, University of Montreal, 2900
Edouard Montpetit, Montreal, Que H3T 1J4, Canada
Location/Qualifiers
1. 2925
                                                                                                                                                                                              Ghaddar,G., Ruchon,A.F., Carpentler,M., Marcinkiewicz,M.,
Seidah,N.G., Crine,P., Desgroseillers,L. and Boileau,G.
Molecular clonding and blochemical characterization of a new mc
testis soluble-zinc-metallopeptidase of the neprilysin family
Blochem. J. 347 (Pt 2), 419-429 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-"NL1; metallo-endopeptidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="testis"
1. .2925
                                                                                                                                                                                        1 (bases 1 to 2722)
Ghaddar,G., Ruchon,A.F.,
                                                                     AF176569.1 GI:7769082
                                                                                                                                                                 Mammalia; Eutheria; 1
1 (bases 1 to 2925)
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gene="N11"
                                                                                                                            Mus musculus
Eukaryota; Metazoa;
                                    complete cds.
                                                                                                      Mus musculus
                                                      AF1
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Matches 199
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Boileau, G. and Desgroseillers, L. New metalloproteases of the neprilysin family Patent: WO 0047750-A 12 17-AG-2000; BOILEAU GUX (CA); DESGROSEILLERS LUC (CA); UNIVERSTIE DE MONTREAL (CA)
                                                  QIVEPAGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNMLDWWSN
FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSLGENIADNGGVRQAYRAYLRWLA
DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
LPGFSEAFHCPRGSPMPMKRCRIW"
774 c 827 g 574 t
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DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                                                                                                                                                                                                                                                                                                                                                                            PAT 21-SEP-2000
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RIGSLSORFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CMNQSVIEKRDSEPLLSVLKMVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVL
                                    DEEY SSLTFY EDLY FENGLONLK NNA ORSLKKLREK VDONLW I IGAAV VNAFY SPNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRR
                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                  Length 2892;
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                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                         Indels
                                                                                                                                                                                  Score 17.8; DB 10;
Pred. No. 1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6;
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                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.8; D
Pred. No. 1e+0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            AX033272 2925 bp
Sequence 12 from Patent WO0047750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  558 CCACCCCAAGCTGTGTATAG 578
                                                                                                                                                                                                                                                                                 CTACCCCAAGCTGCGTGATAG 21
                                                                                                                                                                                                                                                            1 CTACCCCAAGCTGCGTGATAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX033272.1 GI:10280087
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larity 90.5%;
Conservative
                                                                                                                                                                                  sh. 84.8%;
L Similarity 90.5%;
19; Conservative
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es 19; Conserv
                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                717
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Matches 19
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ORIGIN
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
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AX033272
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Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MXII0.
AB005248 BA000015
AB005248.1 GI:2264320
FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLA
DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                    thaliana (strain:Columbia) DNA, clone_lib:Mitsui
                                                                                                                                0
                                                                                     Score 17.8; DB 10; Length 2925;
Pred. No. 1e+02;
): Mismatches 2; Indels 0;
                             LPGFSEAFHCPRGSPMHPMKRCRIW
797 c 836 a 582
                                                836 9
                                                                                                                                                                                    558 CCACCCCAAGCTGTGATAG 578
                                                                                                                                                                  1 CTACCCCAAGCTGCGTGATAG 21
                                                                                                                                  ö
                                                                                                 84.8%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thallana
clone:MXI10.
Arabidopsis thallana
                                                                                                                                  Conservative
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19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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KEYWORDS
SOURCE
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RESULT 10 AF176569

TITLE

COMMENT

CDS

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Address for correspondence: Kaoskazusa.or.jp
Address for correspondence: Kaoskazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgl-bin/agd_graph.cgl?c-MXIIO
Genes with similarity to proteins in the databases are described
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremilini.zool.iastate.edu/Cglibin/Sp.cgl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://genome.wustl.edu/eddy/tRNAscansEk).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.
The 5' clone is MSII7 and the 3' clone is MBB18.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLVKKIDNDKEEAADRRTTVIPRIRENDKIGVDVPWRYRFHVPTILEDHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MTEKIATDVSNMLNNYSPSRDFDGLIGMDAHMKEMESLLCLDSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOEIPOWVKKISHLOTLGLEGCKRLVTIPOLSDSLSOLVVTNCESLERLNFSFONHPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFLWFLNCFKLNNEAREFIQTSSTHAILPSREVPANFTYRANGSSIMVNLNHRPLSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFCTKYLVEIRMKNSKLQNLWQGNQPLGNLKRMDLSESKHLKELPDLSTATNLEYLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :NHKDMELHHLGVAODRLNDKKVLIVLDSIDQSIQLDAIAKETRWFGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRIIITTQDQKLLKAHGINHIYKVEFPSAYEAYQMFCMYAFGQNFPNDGFEELAWEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLHIACLFNNQEMVEVEDYLALSFLDVRQGFHLLAEKSLINLKFLSTNCTRIEMHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQLGKDIVRHKPGHQSICEPGKRQFLIDARDICEVLTDNTGNRNVVGIFLEVRNLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STNIKDLKLTKTAIKEVPSTIKSWSHLRKLEMSYSENLKELPHALDIITTLYINDT
                                                                                                                                      Sato, S., Kotani, H., Nakamura, Y., Kaneko, T., Asamizu, E., Fukami, M., Miyajima, N. and Tabata, S. Structural analysis of Arabidopsis thaliana chromosome 5. I. Structural analysis of the 1.6 Mb regions covered by twenty physically assigned Pl clones DNA Res. 4 (3), 215-230 (1997)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brasslcaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kazusa DNA Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute, Department of Plant Gene Research; 1532-3, Yana, isarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,el:81-438-52-3935, Fax:81-438-52-3934)
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protein_id="BAB09346.1"
db_xref="GI:9758812"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="Mitsul Pl"
|oin(1791. .2912,3016. .3318,3584. .4660)
|note="gene_id:MXI10.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUL-1997) Yasukazu Nakamura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l, .83646
/organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain-"Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone-"MXI10".
                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 83646)
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                                                                                                                           (sites)
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AUTHORS
TITLE
JOURNAL
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MEDLINE
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LVLLMVDPOSOWRCEDMKRHVEXVDIMSATEIPHIAEVVHHQLPVIDTLIIFRCLS"

join(18792 18841,19220, 19412,19494, 19579,19875, 19955

20464, 20607,20697, 20783,20894, 21006,21097, 21162,

21216, 21308,21350, 21509)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MELPSKEYQVPNLEQFMEIEEEDLPPSPRDDPYNLNKCDLPEFTFVPKTKMEKFLGSV
IKSQRKINKWKSYAIGKLLKKVKKLQPPDYVSSEDELVFPSNEEEDRDNILESDENNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'translation="MKDVILVIYSLIKMTKLRSCPLDDCNSSETYFQLDKHLKNEHDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVWNIRGNISRTEQERLFVEIRRSIKRNPCSPIFPYTNDDVLLNVLVLDDVNLSGFIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCNASIKSVRHPVIRYALKLLAHALFGRGETSSTTVSEMCFLFQGVKELLVEDADEN
                                                   LGGGESDEPLGTVAGTLQTHASDIADFIESNLGSSPPVLVGHSFGGLIVQYYLANIVN
KRSLGTENAFPELSGAVMVCSVPPSGNSGLVLRYLFSKPVAAFKVTLSLAAKGFQKSI
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                              KLPSGLKMEVIEQRKSKSERENPPLVFVHGSYHAAWCWAENWLPFFSSSGFDSYAVSL
/translation="MMASSSLPSFPCLSYFKMPIAALTNSPRTTIPYNLKKGQTRLLH
                                                                                                                                                                                                                                                                                                    evidence=not_experimental
product="non-LTR retroelement reverse transcriptase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MMSPKQISDDRGSSHFRHTPFQIIHLIGNFFRIWSVYSMY
                                                                                                                                 Join(7788. 7835,8043. 8777,9032. 9157,9205. 9901,
10085. 12958)
/note="gene_id:MXIIO.3"
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/note="contains similarity to retroelement pol
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product="retroelement pol polyprotein-like"
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/note="gene_id:MXI10.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental/protein_id="BAB09349.1"
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/protein_id="BAB09350.1"
/db_xref="GI:9758816"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
/protein_id="BAB09348.1"
/db_xref="GI:9758814"
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                                                                                                                     PLCRETFFSQAMDDQLVKRYNLAR"
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pir||T02618
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CDS

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(bases 1 to 160601)
                                                                                           Waterston, R.H.
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//note="gene_id:MXII0.13"
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                                                                                                                                                                                         LSIFVDSVFEDDYNLFPKVFENKKLVKLGLSYISWLDGSIFLPMLKTLVLESVLLSVE
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                                                                                                                                                   'translation-"MDLLSNLPYELLCHILSFLTTKEAALTSVLSKRWRNLIAFVPNV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160601)
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.40460,40627. .40767,40853. .41185)
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note="emb|CAB86928.1
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                                                        trong similarity to unknown
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Genome Res. 8 (11), 1097-1108 (1998)
                                                                                            /evidence=not_experimental
/protein_id="BAB09351.1"
/db_xref="GI:9758817"
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'protein_id="BAB09352.1"
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Conservative 0; Mismatche
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/note-"gene_id:MXI10.12
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Indianies. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://pagac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence RP11-178M5 contains a variable CT run from base position 91946 to 91972. The fidelity and length of sequence is uncertain and cannot be confirmed by restriction digest information
                                                                                                                                                                                                                                   Submitted (14-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The RECI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa.K., Woon, P.Y., Zhao, B., Frengen, E. Azteno, M., Catanese, J. J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (14-007-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Sep 10, 2000 this sequence version replaced gi:7212905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
                                                RP11-178M5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://genome.wustl.edu/gsc
            McDonough, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sapiens@watson.wustl.edu
.......... Summary Statistics
Center project name: H_NH0178M05
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Kyung, K., Strowmatt, C. and Mc
The sequence of Homo saplens
Unpublished
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                                                                                                                          (bases 1 to 160601)
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AL607032 208249 bp DNA linear HTG 24-JUL-2002 Mus musculus chromosome 4 clone RP23-15L19, *** SEQUENCING IN PROGRESS ***; 2 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST AA971069 (NID:93146359) op69h07.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST AA644685 (NID:92569903) ab87d10.s1"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 208249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 25, 2002 this sequence version replaced gi:21627906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP. Mus musculus.
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Best Local Similarity 90.5%; Pred. No. 98
Matches 19; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                           family="MER1_type"
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/rpt_family="Alu"
39326. .39426
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9807. 40092
note="similar to
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2669. .43050
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rpt_family-"MalR"
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rpt_family="Alu"
'rpt_fam11y="Alu"
13273; .33454
                                                         pt_family="Alu"
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pt_family="L1"
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                                                             /rpt_family="".
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rpt_family="I
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AUTHORS
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AL607032
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1587. 24976
note="similar to EST AA969211 (NID:93144391) op51d12.s1"
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                                                                                                                                                                                                                                                                                                                                                                                                          ote="similar to EST AI142349 (NID:93658708) qg63g10.rl" 309. 15734
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note="similar to EST AA461577 (NID:92185441) zx51b02.rl"
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note="similar to EST AW181908 (NID:96450368) xj68c06.xl"
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          organism="Homo sapiens'
db_xref="taxon:9606"
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note="similar to EST
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'rpt_family="ERV1"
8809. ....
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59. .23825
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796. 1700.
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pt_family="MER22"
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17. .24849
                                                                                  clone_lib="RPCI-11"
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1663. 1997
17pt_family="ERVK"
3761. 4402
37pt_family="ERVK"
5518. 7103
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/rpt_family="ERV1"

1112. 1374

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1375. 1662
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t_family="MER22"
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1805. .12194
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555. .31007
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rpt_family=""
                                      chromosome="Y"
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32895. .33172
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ILESGREIPRNRIMRIDHKMNYATLGQFLGVLHRTAPIQYGERVTLVLNQRSVAKPYV
DDNRWFYLAADNDHDREWVNELAEDVWTNQLPAYRRFEAEHPTPAPASETQVSGGARG
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                                               i Kaneko, Kazusa DNA Research
for Plant Gene Research; Yana
                 Direct Submission
Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Researc Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; Ya 1532-3, Kisarazu, Chiba 292-0812, Japan
UE.mail:Raneko@kazusa.or.jp,
URL:http://www.kazusa.or.jp/
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
On May II, 2001 this sequence version replaced g1:11994988.
I.catlon/Qualifiers
I. 347950
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/strain="MAFF303099"
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/db_xref="GI:14027325"
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/gene="mll7923"
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                                                                                                                                                                                                                                                                                                              /db_xref-"taxon:381"
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1150. 1007
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2951. .3154
/gene="msr7926"
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gene="mlr7924"
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/gene="mlr7925"
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Phyllobacteriaceae; Mesorhizobium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                              Assembly program: XGAP4; Version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator 11% of reads
Chemistry: Dye-terminator 11% of reads
Consensus quality: 207834 bases at least Q40
Consensus quality: 207956 bases at least Q20
Insert size: 208149; sum-of-contigs
Insert size: 219051; 2.3% error; agarose-fp
Quality coverage: 12.41x in Q20 bases; sum-of-contigs Quality
coverage: 12.08x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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AP003013 BA000012
AP003013 2 GI:14027324
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137404 208249: contig of 70846 bp in length.
Location/Qualiflers
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Mesorhizobium loti
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53647 c 51328 g 49076 t
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0; Mismatches
Information
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                                            Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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/chromosome="4"
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/clone_11b="RPCI-23"
1. .137303
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DNA Res. 7 (6), 331-338 (200
21082930
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                      Center project
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Best Local Similarity
Las 19; Conserve
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ACCESSION
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REFERENCE
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AP003013
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AUTHORS
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ACI03838 62500 bp DNA linear HTG 29-NOV-2001
Homo sapiens chromosome 8 clone RP11-26N14 map 8, LOW-FASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mppssppldsfdlatlavlqrdytpqrligeavnlsapavqrr
Ikrweqagviasnvaliepaavgkpitifvevelesertelidaakrqfsqtpevqqc
Yyvtgeadfilvitvadwgayealtrklffgsnnvrkfrtfvawdrvkvgltvpldd"
                                                                                                                                                                                                                                                                                                 PVIDVGTIGKIREGAIKVAPDITEISQRGARFADGKHGEFDAIIFATGYRPGYARFLE
                                                                                             /prottein_id="BaB53603.1"
/db_xref="c1:14027334"
/translation="MFLTFSGRELSREARLDDTTTVAIIGAGPAGLAVAACLRQAGVI
FIIIEKEQQAAPAWRHYERVHLHTTRYSSLPFVPFPKHYPRYVPRALFVDYLDAYF
                                                                                                                                                                                                                  QRFDLRPQFGETVKAVTQDGRGWRVDAÄSGPLRAKDVVIASGYNAEPLRPAFAGIDTE
                                                                                                                                                                                                                                                 TGKTLHSADYRNAKPFAGQSVLVIGMGNTGAEIALDLAENGAQPTISVRGGVHIVPRE
                                                                                                                                                                                                                                                                  LFGVPIQMYGMAARLGPQRLNDALFPVILDLVLGRLDKYGLKRPGQGLLEQIAVASRI
                                                                                                                                                                                                                                                                                                                     PGIQPDRSGVTPKASDLGLYLIGFHNAVTGLLREIGIEAQAIADDIRHRLNRKKAAEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 62500)
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Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Llu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McDwan, P., McKernan, K., McPbeeters, R., Meldrim, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
/gene="m117934"
/note="similar to dimethylaniline monooxygenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="transcriptional regulator"
/protein_id="BAB53604.1"
/db_xref="G1:14027335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Pred. No. 97;
0; Mismatches
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/protein_id="BAB53605.1"
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                                                                                                                                                                                                                                                                                                                                                                                complement (9426. /gene="ml17935" complement (9426.
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/gene="mlr7936"
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HTG: HTGS_PHASE0.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="m117935"
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ilarity 90.5%;
Conservative
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Best Local Similarity
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DEFINITION
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TITLE
JOURNAL
REFERENCE
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b_xref="GT:1402731"
translation="MRERSLMISMAALLHRTSTLRKALRASWPDRVKTGGSGSALRH
pggikwrrsDfDCQVADDRKTAGTDIEDTGLRNLYYFYSC"
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SDGKFRFRADWTGQAAPURPPKSMGLFGPVERLPEFPDHVDLIEVADDAHPFRLTISP
ARNFLNSTFAETPVSKEKEGRPALLLHPDDAADLGLADGDRVEVGNGRGDLVLHAKFF
                                                                                                                                                                 /translation="mkelsniedktvieltadivsayvgnnplpasglpdliasvsas
/rklagavvvespyslypavnpkksvfpdyiicledgkkfkslkrhlrtdyglspddyr
akwglppdypwvapnysatrsalakstglgrkpaaapaavakkgkaka"
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IRKRIDGIEDELANPAIYEKDPSTATRLAKERSQLAQTLAGHEEKWLTMSAEYEEGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation-"MNCCNAYFEAKGKRSALVLDKMFTLFLELLGGSKPLDRNQHCRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :ranslation="MLIINDLSLRMAGRLLLDHASLTLPAGTKAGLVGRNGTGKTTLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roduct="ABC transporter, ATP-binding component"
rotein_id="BAB53601.1"
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                                                                                     product "transcriptional regulator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAB53599.1"
/db_xref="GI:14027330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4476. .4730)
/gene="ms17931"
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/gene="mll7934"
complement(8203. .9390)
                                                                                                                                                                                                                                                                                                                                                          note-"unknown protein"
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                                                                                                           'protein_id="BAB53598.
'db_xref="GI:14027329"
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| Jene="mlr7932"
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gene="mlr7932"
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/gene="mlr7933"
                                                                                                                                                                                                                                                                                                            916. .4065
gene="msr7929"
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                                                                                                                                                                                                                                                    916. .4065
gene="msr7929"
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Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retter, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Seaman, S., Severti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talans, T., Trayls, R., Trayls, N., Wyman, D., Ye, W.J., Young, G., Zaihoun, J., Zembok, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                               Submitted (29-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                    ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L21835
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# 45626 4625; gap of 100 bp
# 4536 4625; gap of 100 bp
# 4538 43737; contig of 712 bp in length
# 4738 48026; contig of 712 bp in length
# 48027 48126; gap of 100 bp
# 48027 48126; gap of 100 bp
# 48040 48939; contig of 713 bp in length
# 48040 48939; gap of 100 bp
# 48040 48939; gap of 100 bp
# 48040 48939; gap of 100 bp
# 48040 48939; contig of 718 bp in length
# 48040 48057; gap of 100 bp
# 50462 50561; gap of 100 bp
# 50462 50561; gap of 100 bp
# 51371 52030; contig of 660 bp in length
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Query Match 82.9%; Score 17.4; DB 2; Length 62500; Best Local Similarity 90.0%; Pred. No. 1.6+02; Matches 18; Conservative 0; Mismatches 2; Indels 0; G

Search completed: July 8, 2003, 03:34:35 Job time: 234.102 secs

Scoring table:

Searched:

Minimum DB Maximum DB

Database;

Title: Perfect score:

Sequence:

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289 bp mRNA linear EST 13-JAN-2001 CM1-HT0950-031000-465-cll HT0950 Homo sapiens cDNA, mRNA sequence. BF830865. GI:12178097
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BM661988 UI-E-CK1-
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BE464803 hs87all.x
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 289)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.

Nagai, M.A., da Silva, W. Jr., Zaqo, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA075957 zm89c12.s
AW386247 CM4-PT001
BE719507 RC0-HT085
BQ548733 ik94c05.x
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                              AA179588 zp49d10.s
BG994036 PM0-HT091
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N29917 YY12909.s1
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Fax: +55-11-2707001
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AUTHORS
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319.453 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Result

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Reverse transcription of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dias Neto, E., Carcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMI&t2=CMI-HT0950-031000-465-cli&t3=2000-10-03&t4=1);
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF830867 13-JAN-20C 307 bp mRNA linear EST 13-JAN-20C CM1-HT0950-031000-465-901 HT0950 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               profiles into the pUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01509-010, Sao Paulo-SP
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This sequence was derived from the FAPESP/LICR Human Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 307)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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High quality sequence stop: 166.
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/organism~"Homo sapiens

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Site_2: Smal, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwing Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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4044-75 Mouse E14.5 retina lambda ZAP II Library Mus musculus CDNA,
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insertion site: TACGTCCACTGAATTCTGAGTG--->. Other information regarding entire library may be found at http://pga.swmed.edu/Data/Libraries/microarray_cdna_librar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W., White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H. Gene expression in the developing mouse retina by EST sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: pAMP10 (Gibco): Cloned unidirectionally.
Primer: Oligo dT: RNA Isolation: Cytoplasmic RNA preps
(Manniatis): Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies): Average insert size: 1.8 Kb;
                                                              /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Mouse E14.5 retina lambda 2AP II Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                            Score 18.4; DB 12; Length 307;
Pred. No. 1.56+02;
0: Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center. Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA Fax: 713 790 0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.8%; Score 17.8; DB 13; 90.5%; Pred. No. 3.5e+02:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 3.5e+02;
                                                                                                                                                                                              conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="neural retina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10090"
/db_xref-"taxon:9606'
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X., Zhao,S., Pershad,R.,
                                     /dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                       143 CTACCCCAAGCTGTGATA 162
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                                                                                                                                                                                                                                                                                                                                                                              1 CTACCCCAAGCTGCGTGATA 20
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                                                                                                                                                                                                     low stringency
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                                                                                                                                                                                                                                                                                   87.6%;
95.0%;
                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                    19;
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Best Local S
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BI989738
LOCUS
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BJ208146 BJ208146 T. Ogihara unpublished cDNA library, Wh Triticum aestivum cDNA clone wh7a03 5', mRNA sequence.
                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae, Pooideae
                                                                                                                                                                                                                                                                                                                                                                         Expressed genes in Triticum aestivum Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Jap
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.ip.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tshini@genes.nig.ac.jp.
Location/Qualifiers.
                                                                                                                                                              BJ208146.1 GI:19946210
                                                                                                                                                                                                                                                                                                          ; Triticeae; Triticum.
1 (bases 1 to 466)
Ogihara, Y. and Murai, K.
                                                                                                                                                                                                           bread wheat.
Triticum aestivum
                                                                                                                                          BJ208146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                  DEFINITION
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TITLE
JOURNAL
COMMENT
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               RESULT 5
BJ208146
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KEYWORDS
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BE775595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil47321141gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                            GSS 27-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA as blunt end-repaired with T4 DNA polymerase and T4 polymucleotide Armase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: PWD42nv; Purified genomic DNA from M.nusculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance. 72 c 120 g t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.jax.org/resources/documents/dnares/). The DNA
                                               A2962129
A200230P14R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacrer, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref="taxon:10090"
'clone="UUGC2M0230P14"
'clone_lib="Mouse:10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored vector DNA, and transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                      clone UUGC2M0230P14 R; DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 419
                                                                                                                                                                                                                                                                       Mammalia, Eutheria, Rodentia,
1 (bases 1 to 419)
Dunn, D., Aoyagi, A., Barber, M.,
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  column:
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                                                                                                                                                 AZ962129.1 GI:13833356
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid inserts
                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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RESULT 4
AZ962129/c
                                                                      DEFINITION
                                                                                                                                                                                                                  ORGANISM
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ORIGIN
                                                                                                                      ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                           REFERENCE
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Note-Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: ECORI; Site_2: Xho!; Plants were grown under
hydroponic.conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
stssue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled from the two
library was made, and the cDNA clones were in vivo
excised to give paluescript phagemids in the TJ close lab

/clone_lib="Y. Ogihara unpublished cDNA library, Wh" /tissue_type="spike at meiosis" /dev_stage="Feekes' scale 9"

organism="Triticum aestivum" /cultivar="Chinese Spring" /db_xref="taxon:4565"

clone-"wh7a03"

Shizuoka 411-8540, Japan

University of California, Riverside (Akhunov, Chin

Kianian, Otto, Simons, Zhang)

Close, Fenton,

Choi,

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                                                                                                                                                                                                                                                                                                           EST 20-SEP-2000
                                                                                                                                                                                                                                                                                              519 bp mRNA linear EST 20-SEP-2000
MY-04-D-03 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.
BE775595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kamoun, S., Hraber, P.T., Sobral, B.W.S., Nuss, D. and Govers, F. Initial assessment of gene diversity for the oomycete pathogen
                                   (all other authors).
                                                                                                                                                                                                                                                                                                                                                                                        potato late blight agent.
Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                  sequencing were
                                                                                                        Length 466;
                                                                                                                                         Indels
Plasmid DNA preparations and DNA
                                                                                                  Score 17.4; DB 13;
Pred. No. 5e+02;
                               performed in the OD Anderson lab
                                                                                                                                       Mismatches
                                                                                                                                                                                                           430 TACCCCAAGCTACGTGATA 448
                                                                                                                                                                       2 TACCCCAAGCTGCGTGATA 20
                                                                                                                                                                                                                                                                                                                                                          BE775595.1 GI:10229250
                                                                                                82.9%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 519)
                                                                                                                                       Conservative
                                                                                                Ouery Match
Best Local Similarity
Matches 18; Conserv
                                              118
                                                                                                                                                                                                                                                                                                                                                                             EST
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TITLE
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KEYWORDS
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Gaps

Length 419; Indels

Score 17.4; DB 17; Pred. No. 4.9e+02; 0; Mismatches 1;

ch 82.9%; 1 Similarity 94.7%; 18; Conservative

Query Match Best Local Similarity Matches 18; Conserv

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clone_lib="Soares melanocyte 2NbHM"
                                                                                                   'tissue_type="melanocyte"
/clone="IMAGE:269054"
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BF809553/c
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MEDLINE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adev_STage="4-week old vegetative, non-sporulating mycellum in synthetic medium"

"Ala_Dost="E. coli, strain DH5-alpha"

Anote="Vector: pSPORTI; Site_1: Sali; Site_2: NotI; Total RNA was isolated from mycellum of P. infestans DDR7602 cultured for 4 weeks in synthetic medium. EST clones were named by their position in the microtiter plate, preceded by the prefix MY (for mycellal) and the successive number of the microtiter plate (e.g. MY-06-A-04)."
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                                                                                                                                        Laboratory of Phytopathology Mageningen University Binnenhaven 9; P.O.Box 8025, 6700 EE, Wageningen, The Netherlands Binnenhaven 9; P.O.Box 8025, 6700 EE, Mageningen, The Netherlands Fax: 31 317 483 138 Fax: 31 317 483 412 Email: Francine.Govers@medew.fyto.wau.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
High quality sequence stops: 164
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.0%; Score 17; DB 12; Length 519;
1larity 94.4%; Pred. No. 8e+02;
Conservative 0; Mismatches 1; Indeis
   based on expressed sequences (2), 94-106 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Phytophthora infestans"
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/db_xref="taxon:4787"
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High quality sequence stop: 164.
Location/Qualifiers
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MAGE:269054 5', mRNA sequence.
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/db_xref="GDB:3878696"
/db_xref="taxon:9606"
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   Phytophthora infestans
Fungal Genet. Biol. 28
20056376
Contact: Govers F
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Best Local Similarity
Matches 17; Conserv
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208 bp mRNA linear EST 12-JAN-2001
QVO-CI0199-161100-506-f02 CI0199 Homo sapiens cDNA, mRNA sequence.
BF809553
BF809553.1 GI:12138542
BST.
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1 (bases 1 to 208)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Sliva,W. Jr. Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Haia,G.S., Slmpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QVO&t2=QVO-CIO199-
161100-506-f02&t3=2000-11-16&t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 7.5e+02;
0; Mismatches 2;
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20202663
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Best Local Similarity 90.0%;
Matches 18; Conservative
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profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." 42\ c\qquad 39\ g
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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[61100-506-al1st3=2000-11-16st4=1)
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QVO-CI0199-161100-506-all CI0199 Homo sapiens cDNA, mRNA sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/clone_lib="CI0199"
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low stringency cona
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ilarity 90.0%;
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Matches 18; Conserv
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Hiller, L., Lenon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Mortls, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                    r 31-DEC-1996
cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 13-JUN-2001 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="SOLR (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3
                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 286.

Location/Qualifiers
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Ammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                    s3 937216 Homo sapiens
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                                                                                                                      linear
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way, Box 8501, St. 1
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Pred. No. 8.8e+02;
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                                                                                                                  AA179588
zp49d10.s1 Stratagene HeLa cell
                                                                                                                                                        MAGE: 612787 3', mRNA sequence.
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4444 Forest Park Parkway, Box
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       est@watson.wustl.edu
164 CTACCCCAAGCTGTGTAATA 145
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                                                                                                                                                                                            GI:1760974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314.286 1810
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Homo sapiens

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Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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llarity 90.0%;
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Fax: 81-3-5449-5433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
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                                                                                                                                                  rel: +55-11-2704922
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                                                                                                                                                                              7ax: +55-11-2707001
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG994389 130201-007-d12 HT0913 Homo sapiens cDNA, mRNA sequence.
                                                                                   Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dias Neto.E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br This sequence was derived from the {\tt FAPESP/LICR} Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PMOst2=PMO-HT0913
120201-008-g11&t3=2001-02-12&t4=1)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 333)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A. 97 (7), .3491-3496 (2000)
                                                                 Garcia Correa, R., Verjovski-Almeida, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 8.8e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             low stringency conditions."
57 c 71 g 118 t
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/db_xref="taxon:9606"
/clone_lib="HT0913"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 3
High quality sequence stop: 332
Location/Qualifiers
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90.08;
                                                                                                                                                                                                                                                                                                                                                                                             rel: +55-11-2704922
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                                             1 (bases 1 to 332)
Dias Neto, E., Garci
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371 bp mRNA linear EST 30-JUL-1996
CO3725 Human heart cDNA (YNAkamura) Homo sapiens cDNA clone
3NHC2079, mRNA sequence.
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s made by cloning products
Letters Patent application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                    (http://www.ludwig.org.br/scripts/gethtml2.pl?tí-PMO&t2-PMO-HT0913-
130201-007-dl2&t3-2001-02-13&t4-1)
                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostom1;
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Construction of a normalized directionally cloned cDNA library adult heart and analysis of 3040 clones by partial sequencing Genomics 35 (1), 231-235 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catarrhini; Hominidae; Homo
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Pred. No. 8.8e+02;
0; Mismatches 2;
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4-6-1, Shirokanedai, Minato-ku, Tokyo 108,
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57 c 71 g 118
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/db_xref="taxon:9606"
/clone="3NHC2079"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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High quality sequence stop: 333.
Location/Qualifiers
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Location/Qualifiers
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/clone_lib="HT0913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                             Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 CTACCCCAAGCTGTGTAATA 168
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Wed Jul

qq

CTACCCCAAGCTGTGTAATA 310

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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome-
Project. This ends seem in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-FT0010-090
800-300-c04&t3=2000-08-09&t4=1)
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                 /dev_stage="adult" //dev_stage="adult" //dev_stage="double cloned content from adult heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Briones, M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto.E., García Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Rels,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                             BE768673
QV2-FT0010-090800-300-c04 FT0010 Homo sapiens cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                               Gaps
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1 (bases 1 to 376)
                                                                                                                                                 Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/clone_lib="Human heart cDNA (YNakamura)"
                                                                                       3. others
                                                                                                                                                                                           2; Indels
                                                                                                                                               Score 16.8; DB 14;
Pred. No. 9.1e+02;
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90.0%; Pred. No. 9.1e+02;
1ve 0; Mismatches 2;
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High quality sequence stop: 375.
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BE768673.1 GI:10222331
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Best Local Similarity
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BE768673/c
LOCUS
DEFINITION
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1 (bases 1 to 377)
Adams, M.D., Kerlavage, A.R., Fletschmann, R.D., Fuldner, R.A., Bult
Adams, M.D., Kerlavage, A.R., Fletschmann, R.D., Fuldner, R.A., Bult
O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
Gnehm, C.L., Hanna, M.C., Fitchlom, J.L., Geoghagen, N.S., Glodek, A.,
Kelley, J.C., Liu, L. T., Marmaros, S.M., Merrick, J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Moreno-Palaques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, T.F., Li, Y., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Wel, T.F., Hungjun, J., Li, H., Meissen, P.S., Olsen, H., Raymond, L., Wel, Y.F., Wing, J. Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Eraser, C.M. and
                                                         20-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nitial assessment of human gene diversity and expression patterns
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                                                                                                                                                                                                                      Euteleostomi;
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lease check the TIGR Human Gene
                                                AA323181 377 bp mRNA linear EST 20-APR-
EST25923 Cerebellum II Homo sapiens CDNA 5' end, mRNA sequence.
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Catarrhini; Hominidae; Homo.
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Nature 377 (6547 Suppl), 3-174 (1995)
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Pred: No. 9.1e+02;
0; Mismatches 2;
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/db_xref="taxon:9606"
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Fel: 3018699056
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                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                 Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 CTACCCCAAGCTGTGTAATA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
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                                                                                                                 AA323181.1 GI:1975506
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90.0%;
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Eukaryota; Metazoa;
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Conservative

8, 2003, 09:21:30

Search completed: July Job time: 1068.8 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: July 8, 2003, 00:45:33; Search time 231.102 Seconds

10:09-647-780A-10:

Sequence: 15:09-647-780A-10:

Sequence: 16:09-647-780A-10:

Sequence: 16:09-647-780A-10:

Sequence: 16:09-647-780A-10:

Searched: 2034640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum be seq length: 300000000

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Post-processing Maximum Match (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Match) (00 Maximum Max

Novel nep ii membrane metalloprotease and its use for screening inhibitors useful in therapy TITLE Pred. No. is the number of results predicted by chance to have a

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Patent: WO 9953077-A 1 21-OCT-1999;
Patent: WO 9953077-A 10 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS
CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME
MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
LOCATION/Qualifiers
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Schwartz,J.C., Gros,C., Ouimet,T., Rose,C., Bonhomme,M.C. and
Facchinetti,P.
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ilarity 100.0%; Pred. No. 2;
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/db_xref="taxon:10117"
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E. I (Dases I to 17495)

Muzny, D.M.; Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Anely, C., Are, J.R., Banks, T., Barbaria, J., Allentons, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Burdet, C., Burkelburg, K., Bondin, D., Bouck, J., Burkett, C., Burkell, K.L., Byrd, N.C., Carron, T.F., Burkh, P., Burkett, C., Burkell, K.L., Byrd, N.C., Carron, T.F., Carten, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chowdhry, I., Chacko, J., Chavez, D., Chen, G., Chen, R., Chon, Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Dan, A.L., Din, H.H., Douthwaite, K.J., Daraper, H., Dany, A.L., Din, H.H., Douthwaite, K.J., Daraper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elbar, P., Erantz, P., Garcila, A., Garcila, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Haraikton, K., Harris, K., Hart, M., Harlak, P., Hawes, A., Hernandez, J., Hernandez, C., Hodgson, A., Holloway, C., Hollins, B., Homal, F., Howards, S., Huber, J., Huber, S., Hume, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kratosio, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lii, Z., Lichtarge, C., Lieu, C., Liu, J., Liu, M., Mapus, P., Martin, R., Martin
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*** SEQUENCING IN PROGRESS ***,
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Mammalia; Eutheria; Rodentia; Sciurognathí; Muridae; Murinae;
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Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
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Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).NOTE: This is a 'working draft'. sequence. It currently consists of 56 contigs. The true order of the pieces
                                            Consensus quality: 152255 bases at least 040 Consensus quality: 158448 bases at least 030 Consensus quality: 164461 bases at least 020 Estimated insert size: 155965; sum-of-contigs estimation Quality coverage: 0x in 020 bases; agarose-fp estimation Quality coverage: 2.2x in 020 bases; sum-of-contigs estimation
                                                                                                                                                                 is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                          call
                       Assembly program: Phrap; version 0.990329First
                                                                                                                                                                                                                                                      gap of unknown length
contig of 9405 bp in length
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contig of 4694 bp in length
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349498 bp DNA linear BCT 15-MAY-2001
Mesorhizobium loti DNA, complete genome, section 9/21.
AP003002 BA000012
AP003002.2 GI:14023709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                     Novel nep ii membrane metalloprotease and its use for screening
inhibitors useful in therapy
Patent: WO 9953077-A 8 21-OCT-1999;
                                                                                                                                                                                                                                                             INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
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Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research: Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail:kaneko@kazusa.or.jp,
URL:http://www.kazusa.or.jp,
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
On May 11, 2001 this sequence version replaced gi:11994977.
                                                                                                                         artificial sequences.
1 (bases 1 to 19)
Schwartz,J.C., Gros,C., Ouimet,T., Rose,C., Bonhomme,M.C. and
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/note="oligonucleotide"
Sequence 8 from Patent WO9953077.
AX014708
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complement(26, 1600)
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'protein_id="BAB50316.1"
'db_xref="GI:14023711"
'translation="MDVSLIFPRLPFSGKPSMTTGICIGTGRILANWLVSRTASCWRI
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EHDLLVAIAALAPRFLTYALSFLTLTIFWFGQQAQHGLIAKSDRRLATINLCFLAFIA
LLPFSTDLLADFLEFRTAVLVYWLNLLMLGVTLFASWRYADKNGFVAEDADAETKRTV
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QFFVTFKCSDIAYDVLKEQPGLRPAPYLASRGMKWIQRRTSQSMDDAALKDYLRESHR
                                                                                                                                                                                                                                                                                           ALVVSPESTAIMTAVEDKDTGAASGINNAVSRIĞGLIAVAAMGSLATWVYATMLDTSV
RPGIPGFGEPVSTGLPPELEATRLAASDMAFSAISLTTAVLCLLAAIIAWVTVSGQAL
                                                                                                                                                                                                              DLGGGALATLAFGALAYGLTSMSSSSEGHWAGPSIAAGAVLLVVFILFEQRQREPMID
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                                                                                                                                                     LFIVASLACALAPNAVVLIGFRALQGIGAAİMVPGSLAIIAKAYPKKERGRAIGIWA
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                                                                                                                 GSILAIAMPAIRVNLGASLAEAQWISNAYALTLSALILAGGAAGDRFGLRRAFVAG
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complement(2360. .3877)
                                                                                         'translation="MHSPNEAAAIPLTSRLTNGTFCPQSQRRF
/product="transmembrane efflux protein"
/protein_id="BAB50315.1"
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db_xref="GI:14023712"
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/db_xref="G1:14023713"
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/gene="ms13425"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="unknown protein"
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/gene="mll3429"
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VMGVVRASFRPEFLMRVDEVILFHRLRRRDMDRIVEIQFKRLESLLVDRKITLSLDHE
AIEWLAAKGYDPAYGARPLKRVMQKELQDPLAEKILLGEILDGSTVKVTSGSDRLNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aLnrdgrdnrdnggrdnngrnnggrdnnggrhrdrrpnggyggrdhasstegggoodr
Neapaqaeegyepgspaetyavaefaplfesfspaalaaqaelneaaaesgaarrprr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MADPLPEALGPLLREARARLVAAGVGDPALDARLIVEHFSGTTR
FQAIADPERTIDSNAIAAIDAALGRRAGGEPVHRILGYREFYGLRLSLSPETLEPRPD
                                                                                                                                                                                                          ALKKYARDLTADARAGKLDPVIGRDDEIRRTIQVLSRRTKNNPVLIGEPGVGKTAIAE
GIALRIVNGDVPESLKDKQLMALDMGALIAGAKYRGEFEERLKAVLSEVTSANGNIIL
                                                                                                                                                                                                                                                                                FIDEMHTLVGAGKADGAMDASNLLKPALARGELHCVGATTLDEYRKHVEKDPALARRF
                                                                                                                                                                                                                                                                                                              QPVEVDEPTVEDTVSILRGLKEKYEQHHKVRISDSALVAAATLSNRYIADRFLPDKAI
DLVDEAASRLRMQVDSKPEALDEIDRRIMQLKIEREALKVETDDASKDRLVRLEKELV
                                                                                                                                                                                                                                                                                                                                                                                        GLEEESTEITAKWQAEKQKLGLAADLKKQLDEARNELAIAQRKGEFQRAGELAYGKIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKRVVGQGEAVQAVSKAVRRARAGLQDPNRPIGSFIFLGPTGVGKTELTKALASFLFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDSAMVRIDMSEFMEKHSVARLIGAPPGYVGYEEGGALTEAVRRRPYQVVLFDEIEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPDVFNVLLQVLDDGRLTDGQGRTVDFRNTLIIMTSNLGAEYLVNLGEDQDVDAVRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation-"MRPQQQNRRMRGRNNNGGGGGGNNNNNNRKGPNPLTRNYESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OONRDDFDDDGDEDRDDFENAGNNGAGNGCONTVSDPQIPVINHGAGPQPVIEGMPAEV
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LALDGGVDGLNPYRIIAAEAARFLEAESRIAVEIGHTQRDEVTDIFKAAGYASVAALR
                                                                                                   'translation="MNLEKYSERVRGFIQSAQTMALSRNHQQFTPEHILKVLVDDDEG
                                                                                                                                    LAASLIERAGGNVRDVKLGVETALEAMPKVEGGNGQLYLAQPLAKVFSTAEELAKKAG
                                                                                                                                                                         DSFVTVERLLQALTMEKSAKTADILAKAGVTAQALNQVINDVRKGRTADSASAEQNYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDVKIRGSAQQIAEKYATLARDAQSSGDRVMAENYLQHAEHYNRIIAAAQAQMPIQNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PETLVEAVLPFVKAMAAREGTCRILDLGTGTGAIALALLSAVPAATATGVDISAGALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MVNLPRDRMDQVVKRFEMLEAQMSAGPAPDAYVKMASEYAELQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVAKVRQLRSAEHEQADLEAMLADKGTDAEMRALAEADLPDVEERIEALOKDIOILLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEIIATVSGKGVFAHLKFESGVHRVQRVPATEASGRIHTSAATVAVLPEAEEVDIEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEDIRIDTMRASGSGGOHVNTTDSAVRITHLPTGIMVVQAEKSQHQNRAKAMQILRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                ELEKKLKEAEAQDGKAGMVEEVVTPDHVAHIVSRWTGIPVDKMLQGERDKLLRMEDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYDLERSKADEERSESRKSQVGSGDRSERIRTYNFPQGRVTDHRINLTLYKLDRVMMG
product="endopeptidase Clp ATP-binding chain B; ClpB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="protoporphyrinogen oxidase; HemK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRRPRTNADQVDSGSDNADAGEAAAAPADSGNAEPVIVDIDN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="peptide chain release factor 1"
protein_id="BAB50323.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELDEIVDALIADHQSKLLADIGLDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(10498. .12768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="BAB50321.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(9408. .10487)
/gene="ml13435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(9408. .10487)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7276. .8232)
/gene="ml13431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(8543. .9415)
/gene="ml13434"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7276. .8232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(8543. .9415)
                                                                  'db_xref="GI:14023715"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="GI:14023716"
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transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ml13431
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FRT DIGGOKVLPYFKGAIOEENPALGWRAIRLTLDRPGLLRYOIRALLKASGGRELK
LMLPMVTELSEIAQAREIIDREVRHLSRFAHHLPTSLKLGAMLEVPSLLFQLDELMKA
VDFVSVGSNDLFQFVMAVDRGNTQLANRFDTLSAPFLRVLKQIADAGIRNHTPVTLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus NADP+-specific isocitrate dehydrogenase mRNA, complete cds; nuclear gene for mitochondrial product.
                                                                                                 /traislation="MRDQASGPRVLLKRLRELMOEPLEPOERLDRIVRDIASNWVAEV
CSLYVLRADSVLELYATEGLNPNAVHLAQLRLGGGLVGTIAASARPLNLSNAQEHPAF
AYLPETGEEIYNSFLGVPVLRAGRTLGVLVVQNKTMRHYRDDEVEALETTAMVIAEMI
                                                                                                                                                                                                                                              AEAAVEKVQSDWRARWLHWTDPYLRERMSDFDDLANRLLRQLMGRGPEDVAASLEKDA
IIVARSMGAAELLDYPREKMRGLVLEDGAATSHVVIVARAMGIPVAGQMKGAVSMAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jo.S.H., Son.M.K., Koh, H.J., Lee, S.M., Song, I.H., Kim, Y.O., Lee, Y.S., Jeong, K.S., Kim, W.B., Park, J.W., Song, B.J. and Huhe, T.L. Control of mitochondrial redox balance and cellular defense against oxidative damage by mitochondrial NADP+-dependent isocitrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAGYLRAVSSLCRASGSARTWAPAALTVPSWPEQPRRHYAEKRI
KVEKPVVEMDGDEMTRIIWQPIKEKLILPHVDVQLKYFDLGLPNRDQTNDQVTIDSAL
ATOKYSVAVKCATITPDEARVEEFKLKKMWKSPNGTIRNILGGTVFREPIICKNIPRL
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VCPDGKT I EAEAAHGTVTRHYREHQKGRPTSTNP I AS I FAWTRGLEHRGKLDGNQDL.I
RFAQTLEKVCVQTVESGAMTKDLAGC I HGLSNVKLNEHFLNTTDFLDT IKSNLDRALG
                                                                                                                                                                                          ATGDLARLTRPGLELDLRRPVSFTGLSFNDGVGLGHVVLHEPRIVVTNLFNEDSEEEV
                                                                                                                                                                                                                          RRLETSIGSLRLSIDDMLERRDVAFEGEHRQVLEAYRMFANDRGWVRRLEEAIRNGLT
                                                                                                                                                                                                                                                                                                       GDAIIVDGEEGVIHLRPQSDLEAAYAEKVRFRARRQEVYRELRKKPSTTRDGVQVDLL
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                                                                                                                                                                                                                                                                                                                                    MNAGLAVDLPQLAEAGAAGIGLFRTELQFWVASTFPRAEAQEKLYRDVLEAARGKPV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGMYNTDESISGFAHSCFQYSIQKKWPLYLSTKNTILKAYDGRFKDIFQEIFDKHYKT
/product="phosphoenolpyruvate-protein phosphotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 1679)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-DEC-1999) Genetic Engineering, Kyungpook National University, San-Kyuk-dong 1370, Taegu 702-701, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.8%; Score 17.8; DB 1; Length 349498; 90.5%; Pred. No. 1.6e+02; 1ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 276 (19), 16168-16176 (2001)
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    1679
    organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299423 CGGCAGCATCTGATCCCCGAG 299403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1679)
Huh, T.L., Jo, S.H. and Son, M.K.
Direct Submission
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Matches 19; Conservative
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LOCUS
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TITLE
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PUBMED
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SOURCE
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BCO24640 2494 bp mRNA linear ROD 07-AUG-2002
Mus musculus, clone MGC:28430 IMAGE:4038046, mRNA, complete cds
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2494)
                                                                                                                                                                                                                                         Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                        Contract: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.ngsc.bcm.tmc.edu/cdna/
Contact: amg&bon.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                            http://mgc.nc1.nih.gov
                                                             BC024640.1 GI:22137612
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                                                                                                             house mouse:
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Best Local S
Matches 18
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (11:MAR-1996) Hongyu Luo, Notre-Dame Research Center, University of Montreal, 1560 Sherbrooke East, Montreal, Quebec, H2L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASRFGSLGLMTSVLVCPDGKTIEAEAAHGTVTRHYREHQKGRPTSTKGIASIFAWTRG
LEHRGKLDGNQDLIRFAQTREKVCVQTVEGAMTKDLAGCIHGLSNVKLNEHFLMTTDF
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1863)
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Mus musculus isocitrate dehydrogenase mRNA, complete cds.
U51167
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                                           Score 16.8; DB 10;
Pred. No. 4e+02;
0; Mismatches 2;
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Pred. No. 4e+02;
0; Mismatches
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/strain="Balb/c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="MIDH 5.1"
/tissue_type="heart"
/dev_stage="adult"
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90.0%;
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                                             80.0%;
90.0%;
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                                           Query Match 80.0
Best Local Similarity 90.0
Matches 18; Conservative
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Matches 18; Conserv
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BC024640/c
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ORIGIN
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MMU51167/c
                                                                                                                                                                                                                                                                                    DEFINITION
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TITLE
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Hulyk, S.W., Hale, S.M., Martin, R.G., Muzny, D.M.

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/translation="msqaskrkhyvobylgehmypsdhqoivkulrtpgnnilhbyeta
qqqrfivsmpskyrkniwikrgdflivdpieegekvkarisfylcknhyrslqkeghw
peafsbyaekqnnmnresqpelpaepqlsgegssseddsdlfvntnhrqyheseeese
edeeeeeeaa"
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAR Plate: 37.Row: D Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
AF302075
LOCUS AF302075
LOCUS AF302075
DEFINITION Mus musculus neprilysin-like peptidase alpha mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                            'tissue_type="Mammary tumor. WAP-TGF alpha model.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Unknown (protein for MGC:28430)"
/protein id="AAH24640.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 4.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                       /map="C57BL/6J"
/clone="MGC:28430 IMAGE:4038046"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           note-"Vector: pCMV-SPORT6'
                                                                                                                                                                                                                                                                                                                                                                         old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAH24640.
/db_xref="GI:22137613'
                                                                                                                                                                       Location/Qualifiers
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Molecular identification and characterization of novel membrane-bound metalloprotease, the soluble secreted form of which hydrolyzes a variety of vasoactive peptides 174 (45), 32469-32477 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                         /note="SEP(delta); metalloprotease; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GWPVALDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPT
LGMPSREYYFQEDNNHKVRKAYPEFWTSVATWLRKDQNLSKESAMVREEMAEVLELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIVTLGVFYSIALRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKMVG
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LADNONVNGFSSLGENIADNGGVROAYKAYLRWLADGGKDORLPGLNLTYAQLFFINY
                                                                                                                                                                                                                  Direct Submission
Submitted (08-JUN-1999) International Center for Medical Research,
Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
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Mus musculus neprilysin-like peptidase beta mRNA, complete cds.
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Mus musculus
Eukaryotis, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryotis, Metazoa; Chordata; Colurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2652)
Shirotani,K., Tsubuki,S., Iwata,N., Takaki,Y., Harigaya,W.,
Maruyama,K., Kiryu-Seo,S., Kiyama,H., Iwata,H., Tomita,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNSRY
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Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                               /product = soluble secreted endopeptidase delta"
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Pred. No. 4.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                               Ikeda, K., Emoto, N. and Matsuo, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAF13153
/db_xref="G1:6467401"
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Shirotani, K. and Saido, T.C.
Direct Submission
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Best Local Similarity 90.0%;
Matches 18; Conservative
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AF302076
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                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2583)
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                                                                                                                                                               Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T., Iwatsubo, T. and Saido, T.C.
Iwatsubo, T. and Saido, T.C.
Iwatsubo, T. and Saido, T.C.
Iwatsubo, T. and Saido, T.C.
Iwatsubo, T. and Saido, T.C.
Irapidly and efficiently among thiorphan- and
phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELET
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Sciurognathi; Muridae; Murinae; Mus
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele-
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin
1 (bases 1 to 2601)
Ikeda;K., Emoto,N., Raharjo,S.B., Nurhantari,Y., Saiki,K.,
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AF157106
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/protein_id="AAG18446.1"
/db_xref="G1:10505360"
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2 (bases 1 to 2583)
Shirotani, K. and Saido, T.C.
Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience
Science Institutute, RIKEN, 2-1 Hirosawa, Wako-sh
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Pred. No. 4.1e+02;
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/db_xref="taxon:10090"
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                         GI:10505359
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ilarity 90.0%;
Conservative
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AF302075
AF302075.1
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Best Local Similarity
Matches 18; Conserv
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AUTHORS
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Mus musculus neprilysin-like peptidase gamma mRNA, complete cds.
AF302077
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Shirotani, K. and Saido, T.C.
Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OIVEPAGILQPPFESKDQPÖSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNMLDWWSN
FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYRAYLRWLA
DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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                                                                                                                                                                                                                                                                                                       PLLTSLLHESWDERTVVKRALRDSSLKSDICTTPSCVIAAARILENMDGSRNPCENFY
OYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSGHRPAVEKAKTLYRS
                                                                                                                                                                                                                                                                                                                                                                            IDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRK
                                                                                                                                                                                                                                                                                                                                                                                                                     FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLD
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                                                                                                                                                                                                                                                                /db_xref="GI:10505362"
/translation="MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIVTLGVFYSIGKQL
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Iwatsubo, T. and Saido, T.C.
Iwatsubo, T. and Saido, Detamyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan and phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2694)
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saltama
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                                                                                                                                                                                                                       'product="neprilysin-like peptidase beta"
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Pred. No. 4.1e+02;
0; Mismatches 2;
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/db_xref-"taxon:10090"
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                                                                                                                                                                                'note="endopeptidase"
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RIGSLSORFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
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Mus musculus soluble secreted endopeptidase mRNA, complete cds.
AF157105
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2892)
1 (kada, K., Emboto, N., Raharjo, S.B., Nurhantari, Y., Salki, K.,
Yokoyama, M. and Matsuo, M.
Molecular identification and characterization of novel
membrane-bound metalloprotease, the soluble secreted form of which
hydrolyzes a variety of vasoactive peptides
J. Blol. Chem. 274 (45), 32469-32477 (1999)
                                                                                                                                                                                                                                                                                                                                            NFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNG
                                                                                                                                                                                                              NPPASDSRVIGLKGFRWTLFTONVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSA
RTWONYLWWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESA
VGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELMWMDEESKKKAQEKAMNIREQI
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GWPVAMDKWNETMGLKWELERQLAVLNSOFNRRVLIDLFIWNDDONSSRHVIYIDOPT
                                                                                                                                                               LGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELET
                                                                                                                                                                                           HLANATVPQEKRHDVTALYHRMDLMELQERFGLKDRVSLCSPGCPGTHSVDQAGLELG
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Submitted (08-JUN-1999) International Center for Medical Research,
                                                                     /translation="myeragmcrkkspgfveyglmvllllllgaivtlgyfxsialrd
sslksdicttpscviaaarilenmdqsrnpcenfyqyacggwlrhhvipetnsrysyf
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/protein_id="AAF13152.1"
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/note="SEP; metalloprotease"
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/organ1sm="Mus musculus"
/db_xref="taxon:10090"
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Mus musculus neprilysin-like metallopeptidase 1 (N11) mRNA,
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/gene="N11"
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                                            FSARHFQQQSQCMIYQYGNFSWELADNONVNGFSSLGENIADNGSYRQYYRAYLEWIA
DGGKQQRLPGLNLTYAQLFFINYAQYWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
FGPSEAFHCPRGSPWRKCRIW
774 c 577 t 577 t
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New metalloproteases of the neprilysin family
Patent: WO 0047750-A 12 17-AUG-2000;
BOILEAU GUY (CA) ; DESGROSEILLERS LUC (CA) ; UNIVERSTIE DE MONTREAL
KSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHL
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DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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'Organism="Mus musculus"

'db_xref="taxon:10090"
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'db_xref="Gi:10280088"
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RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
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DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2925)
Ghaddar,G., Ruchon,A.F., Carpentier,M., Marcinkiewicz,M.,
                                                                                                                          Seidah, N.G., Crine, P., Desgröseillers, L. and Boileau, G. Molecular cloning and biochemical characterization of a new mctestis soluble-zinc-metallopeptidase of the neprilysin family Biochem. J. 347 (Pt 2), 419-429 (2000)
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Ghaddar,G., Ruchon,A.F., DesGroseillers,L. and Boileau,G.
Direct Submission
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nucleic search, using sw model

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Run on:

Total number of hits satisfying chosen parameters:

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Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_101002:*

Database :

2185239 seqs, 1125999159 residues

IDENTITY_NUC Gapop 10.0 ', Gapext 1.0

Scoring table:

Searched:

US-09-647-780A-10 21 1 cggcaccatgtgatccccgag 21

Title: Perfect score:

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Human metalloprote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; ss; neuron; hormone; pepfide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; probe; hybridsation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amycolatopsis
                                                       Probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat membrane metalloprotease NEPII gene probe #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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ABA70793
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AAK44999
AAI50967
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ABL14849
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ABL12652
ABL28855
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                                                                        ABS19244
                                                                                          ABA58192
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                                                                                                                                                                                                AD2138
                                                                                                                                                                                                                                                                                                                                                                                                                  ABN8427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ28816 standard; DNA; 21 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus rattus.
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Schwartz JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-1999
Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
AAZ28816
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Rat membrane metal
Rat membrane metal
Mouse IDPm encodin
CDNA encoding novel
DNA encoding novel
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                                                                                                                                         (without alignments)
358.431 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                  8, 2003, 00:43:28; Search time 131.941 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
/SIDS2/gcgdata/geneseq-geneseqn-embl/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
/SIDS2/gcgdata/geneseq-geneseqn-embl/NA1988.DAT:*
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              GenCore version 5.1.6
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SUMMARIES

AAZ28816 AAZ28810 AAZ28814

B

Length

Query 100.0

Score

Result Š. ABA95078 AAA63763 AAS88996 AAS94171 AAI90923 AAK84366

2765 19 1667 2925 3939 410 4829

16.8 16.8 16.8 16.8 16.4

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membrane metalloprotease designated neprilysine II (NEPII) gene (AAZ28810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular. or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic- hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the gene for the rat membrane metalloprotease
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neprilysine II; NEPII; inactivation;
                                                                                                          Sequences AAZ28811-Z28827 represent probes for detecting the rat
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to screen for inhibitors,
cardiovascular disease
                 involved in proteolysis of
to screen for inhibitors,
cardiovascular disease
                                                                                                                                                                                                                                                                                                       21;
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                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothalamic-hypophyseal axis; endocrine disorder;
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                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                  0.62;
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                                                                                                                                                                                                                                                                          Sequence 21 BP; 4 A; 8 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                      Score 21; DB Pred. No. 0.63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat membrane metalloprotease NEPII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane metalloprotease NEP II, conal and hormonal peptides, used antially useful for treating e.g.
                 metalloprotease NEP II, hormonal peptides, used
                                                potentially useful for treating e.g.
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                                                                                                                                                                                                                                                                                                                                                                                 1 CGCCACCATGTGATCCCCGAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                            Claim 3; Page 21; 29pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ28810 standard; cDNA; 2765
                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                     Conservative
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P-PSDB; AAY44177.
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                                                                                                                                                                                                                                                                                                                     Similarity
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                               neuronal and
                    membrane
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; ss; neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; probe; hybridsation.
disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                Length 2765;
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                                                                                                                   G; 559 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat membrane metalloprotease NEPII gene probe #4.
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                                                                                                                                                              Score 21; DB 20;
Pred. No. 0.86;
Mismatches 0;
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Mismatches
                                                                                                                     787
                                                                                                                                                                                                                                                                                   467 CGCCACCATGTGATCCCCGAG 487
                                                                                                                                                                                                                                                           21
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0
                                                                                                                     Sequence 2765 BP; 684 A; 735 C;
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                                                                                                                                                                                        llarity 100.0%; P. Conservative 0;
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                                                                                                                                                                                                                                                              1 CGGCACCATGTGATCCCCGAG
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                                                                                                                                                                  100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98FR-0004389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
tes 19; Conserv
                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38-APR-1998;
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                                                                                                                                                                          Local Single 21; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-1998;
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Matches
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19 CGGCACCATGTGATCCCCG 1
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RESULT

ABA95078/C ID ABA95078 standard; CDNA; 1667 BP.

ABA95078;

(first entry) 20-MAY-2002

Mouse IDPm encoding cDNA.

mitochondrial NADP+ dependent isocitrate dehydrogenase; vasotropic; cytoplasmic NADP+ dependent isocitrate dehydrogenase; cerebroprotective; monse; cytoplasmic NADP+ dependent isocitrate dehydrogenase; cerebroprotecantioxidative; nicotinamide adenine dinucleotide phosphate; enzyme; dehydrogenase; NADPH; AOS; GSH; IDPC; IDH; IDPP; antioxidative system; glutathione; aging; gene; ss. Isocitrate

Mus sp.

Location/Qualifiers 46..1404 Key

/product= "IDPm"

WO200208405-A1

31-JAN-2002.

20-JUL-2001; 2001WO-KR01242.

20-JUL-2000; 2000KR-0041516

(TGBI-) TG BIOTECH INC (HUHI/) HUH I.

Park J, Huh T,

Son M; Jo S, Lee S,

WPI; 2002-227047/28. P-PSDB; ABB07641 Isocitrate dehydrogenases and their genes in antioxidative system suppressive of reactive oxygen species-mediated diseases e.g. ischemic stroke, catalyses production of nicotinamide adenine dinucleotide phosphate

Claim 10; Page 104-107; 112pp; English.

nicotinamide adenine dinuclectide phosphate (NADPH), useful in improving antioxidative activity in cells and tissues. An antioxidative system (AOS) for increasing cellular reduced gluttathione (GSH) level, comprising reaction product is solicitate as an enzyme substrate, and NADPH as a reaction product is also provided. The AOS is useful as a cure for or a preventive agent for reactive oxygen species-mediated diseases which include ischemic stroke, aging, and acute pulmonary damage caused by a provision of high pressure oxygen; for use in suppression of radiation-caused diseases, which include UV- or X.ray-induced skin damage and concomitant aging. Materials having decreased IDPm and IDPc gene expression is useful for screening antioxidants inhibitory of reactive DNA damage. The present sequence represents a The invention relates to isocitrate dehydrogenases selected from a cytoplasmic NADP+ dependent isocitrate dehydrogenase (IDPm) or a mitochondrial NADP+ dependent isocitrate dehydrogenase (IDPm). The isocitrate dehydrogenase (IDPm). The isocitrate dehydrogenase are useful catalysing the production of encoding the mouse IDPm protein. oxygen species-mediated

Seguence 1667 BP; 392 A; 438 C; 477 G; 360 T; 0 other;

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Gaps
                       0.
  Length 1667;
                       Indels
  DB 24;
                       5
Score 16.8; Di
Pred. No. 98;
O; Mismatches
                     0;
ch 80.0%;
1 Similarity 90.0%;
18; Conservative
           Best Local Similarity
Matches 18; Conserv
  Query Match
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endopeptidase metallopeptidase-like
                                                                                                                                                                                                                                                                                                                           Neprilysin; neutral endopeptidase metallopeptidase-like enzyme; NBP-like enzyme; prodeln production; protein secretion; neurological disease; Alzheimer's disease; pain; psychiatric disorder; fertility; bone disease; abnormal phosphate metabolism; ss.
                                                                                                                                                                                                                                                                                  cDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme NL-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "neutral
                      1640 GGCACCATGTGATTCCAGAG 1621
21
                                                                                                                                                 AAA63763 standard; cDNA; 2925 BP.
2 GGCACCATGTGATCCCCGAG
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332..2629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                       04-DEC-2000
                                                                                                                                                                                            AAA63763;
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                                                                                                      RESULT 5
AAA63763
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Desgroseillers L, Boileau G; 11-FEB-2000; 2000WO-CA00147: 99CA-2260376. (UYMO-) UNIV MONTREAL. 11-FEB-1999;

WO200047750-A2

17-AUG-2000

2000-549148/50.

P-PSDB; AAB08130

Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders

Disclosure, Fig 3; 59pp; English

The present sequence encodes a murine neutral endopeptidase metallopeptidase-like enzyme, designated NL-1. The specification also describes NL-3 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active blopeptides, using chimeric constructs containing the foreign protein acommand in phase with the N-terminal region. The NL enzymes are have been localised to the brain, and may be useful in the treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders. NL enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide processing by the NL-3 enzyme.

Sequence 2925 BP; 710 A; 797 C; 836 G; 582 T; 0 other;

Gaps ö. Length 2925; Indels 80.0%; Score 16.8; DB 21; 90.0%; Pred. No. 1e+02; ative 0; Mismatches 2; 18; Conservative Similarity Query Match Best Local Matches

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2 GGCACCATGTGATCCCCGAG 21

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss

ONA encoding novel human diagnostic protein #29975.

13-FEB-2002 (first entry)

AAS94171;

AAS94171 standard; cDNA; 3939 BP.

AAS94171

663 GGCACCACGTGATCCCAGAG 682

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in madical immaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypuor equations in a sequence of a sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutations
                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s patent did not appear in the in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     933 A; 1072 C; 1040 G; 894 T; 0 other;
                                                                                                                                                           DNA encoding novel human diagnostic protein #24800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 16.8; DB 23;
llarity 90.0%; Pred. No. 1e+02;
Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 24800; 103pp; English.
                                     AAS88996 standard; cDNA; 3939 BP
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                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631
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23-AUG-2000; 2000US-0649167
                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                   WO200175067-A2.
                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity
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                                                                                                                     13-FEB-2002
                                                                                                                                                                                                                                                                                                                                         11-OCT-2001
                                                                             AAS88996;
RESULT 6
                    AAS88996
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New isolated polynucleotide and encoded polypeptides, useful in

Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73. P-PSDB; ABG29984.

(HYSE-) HYSEQ INC.

30-MAR-2001; 2001WO-US08631 31-MAR-2000; 2000US-0540217 23-AUG-2000; 2000US-0649167

40200175067-A2. Homo sapiens.

11-OCT-2001.

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                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                      diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 80.0%; Score 16.8; DB 23; Length 3939; 90.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3939 BP; 933 A; 1072 C; 1040 G; 894 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid sequences. AAS64197-AAS94564 reprediagnostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 29975; 103pp; English.
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Best Local Similarity 90.0
Matches 18; Conservative
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qq
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printed from WIPO

2; Indels 0;

3790 CGCCACAATGTGATCCCCCA 3809

1 CGGCACCATGTGATCCCCGA 20

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                        cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                        WO200157182-A2
                                                                                                                           Homo sapiens
                                                                                                                                                                                                                              09-AUG-2001
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                     The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemmatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or the teatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.Wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 410 BP; 101 A; 81 C; 136 G; 92 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                     Human polynucleotide SEQ ID NO 10983
                                  410 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 CGCCACCATCTGATCCCC 211
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ID AAK84366 standard; DNA; 4829 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                06-NOV-2001 (first entry)
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AAI90923/c
ID AAI90923 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 94.4
Matches 17; Conservative
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P-PSDB; AA010992.
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                                                                                                                                                                                                                                                                                                                                                                                                                         WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders -
                                                                                AAI90923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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27-SEP-2000; 29-SEP-2000;

39-SEP-2000;

9-SEP-2 -OCT-2 12-OCT-2

2-0CT-

3-SEP-

25-SEP-2000 27-SEP-2000;

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AMK64951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynuclectides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; foetal liver; gene expression; single exon nucleic acid probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 39178; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4829 BP; 922 A; 1179 C; 1681 G; 1047 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human foetal liver single exon nucleic acid probe #19098
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Pred. No. 1.7e+02;
0; Mismatches 1;
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                                                                                                                                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGGCACCATGTGATCCCC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA70793 standard; DNA; 97 BP
11-DEC-2000; 2000US-0254097. 05-JAN-2001; 2001US-0259678.
                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2002 (first entry)
                                                                                                                                Rosen CA, Barash SC,
                                                                                                                                                                               WPI; 2001-483426/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157277-A2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA70793;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
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NOV-

08-DEC-2000; 08-DEC-2000; 08-DEC-2000;

-DEC-2000

NOV-

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Gaps

Indels

Length 4829;

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Gaps

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Indels

Length 97;

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improved diagnosis and treatment of cancers of myeloma. The present sequence is one of
probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                          xpressed exon; gene expression analysis; probe;
leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO: 19556; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed single exon probe SEQ ID NO: 19556
                                                                                                                                        Score 16.2; DB 22;
Pred. No. 1.6e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.2; DB 22;
Pred. No. 1.6e+02;
0; Mismatches 3;
                                                                                                           Sequence 97 BP; 22 A; 20 C; 29 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 97 BP; 22 A; 20 C; 29 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone marrow. They can be used to measure samples, which may enable the improved di such as lymphoma, leukaemia and myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank
                                                                                                                                                                                                       7
                                                                                                                                                                                                                       72 CTGCACCATGTGATCCTGGAG 92
                                                                                                                                                                                                       CGCCACCATGTGATCCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGGCACCATGTGATCCCCGAG
                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.1%;
85.7%;
                                                                                                                                          77.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000; 2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the probes of the invention
                                                                                                                                                                                                                                                                                                                DNA; 97
                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001 (first entry)
                                                                                                                           Query Match
Best Local Similarity 85.7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                              AAK44999 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone marrow microarray; cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40200157276-A2
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                              AAK44999;
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                                                                                                                                                                                                                                                                                   RESULT 12
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   888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                          *6666666
                                                                                                                                                                       measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                               probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uman; brain expressed exon; gene expression analysis; probe;
icroarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                             ome-derived single exon nucleic acid probes useful for gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                       The invention relates to a single exon nucleic acid probe for
                                                                                                                       Claim 4; SEQ ID NO 19098; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                            Length 97;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe SEQ ID NO: 19037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO: 19037; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provides a number of single exon
                                                                                                                                                                                                                                                                                                                                         Score 16.2; DB 22;
Pred. No. 1.6e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                            Sequence 97 BP; 22 A; 20 C; 29 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                        1 CGGCACCATGTGATCCCCGAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCACCATGTGATCCTGGAG 92
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                                                                                                                                                                                                                                                                                                                                           77.18;
85.78;
                Chen
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85./*,
And 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0632366
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US00667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention
                                                                             genome-derived
                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy; cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157275-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo, sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-2001
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0-JUN-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                             analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK19046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK19046
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Gaps

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97;

Length Indels

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sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                    enn SG,
                                                                                                                                                                               3-AUG-2
                                                                                                                                                                                                                                                                                                      The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP)
                                                                                                           Probe #19653 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon probe ORF from lung SEQ ID No 19235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                             microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
77.1%; Score 16.2; DB 22;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 97 BP; 22 A; 20 C; 29 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID No 19653; 654pp; English.
                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGGCACCATGTGATCCCCGAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 CTGCACCATGTGATCCTGGAG 92
72 CTGCACCATGTGATCCTGGAG 92
                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                               AAI50967 standard; DNA; 97 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABS19244 standard; DNA; 97 BP
                                                                                                                                                                                                                                                                                                     2000GB-0024263
                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                           2000US-0236359
                                                                                                                                                                                                                                                                                 2000US-0234687
                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                         genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488897/53
                                                                                                                                                                              WO200157272-A2
                                                                                                                                                             Homo sapiens.
                                                                                      17-0CT-2001
                                                                                                                                                                                                                                                            30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                  09-AUG-2001
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                                                                                                                                                                                                                                                                                           27-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABS19244;
                                                                  AAIS0967;
                                                                                                                                                                                                                                                                                                                                            Penn SG,
                                                                                                                              Probe;
                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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                                       AAI50967
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mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising to a algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon in the above mentioned microarray; assigning exons to a single exon comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types using hybridisation. Or encoded by the configuration and probes/pen reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly cusing human lung derived mRNA and for the study of lung diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a spatially-addressable set of single exonnucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           such as asthma, lung cancer, chronic obstructive pulmonary disease (COOP), interstital lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease. Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spatially addressable set of single exon nucleic acid probes, used to
Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     naemosiderosis, pulmonary histiocytosis, lymphangiolejomyomtosis,
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                           primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID No 19235; 634pp; English.
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8, 2003, 02:18:56

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Search completed: July
Job time: 132.941 secs
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                                                                                                                                                                           Gaps
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Pred. No. 1.6e+02;
0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human foetal liver single exon nucleic acid probe #6497.
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                                                   Sequence 97 BP; 22 A; 20 C; 29 G; 26 T; 0 other;
ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 85.7%;
Matches 18; Conservative
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03-AUG-2000; 2000US-0632366
21-SEP-2000; 2000US-0234587
04-OCT-2000; 2000US-0235359
04-OCT-2000; 2000GS-0024263.
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APPLICANT: BOMMARIUS, ANDREAS
APPLICANT: DRAUZ, KARLHEINZ
APPLICANT: DRAUZ, NACIEYL AMINO ACID RACEMASE
FILE REFERENCE: 192535USO
                       US-09-029-603-1
PCT-US96-12545-5
US-09-335-402-1
US-09-568-102-1
US-09-567-969-1
US-09-568-486-1
US-09-568-486-1
US-09-567-899-1
US-09-567-899-1
US-09-643-501A-2
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US-09-517-347-3
US-09-517-347-7
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Pred. No. 40;
0; Mismatches
                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/624,390
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: DE 19935268.2
PRIOR FILING DATE: 1999-07-27
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CURRENT APPLICATION NUMBER: US/09/624,390
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: DE 19935268.2
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 7
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US-09-624-390-3
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APPLICANT: KULA, MARIA-REGINA
APPLICANT: BOMMARIUS, ANDREAS
APPLICANT: DRAUZ, KARLHEINZ
TITLE OF INVENTION: N-ACTEYL AM
FILE REFERENCE: 192535USO
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Best Local Similarity 89.5
Matches 17; Conservative
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SOFTWARE: Patentin Ve
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APPLICANT: VERSECK,
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                                                                                             July 8, 2003, 01:24:03 ; Search time 28.9902 Seconds (without alignments) 222.151 Million cell updates/sec
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Sequence 6, Ap
Sequence 6, Ap
Sequence 12, 7
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Packfiles1.seq:*
      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-08-792-055-1
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US-09-022-765-73
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                             DB 3;
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT'APPLICATION DATA:
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Pred. No. 87;
0; Mismatches
NAME/KEY: misc_feature
LOCATION: 1624..1679
OTHER INFORMATION: //label= pBluescriptII
                                                                               NAME/KEY: misc_feature
LOCATION: 45..54
OTHER INFORMATION: /label- EcoRI-linker
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OTHER INFORMATION: /label= ECORI-linker
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Pred. No. 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/967,364
FILING DATE: NO. 5989859ember 7, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   857 GGCACCATATGATCGCCGTG 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08967364 Patent No. 5989859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PRIELECOMMUNICATION INFORMATION TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                               Query Match. 72.4%;.
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.4%;
llarity 85.0%;
Conservative
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cerrone, Michael REGISTRATION NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECUMANT: 650 TELEPHONE: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches .17; Conserv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-967-364-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-967-364-6
                                                                                                                                                                                                                          US-08-676-882-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
                                                                                                                                                                  DB 4; Length 1107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Akzo No. 6100241el Patent Department
1300 Piccard Drive, Suite 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /function="Elmeria lactate OTHER INFORMATION: dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                              Kok, Jacobus Johannes
van den Boogaart, Paul
Vermeulen, Arnoldus Nicolaas
WENTION: Coccidiosis poultry vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..51
OTHER INFORMATION: /label= pBluescriptII
                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                  Score 15.8;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,882
FILING DATE: 03-JUL-1996
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: GOTHLEY, MAIY E.
REGIESTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
TELEFAX: (301) 977-0847
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                        TYPE: DNA ORGANISM: Amycolatopsis orientalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Eimeria acervulina
DEVELOMENTAL STAGE: Schizont
IMMEDIATE SOURCE:
CLONE: EASC2_1
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08676882
Patent No. 6100241
                                                                                                                                                                                                                                                                        1 CGGCACCATGTGATCCCCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                Query Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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LENGTH: 1679 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMPUTER READABLE FORM:
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LOCATION: 280..1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Vermeulen
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                              FEATURE:

NAME/KEY: CDS

; LOCATION: (1)..(1107)

US-09-624-390-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Kok, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
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    LENGTH: 1107
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Gaps.
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STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Blue Light Photoreceptors and Methods of TITLE OF INVENTION: Using the Same NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                      Length 1975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1977;
                                                                                                                                                                                                                                                                              Indels
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CHRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,255
FILING DATE: 08-JUL-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                        DB 4;
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                                                                                                                                                                                                                                    Score 15.2; DE
Pred. No. 87;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.2; I
Pred. No. 87;
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CURRENT APPLICATION NUMBER: US/09/328,571A
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: US 08/673,230
PRIOR FILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    1250 GGATCCATGTCATCCCCGAG 1231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 17, Application US/08272255
; Patent No. 5824859
                                                                                                                                                                                                                                                                                                                2 GGCACCATGTGATCCCCGAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cashmore, Anthony R. APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGCACCATGTGATCCCCGAG 21
                                                                                                                                                                          ORGANISM: Rio Mamore hantavirus US-09-328-571A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Leary Ph.D., Kathryn
REGIGSTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.4%;
85.0%;
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Best Local Similarity 85.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 1
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Best Local Similarity 85.08
Matches 17; Conservative
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ADDRESSEE: Woodcock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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                                                                                                                                                            TYPE: DNA
                                                                                                                                        LENGTH:
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Sequence 12, Application US/09328571A
Sequence 12, Application US/09328571A
Sequence 12, Application US/09328571A
Septicant: HABLE, Brian
APPLICANT: HABLE, MARTINEZ, NO. 6416761ah
TITLE OF INVENTION: RO MAMORE HANTAVIRUS NUCLECCAPSID PROTEIN AND
TITLE OF INVENTION: DIAGNOSTIC METHODS EMPLOYING SAID PROTEIN
FILE REFERENCE: 210312.0005/401 [Hjelle]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 1932;
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                                                                                                                                                                                                            APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
NOMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
OFWARE: FRSELSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/368,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                   Incyte Pharmaceuticals, Inc
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Pred. No. 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0417 US
                                      709 GGATCCCTGTGATCCCCGAG 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/967,364
                                                                                                          RESULT 5
US-09-368-408-6/c
; Sequence 6, Application US/09368408
; Patent No. 6071703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGCACCATGTGATCCCCGAG 21
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TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Diskette
IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1932 base pairs
                                                                                                                                                                                                                                                                                                                                                                                 3174 Porter Dr
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                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Palo Alto
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             94304
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                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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APPLICANT: ROSS, Bruce C. TITLE OF INVESTIGES AND USES THEREOF NUMBER OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF CORRESPONDENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 1989;
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                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CANTRUM APPLICATION DATA:
APPLICATION UNMBER: US/08/792,055
FILING DATE: 03-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: ReatSEQ for Windows Version 2.0b
SOFTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.4%; Score 15.2; I
85.0%; Pred. No. 87;
tive 0; Mismatches
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23-DEC-1998
                                                                                                                                                                                                                                                                                              NAME: Spratt, Gwendlyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.622
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 293, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1250 GGATCCATGTCATCCCCGAG 1231
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STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/390,361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGCACCATGTGATCCCCGAG 21
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APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
US-08-792-055-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
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09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-DEC-1997.
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1989 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-JAN-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palo Alto
                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-221-017B-293/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                   APPLICANT: Cashmore, Anthony R.
APPLICANT: Almad, Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 1977;
                                                                                                                                                                                                                      ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: The Black Creek Canal Hantavirus and IIILE OF INVENTION: Related Methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUDIRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, N.E., Suite 1200
CITY: Atlanta
STATE: Georg's
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,255
FILING DATE: 08-UUL-1994
ATTORNEY,AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-1795
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/08565
                                Sequence 17, Application PC/TUS9508565 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1321 GGCACCATCTGATCCTCGCG 1302
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGCACCATGTGATCCCCGAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08792055
Patent No. 5853980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nichol, Stuart T
APPLICANT: Morzunov, Sergey
APPLICANT: Ravkov, Eugeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid_
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                 19103
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Gaps

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IDENTIFICATION METHOD: experimental OTHER INFORMATION: /function= "(translation start:
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                                                                                                                                                                                                                                                                                             /function= "ACHE Promotor"
/standard_name= "ACHE Promotor"
                                                                                                                                                                                                                                                                                                                                                                                                 /function= "non-translated'/
/gene= "ACHE"
/number= 1
                               TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gen
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /Gene= "ACHE" OTHER INFORMATION: /number= 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 4
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    /evidence= EXPERIMENTAL
    /gene= "ACHE"
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OTHER INFORMATION: /gene= "ACI
OTHER INFORMATION: /number= 5
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                                                                                                                                                                       ORGANISM: Homo sapiens
POSITION IN GENOME:
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27005..27274
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28129..28131
                                                                                                                                                                                                                                                   NAME/KEY: promoter
LOCATION: 4089..22464
OTHER INFORMATION: /fi
OTHER INFORMATION: /si
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          double
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OTHER INFORMATION: /e.
OTHER INFORMATION: /g.
OTHER INFORMATION: /n.
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OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
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NAME/KEY:
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FEATURE:
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OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SORGY, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
CORRESPONDEMS: 7
CORRESPONDEMS: 7
CORRESPONDEMS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
                ATORNEY/AGENT INFORMATION.

ATORNEY/AGENT INFORMATION.

NAME: MONTOY, Gladys H
RECISTRATION NUMBER: 37,430

REFERENCE/DOCKET NUMBER: 27340-20021.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-494-0792

TELERA: 650-494-0792

INFORMATION FOR SEG ID NO: 293:

SEGUENCE CHARACTERISTICS:

LENGTH: 4214 base pairs

STRANDEDNES: double

TYPE: nucleic acid

STRANDEDNES: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

""DOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 72.4%; Score 15.2; Best Local Similarity 85.0%; Pred. No. 9; Matches 17; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3755 CGGCTCCATGTGATCGACGA 3736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGGCACCATGTGATCCCCGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08814095
Patent No. 6025183
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 35060 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , LOCATION:
US-09-221-017B-293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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US-08-814-095-7
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Sequence 17, Application US/09128155
Factor No. 611/654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT FILING DATE: 1998-08-03
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1999-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTMARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.4%; Score 15.2; DB 3; Length 152331; 85.0%; Pred. No. 1.1e+02; tive 0; Mismatches 3; Indels 0;
                                                            Length 35060;
                                                                72.4%; Score 15.2; DB 3; 85.0%; Pred. No. 1.1e+02;
                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65542 GGCACCAGGTGATCCCAGTG 65523
                                                                                                                                                                          22585 GGCACCGTGCGCTCCCCGAG 22604
), OTHER INFORMATION: /number= 16 US-08-814-095-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
                                                                                                                                                2 GGCACCATGTGATCCCCGAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGCACCATGTGATCCCCGAG 21
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LOCATION: (1)...(176373)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.09
Matches 17; Conservative
                                                                Query Match
Best Local Similarity 85.03
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 176373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 16
LENGTH: 152331
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US-09-128-155-17
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: complement (32959..33094).
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: complement (2964..29856)
OTHER INFORMATION: /gene= "ARS"
            LUCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: complement (32386.:32468)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: complement (30816..31011)
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                                                                                                                                                                                                                                 LOCATION: complement (33493..33591)
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/number= 14
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OTHER INFORMATION:
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LOCATION: comp]
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OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                          APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAS SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: DAS SEQUENCES;
FILE REFERENCE: 24366-20007:00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH
                                                                                         Gaps
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CUBRENT APPLICATION NUMBER: US/09/103,840R
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4403765;
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                                          Length 176373;
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                                          Score 15.2; DB 3;
Pred. No. 1.1e+02;
0; Mismatches 3;
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Pred. No. 61;
0; Mismatches
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                                                                                                                                              69408 GGCACCAGTGATCCCAGTG 69427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37RV
US-09-103-840A-1
                                                                                                                                                                                                                                                          Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION: APPLICANT: FLEISCHMAN, ROBERT D. APPLICANT: WHITE, OWEN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                        2 GCCACCATGTGATCCCCGAG 21
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                                          72.4%;
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85.0%;
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Best Local Similarity 85.0%;
Matches 17; Conservative
                                                               Best Local Similarity 85.0
Matches 17; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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Best Local Similarity 85.0
Matches 17; Conservative
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US-09-128-155-17
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US-09-103-840A-2/C
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                                            Query Match
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QQ
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OM nucleic - nucleic search, using sw model

July 8, 2003, 19:09:54 Run on:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_NA

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Sequence 27728, A	Sequence 25291, A	Sequence 11096, A	Sequence 22699, A	Sequence 13, Appl	Sequence 4, Appli	Seguence 1, Appli	Seguence 5, Appli	Sequence 5, Appli	Sequence 6591, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 284, App	Sequence 380, App	Sequence 63, Appl	Sequence 31268, A	Sequence 903, App	Sequence 10019, A
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	Length	97	458	460	464	1150	2893	2893	2975	2975	009	1107	1107	9025608	970	356	445	494	569	831
ا مار	Match	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	75.2	75.2	75.2	75.2	73.3	72.4	72.4	72.4	72.4	72.4
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PCT/US01/00661

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## ALIGNMENTS

ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFULLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY TRRENT APPLICATION NUMBER: US/09/864,761 CATION NUMBER: PCT/US01/00667 IG DATE: 2001-01-30 LICATION NUMBER: PCT/US01/00666 PLICATION NUMBER: PCT/US01/00664 PCT/US01/00669 PLICATION NUMBER: PCT/US01/00665 LICATION NUMBER: PCT/US01/00668 PCT/US01/00662 PCT/US01/00663 NUMBER: US 60/180,312 NUMBER: US 60/207,456 Application US/09864761 PLICATION NUMBER: GB 24263.6 000-09-27 1-01-30 US20020048763A1 RIOR APPLIC RIOR FILING LE REFEREN JRRENT PRIOR PRIOR PRIOR RIOR RIOR

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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY SETER REPERENCE: Acomico-x-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
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SOFTWARE. Annomax Sequence Listing Engine vers.
SEQ ID NO 11096
LENGTH: 460
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85.7%; Pred. No. 69;
iive '0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 24263.6
FTLING DATE: 2000-10-04
PPLICATION NUMBER: US 60/236,359
FTLING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLING DATE: 2001-01-30
PPLICATION NUMBER: PCT/US01/00667
ILING DATE: 2001-01-30
PPLICATION NUMBER: PCT/US01/00664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICATION NUMBER: PCT/US01/00661
LLING DATE: 2001-01-30
                                                                                                                                                                                                                                                      RIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-918-995-22699
; Sequence 22699, Application US/09918995
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Best Local Similarity 85.7%
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.92
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.87
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.83
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.83
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Publication No. US20030073623A1
GENERAL INFORMATION
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1200-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLING DATE: 2000-09-21

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SECTION NO 27728

LENTH: 97
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Pred. No. 66;
0; Mismatches
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Pred. No. 69
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SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. US20020048763A1
GENERAL INFORMATION:
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COTHER INFORMATION: n = A,T,C or G
US-09-918-995-25291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.1%;
ilarity 85.7%;
Conservative
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Best Local Similarity 85.7%;
Matches 18; Conservative
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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Best Local Similarity
Matches 18; Conserva
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APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
FILE REPERENCE: PCS10026APME
CURRENT APPLICATION NUMBER: US/09/905,846
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 00/17387.2
PRIOR PILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
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Treatment of Male Sexual Dysfunction
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                                      RRENT APPLICATION NUMBER: US/10/017,273A
TRRENT FILING DATE: 2001-12-12
                                                                                                                                                             PRIOR APPLICATION NUMBER: GB 0108730.3
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: GB 0120679.6
PRIOR APPLICATION NUMBER: 08 09/905,846
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-06-29
RIOR FILING DATE: 2001-06-29
RIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VERSION 3.1
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                                                                              PRIOR APPLICATION NUMBER: US 60/265,358
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: GB 0030647.2
PRIOR FILING DATE: 2000-12-15
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85.78;
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APPLICANT: Ian Dennis Harrow
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Best Local Similarity 85.73
Matches 18; Conservative
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ORGANISM: Homo sapiens
US-09-905-846-1
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TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED ION
TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS
FILE REFERENCE: 2002-09-23
CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: PCT/USO1/09956
PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1150
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                                        APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 77.1%; Score 16.2; L
Best Local Similarity 85.7%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches
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Pred. No. 70;
                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 38054
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 22699
LENGTH: 464
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22699
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; ORGANISM: Dermacentor variabilis
US-10-239-420-13
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Best Local Similarity 85.7%;
Matches 18; Conservative
      Publication No. US20030073623A1
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                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Length 1107;
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APPLICANT: DRAUZ, KARLHBINZ
APPLICANT: VERSECK, STEFAN
TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF AMINO ACIDS
FILE REFERENCE: 214381US-10757-9350-0-X
CURRENT APPLICATION NUMBER: US/09/973,765
CURRENT FILING DATE: 2001-10-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.8; DB 9;
Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                                           APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TILLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262 CURRENT APPLICATION NUMBER: US/10/156,761
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                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
Sequence 6591, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Amycolatopsis orientalis
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                           ISHIKAWA, JUN
HORIKAWA, HIROSH
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6591
                                                                                                                                                                         SHIBA, TADAYOSH
                                                                                                     IKEDA, HARUO
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US-10-156-761-6591
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JS-09-973-765-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh.
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
FILE REFERENCE: PCS1026APME
CURRENT APPLICATION NUMBER: US/09/905,846
CURRENT APPLICATION NUMBER: US/09/905,846
PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-07-26
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Best Local Similarity 85.7%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 3; Indels 0
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                                                PLICANT: Wayman, Christopher P.
TLE OF INVENTION: Treatment of Male Sexual Dysfunction
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Pred. No. 72;
                                                                                                                      CURRENT APPLICATION NUMBER: US/10/017,273A CURRENT FILING DATE: 2001-12-12
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                    CIOR APPLICATION NUMBER: US 60/265,358.
CIOR FILING DATE: 2001-01-31
                                                                                                                                                                                                                                                                                        IOR FILING DATE: 2001-04-06
IOR APPLICATION NUMBER: GB 0120679.6
IOR FILING DATE: 2001-08-24
IOR APPLICATION NUMBER: US 09/905,846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               IOR APPLICATION NUMBER: US 09/895,367
                                                                                                                                                                                                                       APPLICATION NUMBER: GB 0030647.2 FILING DATE: 2000-12-15
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Patent No. US20020102707a1
GENERAL INFORMATION:
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85.78;
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Best Local Similarity 85.75
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-905-846-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-017-273A-5
                                                                                                  LE REFERENCE: PC22013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 5
LENGTH: 2975
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DNA

SEQ ID NO 5

NUMBER OF

Gaps

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Gaps

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TYPE: DNA

RESULT 10

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7913762 GCACCATCTGAGCCCCGAG 7913780

15-09-973-712-1

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Score 15.4; DB 10; Length 970;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 284
LENGTH: 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 380, Application US/09933797

Sequence 380, Application US/09933797

GENERAL INFORMATION:
APPLICANT: Robert A. Sikes et al.
TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
TITLE OF INVENTION: Sinus Expressed Sequences
FILE REFERENCE: 9901-007-999

CURRENT FILING DATE: 2001-08-22

PRIOR FILING DATE: 2001-08-22

PRIOR FILING DATE: 2000-01-14

PRIOR PAPLICATION NUMBER: DCT/US99/10746

PRIOR FILING DATE: 1999-05/14

PRIOR PELING DATE: 1999-05/14

PRIOR PELING DATE: 1998-05-14

NUMBER OF SEQ ID NOS: 811

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 380
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Pred. No. 2.2e+02;
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Job time : 132.338 secs
                                                                                                   US-09-764-864-284/c
; Sequence 284, Application US/09764864
; Patent No. US20020132753A1
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Best Local Similarity 85.0%;
Matches 17; Conservative
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ilarity 94.1%;
Conservative
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CORGANISM: Homo sapiens
US-09-764-864-284
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Matches 16; Conserva
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US-09-933-797-380
                                                                                                                                                                                                          GENERAL INFORMATION
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                                                                                                                                        APPLICANT: DRAUZ, KARLHEINZ
APPLICANT: VERSECK, STEFAN
APPLICANT: VERSECK, STEFAN
APPLICANT: WILA, MARTA-REGINA
TITLE OF INVENTION: CARBAMOYL AMINO ACID RACEMASE FROM AMYCOLATOPSIS ORIENTALIS FOR RACE
TITLE OF INVENTION: CARBAMOYL AMINO ACIDS
CURRENT APPLICATION NUMBER: US/09/973,712
CURRENT FILLE OF STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEPANTON STEP
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: LOCATION: (4187715)

: OTHER INPERMATION: a, t, c, g, other or unknown

US-10-156-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.8; DB
Pred. No. 1.1e+(
0; Mismatches
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Best Local Similarity 89.5%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: IKEDA, HARUO
APPLICANT: ISHIRAMA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHRBA, TADAYOSHI
APPLICANT: HATTORI, WASHIRA
TILE OF INVERTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Amycolatopsis orientalis
Sequence 1, Application US/09973712 Patent No. US20020106752A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 cggaccarcrgarccccg 220
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Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGGCACCATGTGATCCCCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                              APPLICANT: BOMMARIUS, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION:
US-09-973-712-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Gaps

Gaps

Indels

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July 8, 2003, 00:47:28 ; Search time 1064.65 Seconds (without alignments) 319.453 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                         16154066 seqs, 8097743376 residues
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                                                                 OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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21
1 cygcaccatgtgatcccgag 21
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BO990877 GGE21F15 BO980809 GGE2B15. BU010846 GG214473 BQ983268 GGE18K14. BQ868940 GGE3932.5 A1257845 LP06332.5
SUMMARIES		BQ990877 BQ980809 BU010846 BQ983268 BQ868940
	B ID	14 B 14 B 14 B 14 B 14 B 14 B 14 B 14 B
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## ALIGNMENTS

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/clone_lib="QG_EFGHJ lettuce serriola"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jactuca sativa.
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
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QGE12B10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 413)

(kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, R.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                       /note="Vector: pBRcDNaSfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Embryophyta; Tracheophyta; edons; core eudicots;
belongs to contig QG_CA_Contig3186, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               belongs to contlg QG_CA_Contig3186, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trache
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots
Asteridae, euasterids II, Asterales, Asteraceae, Lactuceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
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                                                                                                                                                                                               'clone_lib="QG_EFGHJ lettuce serriola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.3e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  lettuce serriola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.8%; Score 17.8; DB 14; 90.5%; Pred. No. 3.3e+02; ive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_LIB=OG_EFGHJ lettuce ser
TAG_TISSUE=leaves dark grow
                                           F21 row: F column: 15. Location/Qualifiers
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                                                                                                                                   'cultivar="L.serriola
'db_xref="taxon:4236"
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                                                                                                                                                                                                                      /lab_host-"E.coli"
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                                                                                                                                                                           clone="QGF21F15"
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Best Local Similarity
Matches 19; Conserva
                                           Plate: QGF21
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                                                                FEATURES
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GGJ14723.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone BU010846
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Lettuce and Sunflower ESTs from the Compositae Genome Project
fnote="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAS were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAS were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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singleton_ see http://cgpdb.ucdavis.edu/ for details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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/lab_host="E.coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.8; DB 14
Pred. No. 3.9e+02;
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Location/Qualifiers
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/db_xref="taxon:4236"
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52 c 222 q
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Best Local Similarity 90.5%;
Matches 19; Conservative
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Query Match

Matches

BASE COUNT

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

BQ983268/c

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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., Van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                          BQ868940 648 bp mRNA linear EST 14-AUG-200
QGD3903 yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
                       Gaps
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Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        singleton, see http://cgpdb.ucdavis.edu/ for details
Plate: QGD3 row: g column: 03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
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4.5e+02;
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/clone="QGD3g03"
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                                                                  1 CGGCACCATGTGATCCCCGAG
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BQ868940
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Fax: 1-(530)-752-9659
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ilarity 90.5%;
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ983268 555 bp mRNA 11near EST 21-AUG-2002 QGE18K14.9g.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., Van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB-QG_BFGHJ lettuce serriola
TAG_TISSUE-flowers pre-fertilized
TAG_SEQ-GCTTGACGGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    size bias. Details of each source of RNA and library '
construction can be obtained at http://cgpdb.ucdavis.edu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig OG_CA_Contig3575, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Vector: pBRcDNASfiaB; The library was co
from 10 different sources of RNA from a single
                                                                                                                                                                                         Length 557;
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                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="QG_EFGHJ lettuce serriola"
lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_LIB=QG_EFGHJ lettuce serriola
TAG_TISSUE=leaves dark grow
                                                                                                                                                                                    Score 17.8; DB 14;
Pred. No. 4.3e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Lactuca sativa"
                                                                                                              141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E18 row: K column: 14 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compgenomics.ucdavis.edu/
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                                                                                                                                                                                                                                                                                      1 CGGCACCATGTGATCCCCGAG 21
                                                                                                                                                                                                                                                                                                             CGGCACCATGTGATCCTCCAG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone-"QGE18K14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JGE18K14, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ983268.1 GI:22400793
                                                                                                                                                                                 / Match 84.8%;
Local Similarity 90.5%;
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.8%;
90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sativa
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Best Local Similarity
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JOURNAL

COMMENT

TITLE

FEATURES

REFERENCE AUTHORS ö

BASE COUNT ORIGIN

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Query.Match
Best Local Similarity
Matches 17; Conserv
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nad03=01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3432289 3' similar to contains Alu repetitive element; contains element MER22 BG055194.1 GI:12512671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'clone_lib="LP Drosophila melanogaster larval-early pupal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
LP06332.5prime LP Drosophila melanogaster larval-early pupal pOT2 Tosophila melanogaster CDNA clone LP06332 5prime similar to X54997: D.melanogaster Pl gene, mRNA sequence. AI257845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 325)
                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 536)
1 (bases 1 to 536)
1 (bases 1 to 536)
1 (bases 1 to 536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: whole body; Vector: pOT2; Site_1: ECORI; Site_2: Xhol; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 63 row: C column: 8
High quality sequence stop: 476.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="LP06332"
                                                                                                                                                                                                                                                                                                                                      Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.4; DB 9;
Pred. No. 6.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="larvae-pupae"
/lab_host="DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                           Lewis, S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="male and female"
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                                                                         AI257845.1 GI:3865370
                                                                                                                                                                                                                                                                                                   Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.9%;
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                          One Cyclotron Rd,
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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BG055194/C
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                                                                                                                                                                                                                       AUTHORS
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156 bp mRNA linear EST 25-AUG-1999
AVODG955 Mus musculus C57BL/6J heart Mus musculus cDNA clone
1020003M09, mRNA sequence.
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length CDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL, send email to:
Info@inage.llnl.gov
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 156)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pT7T3D-Pac (Pharmacia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharm with a modified polylinker; Plasmid DNA from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB 12; I
Pred. No. 8.7e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:3432289"
/clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.0%; Score 17;
100.0%; Pred. No.
:ive 0; Mismatcl
                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN Mouse ESTS
Unpublished (1999)
Contact: Chie Owa
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Gaps

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Indels

BASE COUNT ORIGIN

AV132551/c DEFINITION

RESULT 9

ò g ACCESSION

VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

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/dev_stage="11-day embryo"
//dev_stage="11-day embryo"
//d
                                                                                                                                                                                                                                                                                                                                             T 3/]; double-stranded cDNA was ligated to Eco RI addedors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pryT3 vector. RNA provided by Dr. Minoru KO, Wayne State Univ. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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1 (bases 1 to 189)
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/clone_lib="Mus musculus C57BL/6J 11-day embryo"
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Pred. No. 8.8e+02;
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Fax: 81-298-36-9098
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Contact: Chie Owa
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                                                                                                                                                                                                                                                                                          /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akipama, J., Fukudad, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Sticchi, N., Kojima, Y., Matsuyama, T., Nittsuma, H., Oda, H., Owa, C., Sato, K., Shipata, Y., Shigamoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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thermostabilization and thermoactivation of thermolabile enzymes
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Pel: 81-298-36-9145
Pax: 81-298-36-9098
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Unpublished (1999)
Contact: Chie Owa
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                                                                                                                                                             T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p17T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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URL.http://genome.gsc.riken.go.jp,
Carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,V., Okazaki,Y., Muramata,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile ensymes by trehalose and its application for the synthesis of full length trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunal,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                            pT7T3D-Pac (Pharmacia
                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(625), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
/dev_stage="13-day embryo" //orde="0rgan: mammary gland; Vector: pT773D-Pac (Pharmaci //orde="0rgan: mammary gland; Vector: pT773D-Pac (Pharmaci ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I: - Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation asystem. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 189;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.8; DB 9;
Pred. No. 9.1e+02;
); Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 GGCACCATGTGATTCCAGAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGCACCATGTGATCCCCGAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB067107.1 GI:8524521
                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 200)
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ax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                          Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Best Local Simi
Matches 18;
                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
BB067107/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 185.0 Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylle, T., Martin, J., Blistain, A., Schmitt, A., Theislain, R., Kitter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

"Brdocrine Pancreas Consortium
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Musmania, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10417729 204 bp mRNA linear EST 23-MAY-200 ik45b05.xl Kaestner ngn3 wt Mus musculus cDNA 3' similar to SW:IDHP_PIG P33198 ISOCITRATE DEHYDROGENASE [NADP], MITOCHONDRIAL PRECURSOR;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched, 15 days embryo
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primed with a primer [5'
GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'],
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.8; DB 10;
Pred. No. 9.3e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="15 days embryo"
/lab_host="DH10B"
                                                                                                                                                   'organism-"Mus musculus"
                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="8030457L12"
                                                                                                                                                                                                                                                                                                                                                                tissue_type="testis"
                                                                                    Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 GCACCATGTGATTCCAGAG 154
                                                                                                                                                                                strain="C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGCACCATGTGATCCCCGAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ417729.1 GI:21122930
                                                                                                                                                                                                                                                                                                       male testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                   sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 204)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90...
Local 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rel: 617-495-1812
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/note-Torgan: pancreas; Vector: pSPORTI (GIBCO); Site_1:
Not I; Site_2: Sal I; The library was prepared by
Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The CDNA's were prepared with an oligo containing a
NotI site, and SalI linkers were added to the ends. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 30-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prevention grants for use in CDNA microarray experiments. Sequence Quality: Sequence ends were trimmed based on percentage of ambigu as base calls or 'N's in windowed segments. Sequencing: All Prism 377 sequencer and analysis software. Sequencing: M3/puC Reverse.
Email: dmeltonebiohp.harvard.edu
bancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For Information on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus 1 (bases 1 to 27)
Gallardo, T.D., Schageman, J.J., Pertsemlidis, A., Garner, H.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inserts were cut with NotI before being cloned into the NotI-SalI sites in the vectors. This is one of two libraries, ngn3 wt and ngn3 -/-. The wt library is in psPoRTI, T7 promoter is 5."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UT Southwestern Medical Center, Adult Mouse Cardiac cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UTSW_H15E9 UTSW Adult Mouse Cardiac Muscle Library Mus musculus CDNa clone UTSW_H15E9, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UTSW_H15E9"
/clone_lib="UTSW Adult Mouse Cardiac Muscle Library"
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cDNA library constructed by UTSW as a component of the Pro
Genomic Applications (PGA) and the Reynolds Heart Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shohet/Garner Labs
University of Texas Southwestern Medical Center
6000 Harry Hines Blvd., NA2.226, Dallas, TX 75390, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 204;
                                                                                                           obtaining a clone please contact: Dr. Marie Scearce (mscearce@mail.med.upenn.edu)
Seg primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                      /strain="129/5v" x cb1"
/db_xref="taxon:10090"
/db_stage="p.c. 14.5"
/lab_host="E. coli-DH125 (GIBCO)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.8; DB 14;.
Pred. No. 9.3e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                organism="Mus musculus"
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                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Schageman JJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
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Best Local Similarity
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BG791763/c
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
                                                                                                                                                                                          FEATURES
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ORIGIN

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Insertion site: TAGGTCACTGATTCTGAGGG--> Other information regarding entire library may be found at thtp://pg.swmed.edu/Data/Libraries/microarray_cdna_libraries htm "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1990) L. Lich, M., Kitsunai, T., Akiyamai, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 30-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB185381 RIKEN full-length enriched, adult male spinal cord Musmusculus cDNA clone A330023112 3' similar to U51167 Mus musculus isocitrate dehydrogenase mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463.470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                       /note-"Vector: pAMP10 (Gibco); Cloned unidirectionally
                                                                                             (CloneAmp,
                                                                                                                                                                                                                                                                                                             Gaps
                                                                         Primer: Oligo df. RNA Isolation: cytoplasmic RNA (Manniatis); Cloning Technique: CUA Cloning (Clonf Life Technologies); Average insert size: 1.8 Kb;
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                       Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                              3 others
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                   Score 16.8; DB 12;
Pred. No. 9.4e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRNA
/tissue_type="Cardiac muscle"
/dev_stage="2 months"
/lab_host="DH5a"
                                                                                                                                                                                                                48 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 bp
                                                                                                                                                                                                              37 g .
                                                                                                                                                                                                                                                                                                                                                 2 GGCACCATGTGATCCCCGAG 21
                                                                                                                                                                                                                                                                                                                                                                     93 GGCACCATGTGATTCCAGAG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB185381.1 GI:8845952
                                                                                                                                                                                                                                                                     80.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                    /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues: 1st strand cDNA was GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                           clone="A330023112"
clone_lib="RIKEN full-length enriched, adult male spinal
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Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                Please visit our web site (http://genome.rtc.riken.go.jp) further details.
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dev_stage="adult"
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
A., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                       ,Y. and Hayashizaki,Y. Automate,I., Ozawa,Y., Muramatsu,M., Okaz, Automated filtration-based high-throughput plasmid preparation system. Ganome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_lib="RIKEN full-length enriched, 6 days neonate
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/lab_host="DH10B"
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                                                                                    Fax: 81-45-503-9216
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nep ii membrane metalloprotease and its use for screening inhibitors useful in therapy patent: WO 9953077-A 1 21-072-1999; INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); GOIMET TANAA (FR); ROSE CHRISTIANE (FR); BONHOWME MARIE CHAWTAL (FR); FACCHINETII PATRICIA (FR)
Patent: WO 9953077-A 11 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
LOCATION/Qualifiers
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Schwartz,J.C., Gros,C., Oulmet,T., Rose,C., Bonhomme,M.C.
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/db_xref="taxon:32630"
/note="oligonucleotide"
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1larity 100.0%; Pred. No. 1.6;
Conservative 0; Mismatches 0
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Pred. No. 2.9;
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/db_xref="taxon:10117"
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ilarity 100.0%;
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1 GCAAAGCACTAGCTTCAGTGTG 22

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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bowie, S. Bilange, K., Blankenburg, K., Bonnin, D., Bouk, J., Bunage, K., Blankenburg, K., Bonnin, D., Buhay, C., Burch, P., Burkett, C., Burchl, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Dathorne, S.R., Darbin, H.H., Douthwaite, K.J., Davis, C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaggo, N., Ford, J., Forster, P., Farantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, J., Hernandez, J., Henandez, J., Henandez, J., Henandez, J., Henandez, J., Henandez, J., Henandez, J., Hune, J., Johnson, R., Leal, B., Lewis, L.C., Li, J., L
     HTG 20-DEC-2001
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On Dec 20, 2001 this sequence version replaced 91:15624568.
ACO94732 174953 bp DNA linear HTG 20-DEC-200
Rattus norvegicus clone CH230-516, *** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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e, T., Sparks, A., Stanley, H.,
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Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B.,
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                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                Consensus quality: 152255 bases at least 040 consensus quality: 158448 bases at least 030 consensus quality: 164461 bases at least 020 Estimated insert size: 155965; sum-of-contigs estimation Quality coverage: 0.x in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
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                         Assembly program: Phrap; version 0.990329First call
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COMMENT

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ACO98965 191911 bp DNA linear PRI 04-FEB-2002
Homo saplens chromosome 16 clone RP11-419L9, complete sequence.
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                                                                                        of 4672
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Best Local Similarity
Matches 19; Conserv
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ORIGIN
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                                                                                                                                                                                                                         Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179141)
Waterston, R. H.
 Homo sapiens chromosome 16 clone RP11-378B23, WORKING DRAFT SEQUENCE, 35 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                     MO 63108, USA
On Jul 16, 2000 this sequence version replaced 91:7023910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 35 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 191000; agarose-fp
Insert size: 175741; sum-of-contigs
Quality coverage: 3.34 in Q20 bases; agarose-fp
Quality coverage: 3.41 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 1710 bp in length
                                                                                                                                                                                                                                                                                                                                           Web site:http://genome.wustl.edu/gsc/index.shtml
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                                       AC019091.3 GI:9230842
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
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                                                                                                                                                                                                Waterston, R.H.
                                                                                     Homo sapiens
                                                                                                                                                                     Unpublished
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ORGANISM
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TITLE
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REFERENCE.
                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                           REFERENCE
                                                                                                                                                                                                                            JOURNAL
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PRI 15-DEC-2000

linear

85668 CAAAGAACTAGATTCAGTGTG 85648

Cambridgeshire;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo

COMMENT

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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with only a small overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Dec 17, 2000 this sequence version replaced g1:11610952. During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sections only once, except for a 100 base overlap.
The true left end of clone RP1-209B5 is at 1 in this sequence. T true left end of clone RP3-479G13 is at 110626 in this sequence. The true right end of clone RP11-692C10 is at 90615 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPI-209B5 is from the library RPCI-1 constructed by the group Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .. .464
"note="L1M4 repeat: matches 3276. .3796 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-DEC-2000) Sanger Centre, Hinxton, Cambridgeshi
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone RPI-209B5 It may be shorter because we sequence overlapping
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1404. .1558
                                                                                                              Human DNA sequence from clone RP1-209B5 on chromosome
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/note="AluJo repeat: matches 85.
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                                                                                       110724 bp
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/organism="Homo sapie
/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates,
1 (bases 1 to 110724)
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note="AluJo repeat:
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'note="L1M4 repeat:
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/clone_lib="RPCI-1"
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                                                                                                                                                                    Submitted (07-NOV-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 19191) DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                             DOE Joint
94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Base-by-base quality values are not generally spart GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        generally visible from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                   Direct Submission
Submitted (04-FEB-2002) Production Sequencing Facility, DO
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94
On Feb 4, 2002 this sequence version replaced gi:16756238
Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS AL683889 Accession AL683889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 191911;
                                                                                                                                                                                                                                                                                                                                                                                          This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Base-by-base quality values are not generally visil GenBank flat file format but are available as part of this entry's ASN.1 file.
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Pred. No. 1.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52176. t
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Pred. No. 69;
                                              Sequencing of Human Chromosome 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
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                                                                                               2 (bases 1 to 191911)
DOE Joint Genome Institute.
                         OOE Joint Genome Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL683889_5 500001
Continuation (3 of 6) of AL683889
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llarity 90.5%;
Conservative
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| Similarity 95.0%;
19; Conservative
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                                                                                                                                                Direct Submission
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Best Local Similarity
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nes 19; Conserv
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AL683889_0
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AL683889_2
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AL683889_2/c
WPCOMMENT
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                                                                        JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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repeat: matches 3000. .3169 of consensus"

/note="L1M4 1644. .2340

repeat_region repeat_region

.310 of consensus"

repeat region	/note="L1ME3A repeat: matches 47215420 of consensus" 2341 2605	
1	/note="LiPB1 repeat: matches 58826155 of consensus"	
1604 -	e- "L	
ear_reg10	.3053044 //note="AluSg/x repeat: matches 126305 of consensus"	
-a-L-1991	0043 note="A	
L_reg1	note-"Al	٠,
pear_regi	e="Alu	٠,
r_regi	te".5	
	/034/540 /note-"AluSx repeat: matches 1293 of consensus" 8010 0038	
1691	note"	
reg	/. te="L	
1601-160	te-".	
regi	// 1000 - 10000 // 1000 - 10000 // 16707 16841	٠.
reat	te-"L1	
4	te="Al	
pear_teg1	13318 Ote="L1P	
peat_reglo	400I ote-"Al	
peat_regio	/11 2 ote="L1	
peat_reg	7412 ote-"MI	,
repeat_region	matches 1898, .2456 of co	
repeat_region	47122782	
repeat_region	pear: marches 1312 Of consensus"	
repeat_region	2634 of consensus"	
repeat_region	t: matches 4495615	
atre	/note="28 copies 2 mer ca 96% conserved" 25603. 25912	
eat regi	te="Alux	٠.
peat region	ote-"L1N	
peat redi	ote-"MAD 77627	
peat redi	ote="L1M	
peat regio	te="MER 9328	
neat read	te-"ML	
**************************************	ote="13	
10-1-09.	ote="Al	
1001	ote="MER21	
1604	ote="Al	
5 6	ote="Al	
cpear_reg	te="M	
repeat_region	3155431865 /note="AluSx repeat: matches 1311 of consensus"	

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AC027421 152464 bp DNA linear HTG 26-MAY-2000
Homo sapiens chromosome 1 clone RP11-1C6 map 1, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ote-"HSMAR2 repeat: matches 1078. .1276 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ote="HSMAR2 repeat: matches 1276. .1299 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 5467. .5515 of consensus"
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                                                                                                                                                                                                                                                                              repeat: matches 2605. .2953 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                          repeat: matches 5927. .6167 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 5238. .5336 of consensus"
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                                                                                                                                                                                                                                                                                                                       repeat: matches 116. .290 of consensus"
                                                                                                                                                                                                                                                                                                                                                               repeat: matches 835. .928 of consensus"
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                                                                                                                                                                                                                                   A repeat: matches 3. .184 of consensus"
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38288
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                                                                                                                                                note-"MLT1A1 repeat: matches 4. .361 of consensus"
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41465
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                  repeat: matches 1. .266 of consensus"
                                                      repeat: matches 1. .354 of consensus"
                                                                                                                                                                                        repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 5. .222 of consensus"
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                                                                                                     note="39 copies 2 mer aa 78% conserved"
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Best Local Similarity 90.5%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 2;
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35358. .3554
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AC027421/c
LOCUS
DEFINITION
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ap of 100 bp contig of 10201 bp in length
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5335 bp in length
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contig of 8399 bp in length
ap of 100 bp
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11933 120415: contig of 8483 bp in length
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2644 bp in length
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3148 bp in length
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3456 bp in length
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contig of 5436 bp in length
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5995 bp in length
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contig of 4698 bp in length
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contig of 6035 bp in length
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of 1770 bp in length
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f 2740 bp in length
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2513 bp in length
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4362 bp in length
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2129 bp in length
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contig of 2449 bp in length
                                                                                                                                                                                                                                                                                                                             26: gap of 100 bp
22448: contig of 2622 bp in length
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contig of 2867 bp in length
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contig of 2277 bp in length
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of 1349 bp in length
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2290 bp in length
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75: contig of 3
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                                                                                                                                                                      9818: gap of .
12558: contig
                                 contig
                                                                       contig
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31012 141212: cont
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                                                 4434: gap of
5783: co
                                                                                       5784 5883; gap of 5884 7653; co
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       2371 2470: gap
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                                                                                                                                                                                                                                                                                                                                                                                     Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Howland, J. LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Looke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M., McEwan, F., McGull, D., McMana, C., Mlenga, V., Morrow, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced g1:7656797.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.
                                                                                                                                                                                                                                                                      Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burket, G.
Boguslavkiy, L., Castle, A., Cheepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ", Riley, R., Rogov, P., Rothman, D.
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s is a 'working draft' sequence. It currently of 37 contigs. The true order of the pieces own and their order in this sequence record is Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 147000; agarose-fp
Insert size: 148864; sum-of-contigs
Quality coverage: 3.3 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Severy, P., Spencer, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 125290 bases at least Q40 Consensus quality: 139114 bases at least Q30 Consensus quality: 145106 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1011: gap of 1011 bp in length 1012 1111: gap of 100 bp 1112 2156: contig of 1045 bp in length 2157 2256: gap of 100 bp
                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 1, clone RP11-1C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815; 100% of Chemistry: Dye-terminator Big Dye: 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. consists of 37 contigs. The true order of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Project Information ject name: L7564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .M., Oliver, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Schauer, S.,
   37 unordered pleces.
                                                           HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is not known and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center clone name:
                                                                                                                                     Mammaîla; Eutherla; Pri
1 (bases 1 to 152464)
                                           GI:8077017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Santos, R
                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary
                                                                                                                                                                                                                Unpublished
                   ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                 ORGANISM
                                                                                                                                                      REFERENCE
AUTHORS
TITLE
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JOURNAL
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REFERENCE
AUTHORS
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COMMENT

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Akher, N., Ayele, K., Beckstrom-Sternberg, S. M., Benjamin, B., Blakesley, N., Ayele, K., Beckstrom-Sternberg, S. M., Benjamin, B., Blakesley, N., Bouffard, G. G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hadhighl, P., Ley, S. L., Idol, J. R., Karlins, E., Laric, P., Lee-Lin, S. -O., Legaspi, R., Maduro, V.B., Masiello, C., Maskerl, B., Mastidan, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vodt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 152502; sum-of-contigs
Quality coverage: 12.78x in Q20 bases; agarose-fp
Quality coverage: 10.48x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 152602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65456: contig of 65456 bp in length 65556; gap of unknown length 152602: contig of 87046 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensy Figure 152288 bases at least 040 consensus quality: 152351 bases at least 030 consensus quality: 152412 bases at least 030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.8; DB 2;
Pred. No. 1.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector_side:right"
30239 c_30430 g_44777 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 125000; agarose-fp
Insert size: 152502; sum-of-cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- Project Information
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1. .65456
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55557. .152602
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .152602
/organism="Felis catus'
/db_xref="taxon:9685"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: azg
Center clone name: 212B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58330 CAAAGCAATAGCTTCAGGGTG 58350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP86-212B12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector_side:right"
65557. .152602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CAAAGCACTAGCTTCAGTGTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_end:SP6
                                                                                                                                                                                                                                                      2 (bases 1 to 152602)
Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65457
65557
                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                                        JOURNAL
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                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                        COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC108898 152602 bp DNA linear HTG 01-FEB-2003
Felis catus clone RP86:212B12, WORKING DRAFT SEQUENCE, 2 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Felis catus.
Felis catus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 152464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                            /clone_lib="RPCI-11 Human Male BAC"
1. 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.8; DB 2;
Pred. No. 1.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47300. .50907 --
/note="assembly_fragment"
51008. .55098
/note="assembly_fragment"
                                                                                                                                                                                                                                                                        135. 5783
lote="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                          119. 12558
lote="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"assembly_fragment"
2549. .24938
note-"assembly_fragment"
5039. .26839
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note="assembly_fragment"
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lote="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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lote="assembly_fragment"
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HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                 ector_side:left"
                                      clone="RP11-1C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.9%;
Best Local Similarity 90.5%;
Matches 19; Conservative
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AC108898
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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õ g /note-"assembly_fragment

clone_end:SP6

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misc_feature
                            misc_feature
                                                                                                                                                                                                                              BASE COUNT
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AL353622/c
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AUTHORS
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SOURCE
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                                                      HTG 18-JAN-2002
                                                 AC107322 152625 bp DNA linear HTG 18-JAN-200
Felis catus clone RP86-198D15, WORKING DRAFT SEQUENCE, 4 unordered
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis
                                                                                                                                                                                                                                                                                                                      Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Blattrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho.S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A. Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (18-JAN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 146000; agarose fp
Insert size: 152225; sum-of-contigs
Quality coverage: 11 37x in Q20 bases; agarose-fp
Quality coverage: 10 90x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 0.990319
Consensus quality: 151720 bases at least 040
Consensus quality: 151988 bases at least 030
Consensus quality: 152043 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93744: contig of 50984 bp in length 93844: gap of unknown length 52625: contig of 58781 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2660: contig of 39590 bp in length 2760: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@hhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; n/a; 100%
Chemistry: Dye-terminator Big Dye; 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone name: 198D15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: azh
                                                                                                                                                   AC107322.1 GI:18201784
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                          naila; Eutheria; Ca:
(bases 1 to 152625)
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93845
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                                                 LOCUS
DEFINITION
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JOURNAL
AUTHORS
TITLE
RESULT 10
AC107322
                                                                                                                            ACCESSION
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KEYWORDS
SOURCE
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/clone_lib="RP86

misc_feature

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On May 2, 2002 this sequence version replaced gill8614033.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation anotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phired quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI 30-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT; Tr:, TREMBL; WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157243 bp DNA linear PRI 30-APR-2003 sequence from clone RP5-1092A3 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157243)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructed by the group of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 152625;
                                                                                                                                                                                                                                                                                                                         300 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.8; DB 2;
Pred. No. 1.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RP5-1092A3 is from the library RPCI-5 co
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                              vector_side:left"
a 30256 c 30622 g 45219 t
vector_side:right"
3071. 42660
/note="assembly_fragment"
42761. 93744
/note="assembly_fragment"
93845. 152625
/note="assembly_fragment"
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Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                            clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human DNA
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ACU25860 157986 bp DNA linear HTG 11-APR-2000
Homo sapiens chromosome 1 clone RP11-692J20 map 1, WORKING DRAFT
SEQUENCE, 46 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                          Gaps
                                                                         Length 157243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   en, B., Linton, L., Nusbaum, C. and Lander, E. sapiens chromosome 1, clone RP11-692J20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coung, G., Zainoun, J., Zimmer, A. and Zody, M
                                                                       80.9%; Score 17.8; DB 9;
llarity 90.5%; Pred. No. 1.5e+02;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seg.wi.mit.edu
/clone="RP5-1092A3"
/clone_lib="RPCI-5"
42538 a 35890 c 36187 g 42628 t
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                           Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                          AC025860.2
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                              BASE COUNT
ORIGIN
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TITLE
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JOURNAL
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                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is
               Insert size: 188000; agarose-fp
Insert size: 153466; sum-of-contigs
Quality coverage: 2.6 in 020 bases; agarose-fp
Quality coverage: 3.1 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                          100 bp
of 1416 bp in length
                                                                                                                                                                                                                         of 100 bp
contig of 1383 bp in length
                                                                                                                                                                                                                                                    100 bp
f 1022 bp in length
                                                                                                                                                                                                                                                                                                                                                                         p of 100 bp contig of 1791 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                    p of 100 bp contig of 1774 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45: gap of 100 bp
16422: contig of 1777 bp in length
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contig of 2183 bp in length
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Length 157986;

Score 17.8; DB 2; Pred. No. 1.5e+02;

Query Match
Best Local Similarity 90.5%;

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ACO74242 164018 bp DNA 11near HTG 07-AUG-2000 Homo sapiens chromosome 6 clone RP11-112M16, WORKING DRAFT SEQUENCE, 34 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Louis,
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164018)
Waterston,R.H.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Aug 3, 2000 this sequence version replaced gi:9369560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center code: WUGSC
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f unknown length
g of 1151 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of 1241 bp in length
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length
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unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1170 bp in length
known length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 1369 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of read Assembly program: Phrap; version 0.990319 Consensus quality: 149547 bases at least 040 Consensus quality: 153517 bases at least 030 Consensus quality: 155530 bases at least 020 Insert size: 152000; agarose-fp Insert size: 160718; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
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Center project name: H_NH0112M16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---- Genome Center
                                                                                    51743 CAAAGAACTAGATTCAGTGTG 51723
                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 100%
Sequencing vector: plasmid; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
gap of
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gap of
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                                           2 CAAAGCACTAGCTTCAGTGTG
                                                                                                                                                                                                                                                                                              AC074242.2 GI:9665200
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6502:
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9099:
9199:
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                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.H
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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misc_feature 920	misc_feature 108	misc_feature 137	misc_feature 156	misc_feature 188	/nc misc_feature 216	/nc misc feature 231	ON ON OTHER PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR	misc_reature 25c/	misc_feature 283	misc_feature 319	misc_feature 365	/nc misc_feature 39°	/nc misc_feature 43	/nc misc_feature 47	misc feature 51	/n misc_feature 56	/n misc_feature 62	/n misc_feature 68	/n misc_feature 74	/m misc_feature 81	misc_feature 87	/nc misc_feature 92	/nc misc_feature 10	misc_feature 11	misc_feature 12	misc_feature 13	misc_feature 14	BASE COUNT 51062 a	OKIGIN	atc	Matches 19; Conserv	· -,	Db 27866 CAAAGCACT	RESULT 14	. LOCUS AC130917 DEFINITION Rattus norve	***, 66 unor ACCESSION AC130917 VERSION AC130917	٠.
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contig of 1593 bp in length gap of unknown length	of 2728 b	of 2057 b	of 2908 b	of 2614 bp i	gap or unknown 1 contig of 1423 b	gap of unknown l	gap of unknown l	gap of unknown 1	contig of 3500 b	contig of 4516 b	contig of 3099 b	gap of unknown I contig of 4064 b	gap of unknown l contig of 3923 b	gap of unknown l contig of 3504 b	gap of unknown length contig of 5098 bp in length	gap of unknown contig. of 5770	gap of contig	<b>-, Δ</b>	of unknown lig of 6797 b	of unknown lig of 6114 b	of unknown ig of 5347	ot unknown ig of 10260	of 7739 b	gap of unknown length contig of 9064 bp in length	ig of 9887 b	of 15211	contig of 18605 bp in length.		dyanism - nomo sapiens db_xref="taxon:9606"	=="6" 1-112M16"	1241 note="assembly_name:Contig28"	1342 .2412 /note="assembly_name:Contig29"	mbly_name:Contig31"	mbly_name:Contig32"	oose."assembly_name:Contig33" 503. 7799	note="assembly_name:Contig34" 900. 9099 note="assembly name:Contig36"	
* 9200 10792: * 10793 10892:	чч	* 13721 15777: * 15778 15877:	1	1.01			* 25772 25871: * 25872 28273	'. v m				٠.	* 43857 43956: * 43957 47879:	* 47880 47979: * 47980 51483:		* 56682 56781: * 56782 62551:	•			* 80992 81091: * 81092 87205:	* 87206 87305: * 87306 92652:	* 92653 92752: * 92753 103012:		* 110952 110951: * 110952 120015: * 120016: 120115:			* 145414 164018: FEATURES 1000701	rce	/organism= /db_xref="t		misc_teature 11241 /note="asse:	•		misc_teature 3764, 4933 /note="asse misc_feature 5034 6402	1 / 6	/note="asse misc_feature 79009099 /note="asse	

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181718 bp DNA linear HTG 15-AUG-2002 vegicus clone CH230-237P19, *** SEQUENCING IN PROGRESS ordered pleces.
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y 90.5%; Pred. No. 1.56+02;

rvative 0; Mismatches 2;
                                                                    note="assembly_name:Contig40"
5878. 18785
note="assembly_name:Contig41"
                                                                                                                                                                                                                                                                             note="assembly_name:Contig46"
1978. .36493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="assembly_name:Contig60"
0952. ..120015
oote="assembly_name:Contig61"
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hote="assembly_name:Contig62"
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                               note="assembly_name:Contig38"
3721. .15777
                                                                                                                                           note="assembly_name:Contig42"
1600. .23022
                                                                                                                                                                                                                                                   lote="assembly_name:Contig45"
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1652. .67979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ote="assembly_name:Contig54"
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:753. .103012
ssembly_name:Contig37"
                                                                                                                                                                       note="assembly_name:Contig43"
3123. .25771
                                                                                                                                                                                                                                                                                                                                       5594. .39692.
hote="assembly_name:Contig48"
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31307 c 31421 g 46923 t
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1306. .92652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ote="assembly_name:Contig59"
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Muzny, D. Marie., Merzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Anguiano, D., Banderdani, M., Barnstead, M., Benahmed, F., Blavalo, K., Blath, P., Brown, M., Brantstead, M., Benahmed, F., Blavalo, K., Blath, P., Brown, M., Brant, M., Blavalo, K., Blath, P., Brown, M., Bryant, M., Blay, C., Burch, P., Brown, M., Bryant, M., Dalay, C., Burch, P., Brown, M., Bryant, M., Dalay, C., Burch, P., Brown, M., Chacker, D., Chen, R., Corkell, M., Chen, R., Gebregeorgis, E., Geer, K., Gill, R., Crady, M., Garner, M., Gebregeorgis, E., Geer, K., Gill, R., Crady, M., Garner, M., Gebregeorgis, E., Geer, K., Gill, R., Crady, M., Garner, M., Gebregeorgis, E., Hadun, S.L., Hodgson, A., Hogues, M., Harnes, S., Huadun, S.L., Hodgson, A., Hogues, M., Jackson, L., Jang, H., Louderson, R., Johnson, B., Johnson, R., Jackson, L., Jacob, L., Liudy, S., Khan, Z., King, L., Kovar, C., Liu, J., Lu, W., Liu, Y., Luh, W., Liu, Y., London, P., Longacre, S., King, L., Kartin, R., Mahneshwari, M., Mahnen, M., Mahmoud, M., Malloy, K., Mandashwari, M., Mahneshwari, M., M
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Submitted (15-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Sorgle, R., Sosa, J., Stelanle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, D., Thomas, D., Tringey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Wardron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Zhou, K., Yoon, L., Yoon, L., Yoon, L., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, S., Dunn, D., Woo Niederhausern, A., Weiss, R., Smith, D.R., Wells, R.A., Smith, D., Welnstock, G. and Gibbs, R.A., Smith, D.R.,
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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------ Summary Statistics
Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: hgsc-help@bcm.tmc.edu
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Rat Genome Sequencing Consortium.
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                                                                   Rattus norvegicus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
HTG; HTGS_PHASE1.
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                                             Norway rat.
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                             AUTHORS
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Chemistry: Dye-terminator Big Dye: 100% of re Assembly program: Phrap: yersion 0.990329 consensus quality: 120233 bases at. least Q40 Consensus quality: 130616 bases at least Q30 Consensus quality: 138732 bases at least Q20
                                                                                                                                                                                                                        1080 bp in length
                                                                                                                                                                                                                                                                               bp in length
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Richard, 320 Chailes Sireet, Cambriage, MA U1141, USA

Birch, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Banderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,

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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Zainoun, J., Zaebek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-AUG-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 13, 2000 this sequence version replaced g1:9280765. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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http://ftp.genome.washington.edu/RW/RepeatMasker.html
http://ftp.genome.washington.edu/RW/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
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Homo sapiens chromosome 15, clone RP11-325L12, complete sequence.
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complement(17245, 17342)
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omplement(13154. .13452)
rpt_family="AluSp"
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complement(4847. 4972).
/rpt_family="MIR"
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complement(1501)
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                                          'rpt_family="AT_rich"
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rpt_family="AluSp"
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rpt_family-"MIR3"
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pt_family="Alux"
/rpt_family-"L2"
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/rpt_family-"L2"
2673. 2700
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"FLAM_A" 2548)

V="L1MB7" 22416)

1y="L1MB7" 459

lement(21460. .21545)
_family="L1MB7"

y-"(TAA)n"

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AluSx"

family="L1MB7"

ly="AluSq"

lement(19342. ... family="L1MB7"

Gaps

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Indels

Score 17.8; DB 9; Pred. No. 1.4e+02; 0; Mismatches 2;

repeat_region

Length 184864;

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(without alignments)
358.431 Million cell updates/sec
                                                                                                     8, 2003, 00:43:28 ; Search time 138.224 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Perfect score;
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N_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

.IES Description		Human secreted pro
SUMMARIES	AAZ28817 AAZ28810 ABK62554 ABL25670 AAD32364 AAK66931 AAK66931	AAC30329
80	004 E 4 C 6 4	21
% Query Match Length DB	2765 2765 2336 2336 7444 30620 563	351
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WPI; 1999-593429/51.

cDNA encoding a hu	Kidney cancer rela	cancer	ZBC gen	ificial ch	- C	encodin	EIF-2alpha kinase	Human low adenosin		low adenos	Human adenosine re	Human reproductive		-	brea	breast	breast	hila me	Sequence encoding	Lactate oxidase va	oxidase	Lactate oxidase va	Aerococcus lactate	Enterococcus faeca	E faecalis EF124 g	Human breast cell	Human foetal liver	4	Human brain expres	Human bone marrow		Probe #4674 used t	Probe #4421 used t	-	Human serine/threo
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## ALIGNMENTS

AAZ28817 standard; DNA; 22 BP

AAZ28817

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neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; probe; hybridsation.
                                                                                                                              inactivation; ss;
on; disorder;
                                                                                                                  neprilysine II; NEPII; inac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Facchinetti P;
                                                                                 Rat membrane metalloprotease NEPII gene probe #7.
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                                                                                                                          membrane metalloprotease;
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                                     01-FEB:2000 (first entry)
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                                                                                                                                                                                                                        Synthetic.
Rattus rattus.
                                                                                                                                                                                                                                                                                FR2777291-A1.
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AAZ28817;
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ABK62554
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                                                                                                                 membrane metalloprotease designated neprilysine II (NEPII) gene (AAZ28810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and itssues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic- hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the gene for the rat membrane metalloprotease designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; deterron; dormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds.
                                                                                                    Sequences AAZ28811-228827 represent probes for detecting the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New membrane metalloprotease NEP II, involved in proteolysis of
neuronal and hormonal peptides, used to screen for inhibitors,
potentially useful for treating e.g. cardiovascular disease
               oţ
          New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardiovascular disease
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                                                                                                                                                                                                                                                                                        Length 22
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Pred. No. 0.23;
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                                                                                                                                                                                                                                                                    Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 other;
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                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ28810 standard; cDNA; 2765 BP
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                                                                     Claim 3; Page 21; 29pp; French.
                                                                                                                                                                                                                                                                                                 100.08;
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P-PSDB; AAY44177.
                                                                                                                                                                                                                                                                                                               Local Similarity
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Schwartz JC;
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Matches
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AAZ28810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat sequence differentially expressed in response to a hepatotoxin #461.
disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine disorders.
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                             Score 22; DB 20; Length 2765;
Pred. No. 0.45;
Mismatches 0; Indels 0;
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                                                                                                                   Sequence 2765 BP; 684 A; 735 C; 787 G; 559 T; 0 other;
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                                                                                                                                                                100.0%;
ilarity 100.0%;
Conservative 0;
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2001US-295798P.
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                                                                                                                                                                                      Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK62554;
                                                                                                                                                                       Query Match
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support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global listed in the specification and for identifying toxicity markers in toxicity markers in drug screening and toxicity assays. The genes and perediction not identification may be used as diagnostic markers for the prediction of the physiological state of tissue or cell procession information of the physiological state of tissue or cell
                                                                                                                                                                                                                                                                                                                                                                          compound or agent. Hepatotoxicity necrosis and steatosis. The present tag (EST) or CDNA derived from a gene in response to a hepatotoxic agent.
                                                                                                                                                                                                                                                                                                                                                                       sample that has been exposed to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                      which is differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                               is an expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                               characterised by centrilobular
                                                                                                                                                                                                                                                                                                                                                                                                                                  sednence
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Sequence 331 BP; 95 A; 78 C; 70 G; 88 T; 0 other;

Score 16.8; DB 24; Length 331; Pred. No. 1.2e+02; 0; Mismatches 2; Indels 0 3 AAAGCACTAGCTTCAGTGTG 22 28 AAAGCACGAGATTCAGTGTG 47 76.48; 90.08; Query Match
Best Local Similarity 90.0
Matches 18; Conservative ð 셤

Drosophila; developmental biology; cell signalling; insecticide; Drosophila melanogaster genomic polynucleotide SEQ ID NO 28483. ABL25670 standard; DNA; 2336 BP. (first entry) 26-MAR-2002 ABL25670; RESULT 4
ABL25670

23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150. 23-MAR-2001; 2001WO-US09231 pharmaceutical; gene; dș Drosophila melanogaster WO200171042-A2 27-SEP-2001. 

(PEKE ) PE CORP NY.

Li PWD, Adams M, Venter JC,

WPI; 2001-656860/75.

E. Myers ייבי באטומופס nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Claim 1; SEQ ID NO 28483; 21pp + Sequence Listing; English..

is The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072) seduences

Gaps

ö

Indels

Score 16.8; DB 24; Pred. No. 1.9e+02; 0; Mismatches 2;

Query Match 76.4%; Best Local Similarity 90.0%; Matches 18; Conservative

Length 7444;

Sequence 7444 BP; 2172 A; 1679 C; 1695 G; 1898 T; 0 other;

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to lung specific genes (LSG) and their corresponding polypeptides. LSG is useful for identifying, diagnosing, monitoring, staging, inaging and treating lung cancer and non-cancerous disease states in lung, identifying lung tissue, monitoring and modifying lung embryonic development and differentiation, in gene therapy, as hybridisation probes, to detect LSG mRNA as a marker for lung cancer, as research reagents and materials for discovery of \text{Vertaupent} treatments and diagnostics to human disease, to detect complementary polynucleotides, and for chromosome identification. An antibody which binds LSG is useful to detect or image localisation of LSG in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel lung specific gene useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous disease states in lung, for gene therapy, and for identifying lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for preventing the
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease; gene
                                                                                                                                                                                     Score 16.8; DB 23; Length 2336;
Pred. No. 1.6e+02;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   onset and treatment of lung cancer, to isolate or to identify expressing LSG polypeptides, to purify LSG polypeptides, and tumours expressing LSG. The present sequence is human LSG DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; lung specific gene; LSG; lung embryonic development;
                                                                                                                 Sequence 2336 BP; 638 A; 505 C; 529 G; 664 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung cancer; vaccine; gene therapy; non-cancerous lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for detecting or diagnosing a disease or condition,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lung specific gene (LSG) #1.
                                                                                                                                                                                                                                                                                                                                                   198 CAAAGCTCTAGCTTCAGTTT 217
                                                                                                                                                                                                                                                                                                            2 CAAAGCACTAGCTTCAGTGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD32364 standard; DNA; 7444 BP
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                                                                                                                                                                                 Query Match 76.4%;
Best Local Similarity 90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-2001; 2001WO-US22949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200208278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-2002
                                                                                                                                                                                                                                               18;
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   222238
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21743
                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                               6812 GCAAAGCACTATCTACAGTG 6831
1 GCAAAGCACTAGCTTCAGTG 20
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97JP-0135716. 96JP-0261132. 97JP-0130236.

14-APR-1997; 19-APR-1997; 26-AUG-1996;

97WO-JP02957

26-AUG-1997;

05-MAR-1998

WO9808944-A1

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AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased carpression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the coroten. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastases of haematopoletic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK54912 to AAK64950 and AAAM82169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 21743; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                              2001US-0259678
                             2000US-0250391
                                                                                                             2000US-0256719
                                                                                                                                                                                                   000US-0251868
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-483426/52.
                                               05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                           05-JAN-2001;
                                                                                                                                                                                                                              38-DEC-2000;
                          01-DEC-2000
                                                                                                                                                                                                   08-DEC-2000;
01-DEC-2000
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                                                                                                                                                                                                                                                                                38-DEC-2
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                                                                                                                                                                     08-DEC
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Gaps
                                    Length 30620;
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Sequence 30620 BP; 7407 A; 7216 C; 7192 G; 8805 T; 0 other;
                                                                    Indels
                                  Score 16.8; DB 22;
Pred. No. 2.3e+02;
0; Mismatches 2;
                                                                                                               20724 GCAAAGAACCAGCTTCAGTG 20705
                                                                                               1 GCAAAGCACTAGCTTCAGTG 20
                               Query Match

Best Local Similarity 90.0%;
Matches 18; Conservative (
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Escherichia coli 0157; bactericide; food;
                                                                                               pathogen; Escherichia co
enteric haemorrhage; ds
                                                                           Bacteriophage DNA SEQ ID NO:2-10
                 AAV26013 standard; DNA; 563 BP
                                                       28-AUG-1998 (first entry)
                                                                                             Bacteriophage;
sterilisation;
                                     AAV26013;
RESULT 7
         AAV2601
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Bacteriophage.

99US-0294093. 98US-082567P 16-APR-1999; 21-APR-1998;

The present sequence represents a DNA sequence from a novel bacteriophage which has high specificity for pathogenic bacteria, especially for strains of Escherichia coli causing enteric haemorrhage, such as E. coli 0157. The bacteriophage can be incorporated into blo-bactericidal compositions. These can contain more than one bacthogen at the same time. The blo-bactericide may also contain an amino-acid or other material to control the pH to 6.5-7.5 and ensure stability of the bacteriophage, such as glycine, arginine or lysine. The bio-bactericidal composition can be used for treating food (such as meat or fish) to prevent bacterial contamination, e.g. in fresh food or in the kitchens of restaurants, schools and other institutions. It may be formulated as a spray. It can also be used to sterilise working the containers. as Bacteriophage with high specificity for particular pathogens such Escherichia coli 0157 is incorporated in bactericides for food Length 563; Sequence 563 BP; 182 A; 93 C; 114 G; 169 T; 5 other; humans but very potent against pathogenic bacteria. Claim 3; Page 39; 54pp; Japanese. (BIOV-) BIO VENTURE BANK CO LID. Takahashi S; WPI; 1998-230262/20. Nishikori K, sterilisation 

0 Indels 74.5%; Score 16.4; DB 19; 89.5%; Pred. No. 2.1e+02; 1ive 0; Mismatches 2; 17; Conservative Query Match Best Local Similarity Matches

328 AAGCACTANCTTCAATGTG 346 4 AAGCACTAGCTTCAGTGTG 22 ò g

RESULT 8 ABL73130

ABL73130 standard; cDNA; 295 (first entry) 14-MAY-2002 ABL73130;

Corn tassel-derived polynucleotide (cdps) SEQ ID NO:2504.

Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss. JS2001051335-A1 13-DEC-2001 Zea mays. 

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 351 BP; 96 A; 89 C; 90 G; 76 T; 0 other;
Duclert A, Glordano J;
                                                                                                                                                                                                                                                Claim 1; SEQ ID 34404; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 CAAGGCACTATCATCAGTGTG 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression and secretion vectors.
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Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200056891-A2
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16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence describes a purified corn tassel-derived polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL70833. The cdps sequences cord tassel-derived polypeptides (CDPs). The cdps sequences con tassel-derived polypeptides (CDPs). The cdps sequences can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a used to produce a tassel-specific profile, independent of colone regulatory elements for use in transformation vectors, to express a polypeptide, to identify, isolate or extend the profile of colone regulatory elements for use in transformation therein a plant isolate or extend the profile of colone regulatory elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                          Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    libraries, in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 2.4e+02;
); Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 295 BP; 70 A; 63 C; 75 G; 86 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 2504; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 CAAAGTACTTGCTTCAGAGTG 113
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                                                                                                                                                        Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (or more) nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
AAC30329/c
ID AAC30329 standard; cDNA; 351 BP.
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Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-2000 (first entry)
                             LALGUDI R V.
ITO L Y.
SHERMAN B K.
                                                                                                                                                     Lalgudi RV, Ito LY,
                                                                                                                                                                                                               WPI; 2002-163647/21
                                                                                                                                                                                                                                                                                                                                                                           breeding programs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1033401-A2.
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                             (LALG/)
                                                                                       (SHER/)
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Gaps

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Indels

Score 16.2; DB 21; Pred. No. 2.5e+02; 0; Mismatches 3;

BP.

Length 351;

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Baughn MR;
                                      rder; myeloma;
ogical disorder;
r syndrome; AIDS;
                                      Human; transmembrane protein; cell proliferation disorder; myelom reproductive disorder; smooth muscle disorder; neurological disord arterioscherosis; leukaemia; acquired immunodeficiency syndrome; A allergy; ovulatory defect; angina; hypertension; stroke; epilepsy; Alzheimer's disease; Tourette's disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reddy R, Bandman O,
cDNA encoding a human transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillman JL,
                                                                                                                                                                                                                                         Location/Qualifiers 195..1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Hi
i Y, Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-2000; 2000WO-US07817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0139565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-579485/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yue H,
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21-FEB-2000; 2000EP-0200610.

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99US-0122487

26-FEB-1999;

(GEST ) GENSET

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ABL68864/C
ID ABL68864 standard; DNA; 2226 BP.
XX
AX
AX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                        The present sequence encodes a human transmembrane proteins (HTWP). Agonists and antagonists of the protein are used to treat a disease or condition associated with overexpression of the protein. Diseases and conditions which can be treated include cell proliferative, immunological, reproductive, smooth muscle and neurological disorders e.g. arteriosclerosis, myeloma tuckemia, acquired immunodeficiency syndrome (AIDS), allergies, ovulatory defects, angina, hypertension, stroke, Alzheimer's disease, epilepsy and fourette's disorder. The bolynucleotides may be used to detect and quantify gene expression in biopsied tissues where protein expression may be correlated with disease e.g. to determine absence, presence or excess expression of HTMP or to monitor regulation of HTMP expression during therapeutic intervention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                       New human transmembrane proteins are used to treat a disease or condition associated with decreased expression of functional HTMP e.g. Tourette's disorder, angina and leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.2; DB 21; Length 2022;
Pred. No. 3.1e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2022 BP; 553 A; 494 C; 459 G; 516 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kidney cancer related gene sequence SEQ ID NO:6581.
                                                                                                                                                                   Claim 4; Page 120-121; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617 CAAGGCACTATCATCAGTGTG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CAAAGCACTAGCTTCAGTGTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
ABL68244/C
ID ABL68244 standard; DNA; 2226 BP. XX
AC ABL68244;
XX
DT 15-MAY-2002 (first entry)
XX
DE Kidney cancer related gene seque
XX
Human; cancer; colon; breast; ov
stomach; lung; prostate; pancrea
XW
YCOStatic; gene therapy; antine
XX
OS Homo sapiens.
XX
NOCO194629-A2.
XX
PN WC200194629-A2.

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ilarity 85.7%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 18; Conserv
     P-PSDB; AAB18979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABLG1664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adentical cancer, infiltrating ductal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        squamous cell carcinoma, neuroendocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carter KC, Ebner R, Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2226 BP; 412 A; 686 C; 666 G; 462 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carcinoma, papillary carcinoma and Wilm's tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID 6581; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1166 GCAGAGCACCAGCTGCAGTGT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infiltrating lobular cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.6%;
Best Local Similarity 85.7%;
Matches 18; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-245084P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Augustus M,
Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-188264/24.
28-SEP-2000;
                                  38-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Young PE, A
Soppet DR,
                                                             28-SEP-2000
                                                                                               -SEP-2000
                                                                                                                              9-SEP-2000
                                                                                                                                                                                               32-0CT-2000;
                                                                                                                                                                                                                              02-0CT-2000;
                                                                                                                                                                                                                                                                32-OCT-2000
                                                                                                                                                                                                                                                                                               02-OCT-2000
                                                                                                                                                                                                                                                                                                                                 02-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                03-0CT-2000
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in capression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises a sequence (S) selected from 8447 sequences (given in ABL61664 cexpression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, coscophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
                                                                                                                                                                                                                                     Sequence 2226 BP; 412 A; 686 C; 666 G; 462 T; 0 other;
                                                                                                                                                                                                              carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                               Query Match 73.6%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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                                           Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endress G,
                             Kidney cancer related gene sequence SEQ ID NO:7201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        · Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carter KC,
                                                                                                                                                                                                                                                                                       000US-234034P
                                                                                                                                                                                               30-MAY-2001; 2001WO-US10838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-245084P
    15-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AVAL-) AVALON PHARM
                                                                                                                                             WO200194629-A2.
                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                 18-SEP-2000;
18-SEP-2000;
20-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8-SEP-2000;
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Gaps

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Score 16.2; DB 24; Length 2226; Pred. No. 3.1e+02; ; Mismatches 3; Indels 0;

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mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine; angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin; fungal toxin; cell surface receptor; plant growth regulator; pigment;
                                                                                                                                                                                                                                        Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation of the expression of at least one zinc binuclear cluster protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to improving the production of a secondary metabolite by a fungus. This involves modulating the expression of at least one ZBC (zinc binuclear cluster protein) gene in a manner to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID 305; 49pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maxon M, Sherman A;
                                                                                                                                                                                                                                                                                                                      insecticide; antineoplastic; gene; ds
                1166 GCAGAGCAGCTGCAGTGT 1146
21
                                                                                                             ABN79910 standard; DNA; 2274 BP.
 1 GCAAAGCACTAGCTTCAGTGT
                                                                                                                                                                                                           Fungal ZBC gene seguence #147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-2001; 2001WO-US29288.
                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MICR-) MICROBIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-352005/38.
P-PSDB; ABP35721.
                                                                                                                                                                                                                                                                                                                                                                                      WO200224865-A2.
                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holtzman D,
                                                                                                                                                                              24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2002.
                                                                                                                                            ABN79910:
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chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set

Claim 1; SEQ ID 7201; 44pp; English

Screening for anti-neoplastic agent involves exposing cells to

WPI; 2002-188264/24.

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may be used for Improving the production of the secondary metabolite e.g antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such as large as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A), as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A), as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds, a fungal toxin, a modulator of cell surface receptor signalling, a plant compound. The method results in a decrease in fermentor run-time, a decrease in the size of the fermentor required for the production of equivalent amounts of the secondary metabolite, or a decrease in the blomass required for the production, which translates into decreased in records ABN79764-ABN79911 repersent ZBC genes of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovarian cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; lymphoma; cancer; vaccine; P1 artificial chromosome;
                                                                                                                                                                                                                                                                                         Score 16.2; DB 24; Length 2274; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                         Sequence 2274 BP; 539 A; 610 C; 594 G; 531 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methods of diagnosis, prognosis and treatment of cancer
                                                                                                                                                                                                                specification, but was obtained directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; therapy;
                                                                                                                                                                                                                                                                                             J.2e+02;
3;
                                                                                                                                                                                                                                                                                                       Pred. No. 3.2e+
0; Mismatches
                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
improve the yield of the secondary may be used for improving the proof.
                                                                                                                                                                                                                                                                                                                                                                210 GCAGAGCCCTAGCTCCAGTGT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S6 kinase-3;
                                                                                                                                                                                                                                                                                                                                                1 GCAAAGCACTAGCTTCAGTGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pl artificial chromosome 427A4.
                                                                                                                                                                                                                                                                                       73.68;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX84531 standard; DNA; 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98GB-0004050.
97GB-0027347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-GB03887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rsk-3; p90 ribosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09934015-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-1998;
24-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX84531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAC; SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                breast
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
AAX84531/c
ID AAX84
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Rsk-3 can be used to treat or ameliorate cancer. Rsk-3 inhibitors can also be used to treat cancer. Vaccines comprising mutant Rsk-3 or nucleic acids encoding mutant Rsk-3, where the mutant is found in cancer cells, are useful for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of 444 movel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat untiliple. Scalerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinfertility; cerebroprotective; cytostatic; rhemmatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkinson's disease. The present sequence is a coding sequence of the threships of the present sequence is a coding sequence of the threships of the present sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asundi V, Zhang J, Zhao QA, Ren F;
F, Drmanac RT;
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                                                                                                                                        Length 2340;
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                                                                                              Sequence 2340 BP; 712 A; 510 C; 508 G; 610 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2840 BP; 763 A; 631 C; 614 G; 832 T; 0 other;
                                                                                                                                  Score 16.2; DB 20;
Pred. No. 3.2e+02;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.2; DB 24;
Pred. No. 3.2e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human coding sequence SEQ ID NO: 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 64; 509pp; English.
                                                                                                                                                                                                                                  | |||||||| |||||| |||||| 491 CCAAGCACTCGCTTCACTGTG 471
                                                                                                                                                                                                             2 CAAAGCACTAGCTTCAGTGTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed sequence tag; gene; ss.
                                                                                                                                                                                                                                                                                                                                             ABN59653 standard; cDNA; 2840 BP
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85.78;
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ilarity 85.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2001; 2001WO-US26015.
                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou P,
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                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserv
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18; Conserv
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ABB97240.
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                                                                                                                                                                                                                                                                                                                                                                                    ABN59653;
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Matches 18
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2 CAAAGCACTAGCTTCAGTGTG 22

This sequence represents a P1 artificial chromosome (PAC), designated 4274, and containing the p90 ribosomal S6 kinase-3 (Rsk-3) gene. The invention relates of diagnosis, prognosis and treatment of cancer related to the Rsk-3 gene. The methods are used for diagnosis, prognosis and treatment of cancer, especially ovarian or breast cancer or lymphoma. Nucleic acids that selectively hybridise to the Rsk-3 gene or cDNA, or a multant Rsk-3 allele, or a molecule that selectively binds to Rsk-3 polypeptide can be used to manufacture reagents for diagnosis of cancer.

Example 1; Fig 16a; 167pp; English.

242 CAAGGCACTATCATCAGTGTG 222

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Search completed: July 8, 2003, 02:18:58 Job time : 140.224 secs 0, Ap Appli

Appli Appli Appli Appli Appli Appli

score:

Title: Perfect :

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

Result ģ

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GENERAL INFORMATION:
APPLICANT: TAKAHASHI, SEISHI
TITLE OF INVENTION: HOVEL BACTERIOPHAGES, METHOD FOR SCREENING SAME AND
TITLE OF INVENTION: BACTERICIDAL COMPOSITIONS USING SAME, AND DETECTION
TITLE OF INVENTION: KITS USING SAME
TITLE OF INVENTION: KITS USING SAME
FILE REPERENCE: 3000-0001
CURRENT APPLICATION NUMBER: US/09/242,901
CURRENT FILING DATE: 1999-02-26
BARLIER APPLICATION NUMBER: PCT/JP97/02957
BARLIER APPLICATION NUMBER: 8/261132
BARLIER FILING DATE: 1996-08-26
BARLIER FILING DATE: 1996-08-26
BARLIER FILING DATE: 1997-04-19
BARLIER APPLICATION NUMBER: 9/135716
BARLIER FILING DATE: 1997-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: "n" at various positions throughout the sequence may CTHER INFORMATION: a, t, g, c other or unknown US-09-242-901-14
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     Sequence 11, Sequence 13, Sequence 31, Sequence 18, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 270 Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Seque
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                                                                                                                                                                                                                                                                                                 US-08-833-310-3
US-09-134-001C-2700
US-09-342-648-1
PCT-US93-03076-1
US-07-807-043B-16
US-08-505-218-1
US-08-505-218-12
US-08-861-774E-33
US-09-152-060-41
US-09-152-060-15
US-09-154-48-18
US-08-294-872-1
PCT-US95-09823-1
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US-08-729-955A-1
US-08-853-948B-1
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Patent No. 5656471
GENERAL INFORMATION:
APPLICANT: MINAGAWA, Hirotaka
APPLICANT: NAKAYAWA, No. 5656471iyuki
APPLICANT: NAKAYAWA, No. 5656471iyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09242901
Patent No. 6322783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AAGCACTAGCTTCAGTGTG 22
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 563
  TYPE: DNA ORGANISM: Bacteriophage
                                                                                                                                   JS-09-242-901-14
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Sequence 20, Appl
Sequence 205, Appl
Sequence 11, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 463, App
Sequence 457, App
Sequence 461, App
Sequence 465, App
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Sequence 3, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 61, Appl
Sequence 1, Appl
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                                                                                                                                                                                                           (without alignments) 222.151 Million cell updates/sec
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                                                                                                                                                                        July 8, 2003, 01:24:03; Search time 30.3707 Seconds
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/cgn2_6/ptodata/1/ina/5B_COKB.seg:*
/cgn2_6/ptodata/1/ina/6A_COKB.seg:*
/cgn2_6/ptodata/1/ina/6B_COKB.seg:*
/cgn2_6/ptodata/1/ina/PcTUS_COKB.seg:*
/cgn2_6/ptodata/1/ina/PcTUS_COKB.seg:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-625-876-5
US-09-071-035-463
US-09-071-035-465
US-09-071-035-465
US-09-071-035-465
US-08-08-450-465
US-08-08-465
US-08-27-610-11
US-08-384-1064-6
US-09-240-906-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441362 seqs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                     - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                         1 gcaaagcactagcttcagtgtg 22
                                                                                                                                                                                                                                                                                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                  US-09-647-780A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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1010
2202
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: LACTATE OXIDASE WITH AN IMPROVED THERMAL : STABILITY AND GENE OF THE SAME

NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:

APPLICANT: NAKAYAMA,
APPLICANT: NAKAMOTO,
TITLE OF INVENTION:
TITLE OF INVENTION:

Sequence 11, Sequence 5, A Sequence 11, Sequence 11,

US-08-525-596B-11

Sequence Sequence

þe

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GENERAL INFORMATION:
APPLICANT: MINAGAMA, No. 56564711yuki
APPLICANT: NAKAYAWA, No. 56564711yuki
APPLICANT: NAKAYAWA, No. 56564711yuki
APPLICANT: NAKAMOTO, Shinya
TITLE OF INVENTION: LACTATE OXIDASE WITH AN IMPROVED THERMAL
TITLE OF INVENTION: STABILITY AND GENE OF THE SAME
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,876
FILING DATE: 01-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.8%; Score 15.8;
89.5%; Pred. No. 49
         UMBER: US/08/625,876
01-APR-1996
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-95947
FILING DATE: 30 MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-146186
FILING DATE: 13-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                           32,925
3R: PF-1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid
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FILING DATE: 13-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-95947
FILING DATE: 30-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CAAAGCACTAGCTTCAGTG 20
                                                                                                                                                                                                                                                                                               TELECOMMUNICATION TREORMATION:
   TELEPHONE: (703) 521-2297
   TELEFAX: (703) 68-0573
   TELEX: 248425 EMBON
   INFORMATION FOR SEQ ID NO: 3:
   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THOMPSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                NAME: PATCH, Andrew J
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1122 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.8
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1...1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: · linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 01 CLASSIFICATION:
                                        FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-625-876-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-08-625-876-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LACTATE OXIDASE WITH AN IMPROVED THERMAL STABILITY AND GENE OF THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1122;
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                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MINAGAWA, HITOTAKA
APPLICANT: NAKAYAMA, NO. 56564711yuki
APPLICANT: NAKAYAMA, NO. 56564711yuki
APPLICANT: NAKAMOTO, Shinya
TITLE OF INVENTION: LACTATE OXIDASE WITH
TITLE OF INVENTION: STABILITY AND GENE (
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,876
FILING DATE: 01-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/625,876
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-95947
FILING DATE: 30-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-146186
FILING DATE: 13-UN-1995
APPLICATION NUMBER: JP 7-146186
FILING DATE: 13-UN-1995
APPRICATION NUMBER: JP 7-1612
REGISTRATION NUMBER: 32,925
REGISTRATION NUMBER: PF-1612
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WOLECULE TYPE: other nucleic acid
SEE: YOUNG & THOMPSON
: 745 South 23rd Street
Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08625876
Patent No. 5656471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               918 CAAAGCGCTAGCTTCAGGG 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CAAAGCACTAGCTTCAGTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YOUNG & THOMPSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 248425 EMBON INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703) 521-2297
(703) 685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1122 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.59
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
                                                                                 COUNTRY: · U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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US-08-625-876-3
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Patentin Release #1:0, Version #1.30

SOFTWARE:

PATCH, Andrew J

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Sequence 457, Application US/09071035
Patent No. 648043
GENERAL INFORMATION:
GENERAL INFORMATION: GI1 H. Chol
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 4; Length 6168; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-071-035-461/c; Sequence 461, Application US/09071035; Patent No. 6448043
                                           1635 AAAGCACTIGGITCAGIGT 1617
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                        3 AAAGCACTAGCTTCAGTGT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                          STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                    JS-09-071-035-457/c
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                                                                                                                                                                                                                                                                                                                                                                                                   20850
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APPLICANT: G11 H. Cho1
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                         Length 1122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Score 15.8;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; Pred: No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
REGISTRATION NUMBER: 32,925
REFREENCE/DOCKET NUMBER: PF-1612
TELEPHONE: (703) 521-237
TELEPHONE: (703) 685-0573
TELEFAX: (703) 685-0573
TELEFAX: 248425 EMBON
INPOMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENTH: 1122 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSDOS version 6.2
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                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 463, Application US/09071035
Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       918 CAAAGCGCTAGCTTCAGGG 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: ANAMER BLOOKES
NAME: A. ANGERS BLOOKES
RESISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 463:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                Ouery Match 71.8%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 71.8%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                            LENGTH: 1122 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTKI.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
"THE VECTOR 486
MEDIUM TYPE: MEDIUM 4800'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         1.:1122
                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-071-035-463/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-09-071-035-463
                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-625-876-5
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Gaps ö

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APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: DePinho, Ronald A.
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Regulation
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0
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                                                                            Length 6168;
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                                                                                                                  Indels
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                                                                          Score 15.8; DE Pred. No. 63; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: 04 APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08384106A Patent No. 6033847
                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08627610 Patent No. 5919997 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 904 AAAGCCCTAGCCTCAGAGTG 923
                                                                                                                                                                                               4151 AAAGCACTIGGTICAGIGI 4133
                                                                                                                                                           3 AAAGCACTAGCTTCAGTGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AAAGCACTAGCTTCAGTGTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: LAHIVE & COCKFIELD 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 69.1%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                          vuery match 71.8%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           941 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: both
                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02109
                                     US-09-071-035-465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-627-610-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-384-106A-6
                                                                                                                                                                                                                                                                               US-08-627-610-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 465, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 6168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.50 inch, 1.4Mb storage
3: Diskette, 3.50 inch, 1.4Mb storage
HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 71.8%; Score 15.8; DB Best Local Similarity 89.5%; Pred. No. 63; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSDOS version 6.2
                                       MSDOS version 6.2
                                                                                                                                                                                                           ATOCNEY AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 136,373
REFERENCE/DOCKET NUMBER: PB369P2
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 461:
SEQUENCE CHARACTERISTICS:
LENGTH: 6168 base pairs
                                                                                                 APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: A. Anders Brookes
REGISSPRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AAAGCACTAGCTTCAGTGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (301) 309-8504
TELEBAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 465:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Diskette, 3.5
HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: . 6168 base pairs
                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: double
                             COMPUTER: RE VECLIA OPERATING SYSTEM: MSI SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-071-035-465/c
                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
US-09-071-035-461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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Gaps

Sherr Ph.D., Charles J

us-09-647-780a-11.rni

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APPLICANT: St. Jude Children's Research Hospital
TITLE OF INVENTION: INK4c-pl8 and InK4d-Pl9, Inhibitors of
TITLE OF INVENTION: Cyclin Dependent Kinases, CDK4 and CDK6, and Uses Thereof
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 941;
                                                                                                                                                                                                                                                                                                ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 New York Ave., N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PCT/US96/01643 FILING DATE: 06-PEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
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Pred. No. 96;
                                                                                                                                                Sequence 6, Application PC/TUS9601643 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-641-638-601
; Sequence 601, Application US/09641638
; Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/384,106
FILING DATE: 06-FEB-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                              904 AAAGCCCTAGCCTCAGAGTG 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        904 AAAGCCCTAGCCTCAGAGTG 923
      3 AAAGCACTAGCTTCAGTGTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fox, Samuel L. REGISTRATION NUMBER: 30,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 0
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.1%;
85.0%;
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APPLICANT: Bougueleret, Lydie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C57 Black Kaplan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 941 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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Best Local Similarity
Matches 17; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                 20005
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APPLICANT:
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                                             q
                                  APPLICANT: Okuda, Tsukasa
TITLE OF INVENTION: INK4C-p18 and INK4d-P19, Inhibitors of
TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
CORRESPONDENCE: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROUSSEL, MARTINE F.
APPLICANT: SMEYNE, RICHARD
APPLICANT: ZINDY, FREDERIQUE
APPLICANT: ZUNIY, JUSTINE
TITLE OF INVENTION: CELLS THAY LACK P19INK4D AND P27KIP1 ACTIVITY AND TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length .941;
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                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                         E: STERNE, KESSLER, GOLDSTEIN & FOX 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.2; DB.
Pred. No. 96;
0; Mismatches
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85.0%; Pred. No. 96;
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CURRENT FILING DATE: 1999-01-29.
NUMBER OF SEQ ID NOS: 8
SEQ TWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 941
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-FEB-1994
CLASSIFICATION: 435
TORNEV.A.
                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      904 AAAGCCCTAGCCTCAGAGTG 923
Downing M.D., James
Hirai Ph.D., Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-09-240-906-3
Sequence 3, Application US/09240906
Patent No. 6245965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORREY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
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Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              941 base pairs
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
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                                                                                                                                                                                  Washington
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                                                                                                                                                                                                                                            20005
                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                   APPLICANT:
                                                                                                                                                                                                                           COUNTRY:
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Gaps

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LOCATION: 28.525
OTHER INFORMATION: /product- "murine p19"
PCT-US96-05252-3
                                                                           NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 02307B-059910PC
TELECOMMUNICATION INFORMATION:
       US 08/425,093
                                                                                                                                                         TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEGUENCE CHARACTERISTICS:
LENGTH: 1010 base pairs
                        FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Curcuma zedoaria
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (130)...(1974)
US-09-388-743-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-388-743-1/c
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 2202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
ITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING ITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM ILE REFERENCE: GENSET.0510F10
URRENT APPLICATION NUMBER: US/09/641, 638
URRENT FILING DATE: 2000-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 535.552
OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THER INFORMATION: 10-387-371 : polymorphic base C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: p19: A Cell Cycle Inhibitor NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
URRENT APPLICATION DATA:
APPLICATION UNBER: PCT/US96/05252
FILING DATE: Not yet assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 69.1%; Score 15.2; DB 4; Best Local Similarity 85.0%; Pred. No. 97; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: upstream amplification primer NAME/KEY: primer_blod
LOCATION: 535.552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: 10-387-371.mis2, potential NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: 10-387-371 potential probe 09-641-638-601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WAME/KEY: misc_binding
LOCATION: 481..500
JTHER INFORMATION: 10-387-371.mis1, potential
                                                                                          CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR PILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application PC/TUS9605252 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             770 AGAGCACTAGCTTCATAGTG 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AAAGCACTAGCTTCAGTGTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: One marricelly: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AME/KEY: misc_binding
OCATION: 502..521
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94105-1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                 SOFTWARE: P
                                                                                                                                                                                                                                                                                                                                                                                                        PE: DNA
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TITLE OF INVENTION: Use in the Production of New Starches
TITLE OF INVENTION: Use in the Production of New Starches
TITLE OF INVENTION: Use in the Production of New Starches
FILE REFERENCE: 1144
CURRENT APPLICATION NUMBER: US/09/388,743
CURRENT FILING DATE: 1999-09-02
NUMBER OF SED ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2202;
                 Length 1010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.2; DB 4;
Pred. No. 1.1e+02;
0; Mismatches 3;
69.1%; Score 15.2;
nilarity 85.0%; Pred. No. 97;
Conservative 0; Mismatchen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: July 8, 2003, 09:31:46
Job time : 32.4207 secs
                                                                                                                                           |||||| |||||| ||||| |||| |||| |||| 802 AAAGCCCTAGCCTCAGAGTG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 CAAATCACTAGCTCCATTGT 188
                                                                                                                 3 AAAGCACTAGCTTCAGTGTG 22
                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09388743
Patent No. 6423886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CAAAGCACTAGCTTCAGTGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.18;
85.08;
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Singletary, George
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GenCore version 5.1.6.

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 19:09:54; Search time 127.063 Seconds

(without alignments)
273.390 Million cell updates/sec

Perfect score: 2
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Sequence: 10S-09-647-780A-11
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4: /cgn2_6/ptodata/2/pubpna/USG6_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/USGB_PUBCOMB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 461, Apple Sequence 371, Apple Sequence 9811, Apple Sequence 24, Apple Sequence 24, Apple Sequence 30, Apple Sequence 916, Apple Sequence 12317, Apple Sequence 12317, Apple Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli
SUMMARIES	US-09-917-800A-461 US-09-909-567B-37 US-10-198-846-9851 US-10-13-864- US-09-294-093B-2504- US-10-071-766-30 US-10-071-766-30 US-10-071-766-30 US-10-071-766-30 US-10-29-180-91 US-09-764-891-9765 US-09-764-891-9765 US-09-764-891-9765 US-10-198-846-12317 US-10-198-846-12317 US-10-198-846-12317 US-10-198-846-12317 US-10-198-846-12317 US-10-217-357-3 US-09-975-326-3 US-09-975-326-3 US-09-975-326-1 US-09-975-326-1
DB .	
Length DB	331 7444 78444 2019 682 2019 2019 872 1067 2019 1067 1067 107 107 107 107 107 107 107 107 107 10
& Query Match	7.66 7.66 7.36 7.36 7.36 7.36 7.36 7.36
Score	10000000000000000000000000000000000000
Result No.	0 000

	Sequence 164. App	Sequence 3, Appli		Sequence 44. Appl	790.	Sequence 3579. Ap	Sequence 3580. An		•••	4	Sequence 4209, Ap	Sequence 4041. Ap	-		_	741	Sequence 3. Appli	Sequence 59, Appl	Sequence 8, Appli	Sequence 58, Appl	Sequence 3171, Ap	Sequence 10718. A	Sequence 2, Appl 1	'n	121		
	10 US-09-070-927A-164	9 US-10-270-336-3	9 US-09-918-995-34956	10 US-09-864-761-44	10 US-09-764-877-790	10 US-09-764-877-3579	10 US-09-764-877-3580	10 US-09-764-877-3581	10 US-09-764-877-3582	-0	9 US-10-198-846-4209	9 US-10-198-846-4041	9 US-10-198-846-4087	-0	9 US-09-764-881-61	9 US-10-106-698-741	9 US-10-232-484-3	US-10-098-841-59	US-10-213-948-8	) US-10-098-841-58	10 US-09-764-877-3171	US-10-198-846-10718	US-09-754-853A-2	US-09-754-853A-3	US-10-098-263B-121417	10 US-09-764-877-534	
	27360	119596	421	499	573	573	573	573	573	785	844	855	860	806	939	1057	2438	5207	5230	5261	32185 1	1197	335913 9	335913 9	25	223	
	71.8	71.8	70.9	70.9	.70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.9	70.0	70.0	70.0	69.1	69.1	
•	15.8	15.8	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6.	15.6	15,6	15.4	15.4	15.4	15.2	15.2	
	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	36	40	41,	42	43	44	45	
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## ALIGNMENTS

RESULT 1

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	17800A									Toxicology Modeling		APPLICATION NUMBER: US/09/917,800A		60/222,040		60/222,880		60/290,029		60/290,645		60/292,336		60/295,798	•	60/297,457		60/298,884		60/303,459						;		ssion No.
•	-03-31/-600A-461 Sequence 461, Application US/09917800A	2A1		Donna	Mark	Kory	Arthur	Michael	, Inc.		44921-5038-US	MBER: US/			2000-07-31	NUMBER: US 60,		NUMBER: US 60,		NUMBER: US 60/		NUMBER: US 60/		NUMBER: US 60/		NUMBER: US 60/		NUMBER: US 60/		NUMBER: US 60/	2001-07-09	1/40	1.2.			norvegicus		Genbank Accession No.
	Applicati	Patent No. US20020119462A1			2		Castle, Ar	Elashoff, Michael	Gene Logic, Inc.	OF INVENTION: Molecular	E: 44921-	CATION NO	FILING DATE:			Z		z		z		z		z		z		z				SEC ID NOS: 1/40	racentin ver			Rattus norve		NOI:
12-00-017-000%	1/-000A-4 nce 461,	t No. US2	0								1		ENT FILLIN		7	APPLICA	FILLING	APPLICA	FILING	-				٠.		APPLICA	FILING				1 1 1	ž į	. •	LENCTH: 321	: ă	<u>::</u>	FEATURE:	-09-917-800A-461
100-01	Seque ;	; Paten	; GENER	, APPL	; APPL	; APPL	; APPL	; APPL	; APPL	; TITLE	FILE	; CURRENT	; CURRENT	; PRIOR	, PRIOR	PRIOR	PRIOR	; PRIOR	; PRIOR	; PRIOR	; PRIOR	; PRIOR	; PRIOR	; PRIOR	, PRIOR	PRIOR	; PRIOR	PRIOR	PRIOR	; PRIOR	FRIOR	NOMBER	CEO TO NO.	1. 520 .	TYPE:	; ORG2	FEA	; US-09-91

Wed Jul

6812 GCAAAGCACTATCTACAGTG 6831

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APPLICANT: Macina, Roberto A.
APPLICANT: Main Manoj
APPLICANT: Nair, Manoj
APPLICANT: Chen, Selyu
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
FILE REFERENCE: DEX-0214
CURRENT APPLICATION NUMBER: US/09/909,567B
PRIOR APPLICATION NUMBER: 60/219,834
PRIOR FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youchen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILLE OF INVENTION: THERAPY OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 7444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 7879;
    Length 331;
                                            Indels
  DB 10;
Score 16.8; DE
Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.8; Di
Pred. No. 88;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLECATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9851, Application US/10198846
Publication No. US20030099974A1
GENERAL INFORMATION:
                                                                                                                                                                                                         6812 GCAAAGCACTATCTACAGTG 6831
                                                                                    3 AAAGCACTAGCTTCAGTGTG 22
                                                                                                                            28 AAAGCACGAGATTCAGTGTG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1, 2, 7877, 7878, 7879
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 7444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.4%;
ilarity 90.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapien
US-09-909-567B-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-10-198-846-9851
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LENGTH: 7879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REPERBNCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: G0/082,567
PRIOR FILING DATE: April 21, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 219;
                                                                                                 APPLICANT: Yuanhao Yu,
TITLE OF INVENTION: Recombinant Oncolytic Adenovirus for
TITLE OF INVENTION: Human Melanoma
FILE REFERENCE: CELL-021
CURRENT APPLICATION NUMBER: US/10/053,886
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 09/814,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.6%; Score 16.2; DB 9;
85.7%; Pred. No. 1e+02;
vative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCATION: (214)...(219); OTHER INFORMATION: XhoI restriction site US-10-053-886-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)...(6)
OTHER INFORMATION: EagI restriction site
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
EQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2504, Application US/09294093B Patent No. US20010051335Al GENERAL INFORMATION:
APPLICANT: Lalgudi, Raqhunath. V
                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 09/814,351
PRIOR APPLICATION NUMBER: 09/814,351
PRIOR APPLICATION NUMBER: 60/192,156
PRIOR FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CAAAGCACTAGCTTCAGTGTG 22
Sequence 4, Application US/10053886 Publication No. US20030039633A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: (1)...(6)
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NAME/KEY: misc_feature
LOCATION: (214)...(219)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: M. musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEO ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Zea mays FEATURE:
                                                     GENERAL INFORMATION:
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SEQ ID NO 2504
LENGTH: 295
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Gaps

Indels

OTHER INFORMATION: Incyte ID No. US20010051335A1 700346213H1

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APPLICANT: Sliva, Jeffry C.
APPLICANT: Trueheart, Josh
APPLICANT: Trueheart, Josh
APPLICANT: Trueheart, Josh
APPLICANT: Trueheart, Josh
APPLICANT: Trueheart, Josh
TITLE OF INVENTION: No. US20020182708Alel Regulators of Fungal Gene Expression
FILE REFERENCE: MIC-004
CURRENT APPLICATION NUMBER: US/10/029,180
CURRENT FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: US 60/257,431
PRIOR FILING DATE: 2000112-22
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NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.6%; Score 16.2; DB 9; 85.7%; Pred. No. 2.1e+02;
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SOFTWARE: FastSEC for Windows Version 4.0
SEQ ID NO 91
LENGTH: 2274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9766, Application US/09764891
Publication No. US20030077808A1
                                                         951 GCAAATACTAGCTTCAGTAT 971
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           . 1 GCAAAGCACTAGCTTCAGTGT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9766
LENGTH: 25701
                                                                                                                                                                                                                                         Cali, Brian M.
Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                                                                                                                              Milna, G. Todd
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US-09-764-891-9766
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nes 18; Conserv
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US-09-764-891-9766/c
                                                                                                                                                 S-10-029-180-91/c
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                                                                                                                                                                                                                                                                                                              RESULT 6
US-10-043-487-24/C
Sequence 24, Application US/10043487
; Sequence 24, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
; TITLE OF INVENTION: Protein Protein interactions between Shigella Flexneri polypeptid
; TITLE OF INVENTION: mammalian polypeptides
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
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                                                                                                                  Score 16.2; DB 10; Length 295; Pred. No. 1.1e+02;
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Pred. No. 1.3e+02;
0; Mismatches 3; Indels 0;
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OTHER INFORMATION: Incyte ID No. US20020192678A1 1100140.10
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FUDLICATION NO. US20020192678A1
GENERAL INFORMATION:
APPLICAMT: Huel-Mei Chen
TITLE OF INVENTION: GENES EXPRESSED IN SENESCENCE
FILE REFERENCE: PA-0043 US
CURRENT APPLICATION UNMBER: US/10/071,766
CURRENT PILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PERL Program
SEQ ID NO 30
LENGTH: 1067
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Pred. No. 1.2e+02;
0; Mismatches 3;
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; NAME/KEY: unsure
; LOCATION: 273
: OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-2504
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; LOCATION: 717-759
: OTHER INFORMATION: a, t, c, g, or other
US-10-071-766-30
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PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SEQ ID NO 24
LENGTH: 682
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85.7%; Pre
ative 0;
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Best Local Similarity 85.7%;
Matches 18; Conservative
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Best Local Similarity 85.7%;
Matches 18; Conservative
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US-10-043-487-24
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Matches 18; Conserv
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
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                Sequence 9765, Application US/09764891
Publication No. US20030077808a1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
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Pred. No. 1.9e+02;
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APPLICANT: Wang, Youchen
APPLICANT: Wang, Youchen
APPLICANT: Steinmann, Kathleen
TILE OF INVENTION: NOVEL GENES, COMPOSITIONS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSES
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
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PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SEQ ID NO 12317
LENGTH: 522
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Publication No. US20030099974A1
GENERAL INFORMATION:
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Publication No. US20030099974A1
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lillie, James
                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-764-891-9765
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; ORGANISM: Homo sapiens
US-10-198-846-12317
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US-09-764-891-9765/c
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US-10-198-846-7129
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LENGTH: 25758
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PPLICANT: Chen, Wensheng
ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                 ) NAME/KET: misc_feature

; LOCATION: 555, 558, 583, 618, 675, 681, 706, 712, 733, 734, 736, 774,

; LOCATION: 785, 789, 796, 803, 814, 842, 859.

; COTHER INFORMATION: n = A,T,C or G

US-10-198-846-7129
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Pred. No. 2.1e+02;
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ENCE: MRI-049
PLICATION NUMBER: US/10/198,846
                                                                                                                      NUMBER OF SEQ ID NOS: 14084
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7129
LENGTH: 872
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LING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICATION NUMBER: PCT/US01/00669
ILING DATE: 2001-01-30
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ILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/632,366
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APPLICATION NUMBER: US 60/236,359
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Patent No. US20020048763A1
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FILING DATE: 2000;10-04
                       CURRENT APPLICATION NUMBER: US/10/198 CURRENT FILING DATE: 2002-07-18 PRIOR APPLICATION NUMBER: 60/306,220 PRIOR FILING DATE: 2001-07-18
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
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Gaps

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Length 2298; Indels

Score 15.8; DB 10; Pred. No. 2.4e+02; A. Mismatches: 2;

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FILE REFERENCE: LEX-0254-USA
CURRENT APPLICATION NUMBER: US/09/975,326
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 60/239,821
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9, 2003, 02:22:05
                                                                                                                                                                                                                                                                                                                                                                                                        944 GCAAATCACCAGCTTCAGT 962
                                                                                                                                                                                                                                                                                                                                                                                  1 GCAAAGCACTAGCTTCAGT 19
                                                                                                                                                                                                                                                                                           Ouery Match 71.8%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                LENGTH: 2298
TYPE: DNA
ORGANISM: homo sapiens
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IN FETAL LIVER, SIGNAL
                                                                                      NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
ED ID NO 4452
LENGTH: 1947
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Pred. No. 2.3e+02;
0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/10/217,357
CURRENT FILING DATE: 2002-08-09
PRIOR PELICATION NUMBER: US/09/975,326
PRIOR PELICATION NUMBER: US 60/239,821
PRIOR PELICATION NUMBER: US 60/239,821
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 2.
APPLICATION NUMBER: US 09/608,408
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APPLICANT: Turner, C. Alexander Jr.
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Patent No. US20020128458A1
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89.5%;
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                                                 ORGANISM: Homo sapiens
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; ORGANISM: homo sapiens
US-10-217-357-3
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Best Local Similarity
Matches 17; Conserva
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JS-09-864-761-4452
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LENGTH: 2298
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7.4 79.1 822 12 BG676524 7.2 78.2 165 10 BB061457 7.2 78.2 229 17 BH058084	7.2 78.2 277 9 AV293838 7.2 78.2 277 9 AV28045 7.2 78.2 402 17 AQ586256 7.2 78.2 427 17 BH121214 7.2 78.2 454 13 BI536125	78.2 524 10 BE341990 .2 78.2 559 12 BG081637 .2 78.2 598 17 BH533618 .2 78.2 610 17 AQ656158 .2 78.2 613 17 BH351842 /	7.2 78.2 762 17 AZ703949 7.2 78.2 968 12 BF138199 7.2 78.2 1101 17 CNS017M8 17 77.3 832 9 AL579993 8 76 4 274 9 AV712423	8 76.4 287 9 A1472268 8 76.4 289 9 AV099156 8 76.4 31 9 AA998276	6.8 76.4 398 10 AW285513 6.8 76.4 400 10 AW285496 6.8 76.4 406 10 AW680420 6.8 76.4 406 10 AW580420 6.8 76.4 4.2 9 AA754067	4 4 4 4 1 2 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6.8 76.4 499 17 AQ33196 6.8 76.4 506 13 BM328697 6.8 76.4 520 17 AQ565228 6.8 76.4 542 17 AQ685473 6.8 76.4 563 10 BB363430	ALIGNMENTS	AV383817 AV383817 Hal CDNA CLONE 0 AV383817	. 🛥		Fax: 81-75-705-1 Email: kwmakabe@ Locatio 1 .684 /organi /db_xre /clone=
		c 15 c 17 18 19	•		00000000000000000000000000000000000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	) O O O O		RESULT 1 AV383817/C LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM REFERENCE	AUTHORS TITLE JOURNAL COMMENT	FEATURES
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model  Run on: July 8, 2003, 00:47:28; Search time 1115.35 Seconds	Title: US-09-647-780A-11 Perfect score: 22 Sequence: 1 gcaaagcactagcttc	able: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 16154066 seqs, 8097743376	f hits satisfying chosen par length: 0	DB seq		5: em_estov:* 6: em_estpl:* 7: em_estro:* 8: em_htc:* 9: gb_estl:* 10: ch est2:*			21: em_gss_vrt:* 22: em_gss_fun:* 23: em_gss_man:* 24: em_gss_man:* 25: em_gss_puter:* 26: em_gss_prod:* 27: em_gss_rod:*	Pred. No. is the score greater than is derived by and is derived by a score greater the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of the score of	No. Score Match Length DB ID Description  C 1 18 81.8 664 10 AV383817 AV383817 AV383817 AV383817 AV383817 AV383817 AV383817 AV383817 AV383817 AV370100 BMBAC369H  C 2 17.8 80.9 526 17 AA443237 AA443237 IMC037M14  4 17.8 80.9 526 17 AA443237 BH477117 BH477117 BH477117 BH477117 BH477117 BH477117 BH477117 BH477117 BH477117 BH477117 AV315638 AV315638 RPCT-24-1  C 6 17.4 79.1 768 17 BH117517 BH117517 RPCI-24-2

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 gb)RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicilin resistance. Tell 187 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                       A2443237 190237M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC1M0237M14 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                          Mus musculus
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'lab_host-"E. Coli strain XL10-Gold, Ti-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:10090"
clone="UUGC1M0237M14"
clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No. 8.1e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0237 row: M column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 526.
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/organism="Mus musculus"
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Best Local Similarity 90.5%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                (bases 1 to 526)
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Fax: 801 585 7177
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ORIGIN
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AZ443237/C
                                                                                                                    DEFINITION
                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                      KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                                                                                                                                                             HWBAC369H02T7_PSU Brugia malayi Genomic Bac Library 3 Brugia malayi BH770100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.

1 (bases I to 459)

Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster,J., Guiliano,D., Slatko,B. and Blaxter,M.

Genome survey sequences from the human parasitic nematode Brugia
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Fax: +44 131 650 6550

Email: mark.blaster@ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire
Whitton and Dr Mike Quall. The Sequence was generated by The
Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
Bdinburgh, UK.
Seq primer: T? (TAMTACGACTCACTATAGGG)
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBACe3.6; Site_1: BamH I; Brugia malay1
                                                                                                                                                                          Gaps
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                                                                                                                         Length 684;
                                                 others
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Institute of Cell, Animal and Population Biology
University of Edinburgh
                                                                                                                    Ouery Match 81.8%; Score 18; DB 10; L. Best Local Similarity 100.0%; Pred. No. 7.8e+02; Matches 18; Conservative 0; Mismatches 0;
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llarity 90.5%; Pred. No. 7.4e+02;
Conservative 0; Mismatches 2;
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/tissue_type="whole parasite"
/dev_stage="microfilaria (11)"
                                                 182 t
/dev_stage="Fertilized egg"
/note="Organ: embryo"
132 c 148 g 182 t
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/strain="TRS"
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                                                                                                                                                                                                                      4 AAGCACTAGCTTCAGTGT 21
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                                              BASE COUNT
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BH770100/c
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E., SLC, UT

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Gaps

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Length 526; Indels end

us-09-647-780a-11.rst

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library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chorl.org/bacpac/orderingframe.htm). BAC epage: http://ww.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 177 row: N column: 20
                                    Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                                                                                     1. .473
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="RPCI-24-177N20"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_GSSs: RPCI-24-283H21.TV
Contact: Shaying Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.1%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                        /sex-"Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 79.1
Best Local Similarity 94.7
Matches 18; Conservative
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                            Seq primer: SP6
Class: BAC ends.
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BH117517/c
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mamanla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muss.
E. (Abases 1 to 473)
S. Alexman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RFCI-24-177N20.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                       BH477117 590 bp DNA linear GSS 13-DEC-2001
BOHFH90TR BOHF Brassica oleracea genomic clone BOHFH90, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A2915638 1177020.TJ RPCI-24 Mus musculus genomic clone RPCI-24-177020
                                                                                                                                                                                                           Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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//nctor: pHOSI, Site_1: BstXI; 2-3 kb sheared
//nctor: pHOSI, Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOSI using BstXI linkers"
124 c 106 g 207 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cdtcwn@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TR
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                  Whole genome shotgun sequencing of Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                    MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHFH90"
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1. .590
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                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Other_GSSs: BOHFH90TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chris Town
                                                                                                                                                                                          Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301-838-3523
Fax: 301-838-0208
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AZ915638
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BH477117
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A2915638
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BH117517 768 bp DNA linear GSS 19-JUL-2001
RPCI-24-283H21.TJ RPCI-24 Mus musculus genomic clone RPCI-24-283H21
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/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCT-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end
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Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 768)
                                                                                                                               BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejongémail.cho.org). Clonnes may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC eppge: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 283 row: H column: 21
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Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                     Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                        Score 17.4; DB 17;
Pred. No. 1.2e+03;
                                                                                                                                                                                             187 t
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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1. 768
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RESULT 8
BE061457/c
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                                                                              /gcw."Male"
/cell_type="Spleen/Brain"
/cell_type="Spleen/Brain"
/coll_type="Spleen/Brain"
/note="Vector: prakBAG1; Site_1: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTAKBAG1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG676524 822 bp mRNA linear EST 01-MAY-2001 602622988F1 NCI_CGAP_SKn4 Homo sapiens cDNA clone IMAGE:4748036 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7. Primer: Oligo u. . constructed by Life
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Amamalia, Eutherla, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo Average insert size 1.5kb. Library constructed by Life 24chnologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nc1.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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/lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                                                                                                                        Score 17.4; DB 17;
Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.4; DB 12;
Pred. No. 1.7e+03;
0; Mismatches 1;
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Plate: LLAM10598 row: p column: 21
High quality sequence stop: 740.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                              0; Mismatches
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/clone_lib="NCI_CGAP_Skn4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo saptens"
musculus,
                                /db_xref="taxon:10090"
/clone="RPCI-24-283H21"
/clone_lib="RPCI-24"
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94.78;
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94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG676524
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229 bp DNA linear GSS 18-JUL-2001
, DNA sequence.
BH058084
BH058084.1 GI:14866697
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/db_xref="taxon:9666"
/clone_lib="BT00247"
/clov_stage="Abro247"
/dev_stage="Abro247"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716. - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This isoquence was derived from the FAPESP/LiCR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=&t2=RC6-BT0247-240
999-002-c05&t3=1999-09-24&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Slmpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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EST 09-JUN-2000
BE061457 165 bp mRNA linear EST 09-JUN-200 RC6-BT0247-240999-002-c05 BT0247 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                          Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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Pred. No. 7,3e+02;
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High quality sequence stop: 165
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/organism="Homo
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86.4%;
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us-09-647-780a-11.rst

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/organism="Solanum tuberosum"
            Location/Qualifiers
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                                                                       Zhao, S., Nlerman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Generation of ESTs from potato leaves and petioles
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potato leaves and petioles Solanum tuberosum cDNA clone
'' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                     library availability, please contact Pieter d. Jong (pde)ong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC epage: http://www.iigr.org/tdb/bac_ends/mouse/bac_end_intro.htmlPlate: 337 row: N column: 15
                                                                                                                                                                                                                                                                                            Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
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                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
Thy Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Unpublished (1999)
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/clone_lib="RPCI-24"
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                                                                                                                                                                             Contact: Shaying Zhao
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86.4%;
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90 د
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van der Hoeven, R.S.
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AV270745 AV270745 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930551J19 3', mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9222
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Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki
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Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Carninci,P. and Hayashizaki,Y.
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                                                                                                                                                                     /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.2; DB 12;
Pred. No. 9.7e+02;
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URL:http://genome.gsc.riken.go.jp/
                                                     /db_xref="taxon:4113"
/clone="cSTB41L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
/cultivar="Kennebec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 g
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                                                                                                                                                                                                                                                                                                                                                /lab_host-"SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                liquid nitrogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.2%;
llarity 86.4%;
Conservative
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/sex="Male"
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Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepared by using trehalose thermo-activated reverse
transcriptuse and subsequently enriched for full-length by
cap-trapper. Second strand CDNA was prepared with the
primer adapter of sequence [5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ586256
RPCI-11-451J22.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-451J22
                                                                                                                                                                                                                                                                                                                                                                                                                                                    primed with a primer [5'
GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                     clone_lib="RIKEN full-length enriched, adult male testis
                                                                                                                                                                                                                                                                                                                                                                                                                               contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 402)
                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                   Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                             note-"Site_1: Sall; Site_2: BamHI; cDNA library was
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Pred. No. 1e+03;
0; Mismatches 3; Indels C
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Other_GSSs: RPCI-11-451J22.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
                                                                                                                     'organism="Mus musculus"
'strain="C57BL/6J"
                                                                                                                                                               'db_xref " taxon:10090"
                                                                                                                                                                                                                                                                  tissue_type="testis"
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                                                                             Location/Qualifiers
                                                                                                                                                                                    clone="4930551J19"
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                                                                                                                                                                                                                                                                                     dev_stage="adult'
lab_host="DH10B"
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Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                               sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , DNA sequence.
AQ586256
                                                               further details
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                     19-44 (1999)
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AQS86256/c
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                                                                               FEATURES
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PRCI-24-374F2.TV RPCI-24 Mus musculus genomic clone RPCI-24-374F2, DNA sequence.
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other, GSSS: RPCI-24-374F2.TJ
Contact: Shaying Jahao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
The: 301 838 0208
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chort.org/bacpac/orderingframe.htm). BAC epage: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 374 row: F. column: 2
                                                                                                                                                                                                                                                                                                                                                                EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17;
                                                                                                                                                                                                                                                                                                                           /set__turn_
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1
RPCIII. Human Male BAC Library"
RA n n 131 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.2;
Pred. No. 1.
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                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="RPCI-11-451J22"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="RPCI-24-374F2"
                                                                                                                                                                                                            /db_xref="GDB:7673037
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                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 GCAAAGCACTAGCTGTACTGTG 132
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                                                                                                                                                           1. .402
/organism="Homo
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86.4%;
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potato.
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                                      LOCUS
DEFINITION
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                                                                                                                                         SOURCE
                        BE341990/c
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AUTHORS
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KEYWORDS
        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                            EST 30-AUG-2001
   cloned in the pTARBAC1 cloning vector at the using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 454)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from day 20 and day 40
                                                                                                                                         Gaps
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                                                                                                        Length 427;
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                                                                                                                                                                                                                                                                                       BI536125 454 bp mRNA linear 390375 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4396
Fax: 402 762 4390
                                                                                                        DB 17;
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0; Mismatches 3;
                                                                                                                    Pred. No. 1.4e+03;
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                                                                                                      Score 17.2;
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Seq primer: ATTAGGTGACACTATAG
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/lab_host="DH10B"
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BACKWARD: GTTTTCCCAGTCACGACG
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9; Conservative
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86.4%;
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BI536125
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264 GCAAAGCAAGAACTTCAGTGTG 285

1 GCAAAGCACTAGCTTCAGTGTG 22

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524 bp mRNA linear EST 17-JUL-2000 Cornell University Solanum tuberosum cDNA
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                                                                                                                                                                                            Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

[ (Dases 1 to 524)

van der Hoven,R., Bezzerides,J., Bachem,C., Horvath,B., Visser,R.,Holt,T.E., Liang,F., Hansen,T.S., Utterback,T., Bowman,C.L., Doan,B., Bougti,O., Buell,C.R., Ronning,C.M., Tanksley,S.D. and Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; RNA was supplied by Christian Bachem & Beatrix Horvath(Laboratory of Plant Breeding, Dept. of Plant Sciences, Wageningen University, The Netherlands). Total RNA was isolated from developing axillary buds of potato nodal stem cuttings cultured on medium for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        taken of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="potato stolon, Cornell University"
/tissue_type="axillary buds of stem explants, swelling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al. (Plant Journal 1996). Tissue samples were taken stages corresponding to growing stolons and the early
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.2%; Score 17.2; DB 10;
86.4%; Pred. No. 1.6e+03;
ilve 0; Mismatches 3;
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'lab_host="SOLR"
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clone cSTA18117, mRNA sequence
BE341990
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/clone="cSTA18117"
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Job time : 1119.5 secs
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Matches 19; Conserv
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 8, 2003, 00:45:53; Search time 242.107 Seconds (without alignments) 2644.537 Million cell updates/sec Run on:

US-09-647-780A-12 22 1 ggtcatcattccagatgaagag 22 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4109280 Total number of hits satisfying chosen parameters:

2054640 segs, 14551402878 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 100 Listing first 45

Gen Emb1 Database :

em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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## ALIGNMENTS

	12 22 bp DNA 11near PAT 07-SEP-2000	ce 12 from Patent W09953077.	1.2	12.1 GI:10040985		tic construct.	tic construct	cial sequences.	ses 1 to 22)	Schwartz, J.C., Gros, C., Ouimet, T., Rose, C., Bonhomme, M.C. and	netti,p.	Novel nep ii membrane metalloprotease and its use for screening	tors useful in therapy
	AX014712 22 b	DEFINITION Sequence 12 from Patent W09953077	AX014712	AX014712.1 GI:10040985		synthetic construct.	synthetic construct	artificial sequences.	l (bases 1 to 22)	Schwartz, J.C., Gros, C., Ouimet	Facchinetti, P.	Novel nep it membrane metallop	inhibitors useful in therapy
RESULT 1 AX014712	rocus !	DEFINITION	ACCESSION AX014712	VERSION	KEYWORDS .	SOURCE	ORGANISM		REFERENCE 1	AUTHORS		TITLE	

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818 GGTCATCATTCCAGATGAAGAG 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Novel nep ii membrane metalloprotease and its use for screening inhibitors useful in therapy inhibitors useful 10 therapy Patent: WO 953077-A 1 21-0CT-1999; INST NAT SANTE RECH WED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
LOCATION/QUALIFIERS
Patent: WO 9953077-A 12 21-OCT-1999;
INST NAT SAUTE RECH MED (FR): SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR): OUIMET TANJA (FR): ROSE CHRISTIANE (FR); BONHOWME MARIE CHANTAL (FR): FACCHINETTI PATRICIA (FR)
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Schwartz,J.C., Gros,C., Ouimet,T.; Rose,C., Bonhomme,M.C. and
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                                                                                        1. .22
/organism="synthetic construct"
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/note="oligonucleotide"
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db_xref="taxon:10117"
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                         DNA Linear nac == ***, *** SEQUENCING IN PROGRESS ***,
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Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.,
Manl, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S.,
Worley, K., Wu, C., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Contact: hgsc-help@bcm.tmc.edu
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Tang, H., Tansey, J., Taylor, C., Taylor, T.
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Rattus norvegicus clone CH230-516,
56 unordered pieces.
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Direct Submission
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ROD 11-JUN-2001
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                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                               Consensus quality: 152255 bases at least 040
Consensus quality: 158448 bases at least 030
Consensus quality: 1646461 bases at least 020
Estimated insert size: 155965; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
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Raharjo, S.B., Nurhantari, Y., Saiki, K.
      \label{eq:continuous} Kkeda,\dot{K}., \; Emoto,N., \; Raharjo,S.B., \; Nurhantari,Y., \; fokoyama,M. \; and \; Matsuo,M. \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; of \; \\ 40lecular \; identification \; and \; characterization \; and \; characteriza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain Science Institutute, RIKEN, 2-1 Hirosawa, Wako-shi, Saltama 351-0198, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRKDONLSKESAMVREEMAEVLELET
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2601)
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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      musculus neprilysin-like peptidase alpha mRNA, complete cds
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Maruyama,K., Kiryu-Seo,S., Kiyama,H., Iwata,H., Tomita,T.,
Iwatsubo,T. and Saido,T.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MVERAGWCRKKSPGFVEYGLMYLLLLLGAIVTL
SSLKSDICTTPSCVIAAARILENMDOSRNPCENFYQYACGGWLRHYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="neprilysin-like peptidase alpha"
protein_id="AAG18446.1"
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/db_xref="taxon:10090"
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Shirotani, K. and Saido, T.C.
Direct Submission
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                                                                AF302075.1 GI:10505359
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AF157106.1 GI:6467400
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      DEFINITION
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Mus musculus neprilysin-like peptidase beta mRNA, complete cds.
AF302076
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WMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLK
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IW"
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SSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNSRYSVF
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membrane-bound metalloprotease, the soluble secreted form of which hydrolyzes a variety of vasoactive peptides J. Biol. Chem. 274 (45), 32469-32477 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKMVG
                                                                                                                                                                                     (bases 1 to 2601)
Ikeda,K., Emoto,N. and Matsuo,M.
Direct Submission
Submitsed (08-JUN-1999) International Center for Medical Research,
Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe 6500017, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus I. (bases I to 2652)
Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T., Iwatsubo, T. and Saido, T.C.
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/protein_id="AAF13153.1"
/db_xref="GI:6467401"
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Mus musculus neprilysin-like peptidase gamma mRNA, complete cds.
AF302077
Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
                                                                                                                                                                                                                                                                                                                                                       DQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQERFGLKG
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                                                                                                                                                                                                                                                              translation="MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIGKQI
                                                                                                                                                                                                                                                                                                                    ANQSVIEKRDSEPLLSVLKMVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVL
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Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Institute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
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Shirotani K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Twata, H., Tomita, T., Iwatsubo, T. and Saido, T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases
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                                                                                                                                                                                                        product="neprilysin-like peptidase beta"
protein_id="AAG18447.1"
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Pred. No. 8.8;
0; Mismatches 1;
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                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
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/db_xref="taxon:10090"
25. .2364
/note="endopeptidase"
                                                                                                                                                                     note="endopeptidase"
                                                                           Location/Qualifiers
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Location/Qualifiers
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Shirotani, K. and Saldo, T.C.
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ilarity 95.5%;
Conservative
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Matches 21; Conserv
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21293028
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GAAVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMYIGHEITHGFDDNGR
NFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNG
GVRQAYKAYLRWLADGGKDQRLPGLNIIYAQLFFINYAQVWCGSYRPEFAVQSIKTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF157105 25-NOV-1999 MRNA linear ROD 25-NOV-1999 Mus musculus soluble secreted endopeptidase mRNA, complete cds. AF157105
                                                                                                                                                                                                                                                HLANATVPQEKRHDVTALYHRMDLMELQERFGLKDRVSLCSPGCPGTHSVDQAGLELG
NPPASDSRVLGLKGFNWTLF1QNVLSSVEVELFPDEEVVVYG1PYLENLEDIIDSYSA
                                                                                                                                                                                                                                                                                                             RTMONYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESA
                                                                                                                                                                                                                                                                                                                                       VGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQI
                                                                                                                                                          DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKMVG
                                                                                                                                                                                   GWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPT
                                                                                                                                                                                                                       LGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELET
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FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLD
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ikeda, K., Emoto, N., Raharjo, S.B., Nurhantari, Y., Saiki, K.,
Yokoyama, M. and Matsuo, M.
Molecular identification and characterization of novel
membrane-bound metalloprotease, the soluble secreted form of which
hydrolyzes a variety of vasoactive peptides
J. Biol. Chem. 274 (45), 32469-32477 (1999)
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/product="neprilysin-like peptidase gamma"
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700 c 766 g 542 t
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/db_xref="G1:6467399"

    .2892
    /organism="Mus musculus"

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95.58;
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Query Match Local

Best Loc Matches

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BASE COUNT ORIGIN

RESULT 9' AX033272/c LOCUS

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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AL607032 208249 bp DNA linear HTG 24-JUL-2002 Mus musculus chromosome 4 clone RP23-15L19, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
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DGGKDQRLFGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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IDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRK
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AF176569 2925 bp mRNA linear ROD 11-MAY-2000
Mus musculus neprilysin-like metallopeptidase 1 (N11) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 2925)
Ghaddar,G., Ruchon,A.F., DesGroseillers,L. and Boileau,G.
Direct Submission
Submitted (09-AUG-1999) Biochemistry, University of Montreal, 2900
Edouard Montpetit, Montreal, Que H3T 1J4, Canada
Location/Qualifiers
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Ghaddar,G., Ruchon,A.F., Carpentier,M., Marcinkiewicz,M., Seidah,M.G., Crine,P., Desgroselllers,L. and Boileau,G. Molecular cloning and biochemical characterization of a new mouse testis soluble-zinc-metallopeptidase of the neprilysin family Blochem. J. 347 (Pt 2), 419-429 (2000)
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MUS MUSCULUS
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'protein_id="AAF69247.1"
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Pred. No. 8.8;
0; Mismatches 1;
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797 c 836 g 582
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/db_xref="taxon:10090"
/tissue_type="testis"
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Best Local Similarity 95.5%;
Matches 21; Conservative
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/gene="N11"
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Mus musculus
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AL607032/c
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Boileau, G. and Desgroseillers, L.

New metalloproteases of the neprilysin family

Patent: WO 0047750-A 12 17-ANG-2000;

BOILEAU GUY (CA); DESGROSEILLERS LUC (CA); UNIVERSTIE DE MONTREAL
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DQNLSKESAMVREEWAEVLELETHLANATVPQEKRHDVTALYHRWDLMELQERFGLKG
                                                                               QIVFPAGILQPPFFSKDQPQSLNFGGIGMYIGHEITHGFDDNGRNFDKNGNMLDWWSN
FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSLGENIADNGGVRQAYRAYLRWLA
DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                  KSTVRELIEKIRSVEYDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHL
DEEYSSLIFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLMIIGAAVVNAFYSPNRN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                     Length 2892;
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'db_xref="GI:10280088"
'translation-"MVERAGWCRKKSPGFVEYGLMVLLLI
                                                                                                                                                                                                                                                     Score 20.4; DB 10;
Pred. No. 8.8;
); Mismatches 1;
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Pred. No. 8.8;
0; Mismatches 1;
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                                                                                                                                                       LPGFSEAFHCPRGSPMHPMKRCRIW"
774 c 827 g 574 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX033272 2925 bp
Sequence 12 from Patent WO0047750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1013 GETCGTCATTCCAGATGAAGAG 992
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                                                                                                                                                                                                                                                                                                                                                                         962 GGTCGTCATTCCAGATGAAGAG 941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AX033272.1 GI:10280087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 92.7%;
l Similarity 95.5%;
21; Conservative
                                                                                                                                                                                                                                                  92.7%;
ilarity 95.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX033272
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BASE COUNT ORIGIN

RESULT 10 AF176569/c

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Length 2925;

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complement(join(184. .261,357. .512,992. .1073,1554. .1893,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/), searches of the complete sequence against NCBI none redundant protein database (nr) (ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RMIPSAKLPVFQNGAHVIYRAFDIIQYLDRLSVHLSGEIVPVNTEVYQWMQKVDSWNP
WYELTHPPIKTEYSKFISRVLLARMBARDJLASNYHAKIRBAYETBUKLKDPDIM
KOSEBELSKLLDDVBAQLNNGKYLAGDEFSPADSVFIPILARITLLDDEEYINCRPR
LLEYYTLVKQRPSYKVAIGKFFGGWKKYRTLFKTSFFLCVRTLFRKY
                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (27-JUW-2002) Han Bin, National Center for Gene Research,
Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233,
CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGDFGRLGHGNSSDVFTPQPVKALQGIKIKQIACGDSHCLAVTWAGEVQSWGRNONGQ
LGLGTTEDSLLPQKIQSFEGVCVKMIAAGAEHTAAVTEDGDLYGWGWGRYGNLGLGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWGRGEDGQLGHGDAEDRLVPTVLSGFDAAAPGITSVICGADHTTAYSEDEQQVYSWG
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                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                               Fu,G., Wang,S.Y., Ren,S.X., Lv,G., Lin,W., Gu,W.O., Zhu,G.F.,
Tu,Y.F., Jia,J., Yin,H.F., Zhang,Y., Cai,Z., Chen,J., Kang,H.,
Chen,X.Y., Shao,C.Y., Sun,Y., Hu,O.P., Zhang,X.L., Zhang,W.,
Wang,L.J., Ding,C.W., Sheng,H.H., Gu,J.L., Chen,S.T., Ni,L.,
Zhu,F.H., Han,B., Feng,Q., Huang,Y.C., Li,Y., Zhu,J.J., Zhao,Q.,
Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L., Weng,Q.J.,
Zhang,L., Lu,Y.Q., Yu,S.L., Liu,X.H., Lu,T.T., Zhang,Y.J., Lu,Y.,
Li,C., Li,T., Zhang,Y., Hu,H., Jia,P.X., Qian,Y.M., Ying;K.,
Zhou,B., Chen,Z.H., Hao,P., Zhang,L., Wu,M., Zhang,R.Q., Guan,J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Organ sativa Japonica (nipponbare) genomic DNA, chromosome 4, BAC clone: OSJNBD0086G13.
On Jul 12, 2002 this sequence version replaced g1:15620782.
Web site: http://www.ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prediction programs including Fgenesh (http://www.softberry.com/),
genscan (http://CCR-081.mit.edu/GENSCAN.html), GenemarkHMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes were identified by a combination of several methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MDAVMSAADDAGAASGREDPPPAVVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDRLVPEKVSSVENMFLKIPSLYATGLYCQSVTISLLS'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAD41017.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /variety="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CUGI-OSJNBb
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                                                                                                                   Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bhan@ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                             and Hong, G.F.
             Oryza sativa.
        SOURCE
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JOURNAL'
                                                                                                                                         REFERENCE
AUTHORS
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OSJNBb0086G13,
        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                           Insert size: 208149; sum-of-contigs
Insert size: 219051; 2.3% error; agarose-fp
Quality coverage: 12.41x in Q20 bases; sum-of-contigs Quality
coverage: 12.08x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 208249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid; 108752; 100% of reads Chemistry: Dye-terminator; 11% of reads Chemistry: Dye-terminator Big Dye; 88% of reads Consensus quality: 207934 bases at least 040 Consensus quality: 207956 bases at least 020 Consensus quality: 208060 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137304 137403: gap of 100 bp
137404 208249: contig of 70846 bp in length.
Location/Qualifiers
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/note="assembly_fragment:01838
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53647 c 51328 g 49076 t
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Pred. No. 9.3;
0; Mismatches

    Project Information

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/db_xref="taxon:10090"
/chromosome="4"
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aryota, Metazoa, Chordata,
umalia, Eutheria, Rodentia,
(bases 1 to 208249)
                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: bM15L19
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AL606706
AL606706.2 GI:21741205
HTG.
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ilarity 95.5%;
Conservative
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                                                                                                        Submission
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AUTHORS
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JOURNAL
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OSJN00063
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AX146976/c
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LLTTRRAASAASLLLAALPPFPASSPQLPVASAKEDDEAEAREGEGELELELELELER
YTDRDEGFTLLKPVSWPKVEKAGATALFQQEGKGSNNIGIVVNPVRLSTLTEFGTPQF
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EKYAEDQEAFFKDYAGAHAKLSNLGAKFNPPELYQPDAPPTTGAADLQTAAHTPQGPG
                                                                                                                                                                                                                                           PVWGPLASWCCAWLEAIGLIAGIGTQAFAGSQVLQSIILLCTGTNKGGGYLTPRWLFL
                                                                                                                                                                                                                                                                          LMYIGLTFIWAVLNTFALEVIAFLDLISMWWQVIGGTVIVIVLPLVAKTTQPASYVFT
HFBTAPEATGIRSSAYATILSLLVSQYSLYGYDAAAHLTEETKGADKNGPIAILSSIG
                                                                                                                                                                                                                                                                                                                                        IITVFGWAYILALTFSIQDFSYLFDPSNETAGTFVPAQILFDAFHGRYGSSAGAIALL
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SSRSDAI"
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GITPLYGSSLRYTGPASLVWGWVVVSFFTWFVGFAMAEICSSFPTTGSLYFWAAHLAG
                                                                                                                                                                                                                                                                                                                                                                                                          ALLGLPILWINVVFTAITSIATIGWVGGYAVPIFARMVMREEDFSPGPFYLRRASRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLVAFLWICYTCTVFLLPTAYPISAGNFNYAPVALGACLGLIGLWWVLDARRWFKGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MAAQRLAALHAAAPSAFSSTSSASHGRPAARSSTTALLPVALPR
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                                                                                                                                                                                                                                                                                                                                                                              FVIWGSFFFGGLSITTSAARVVYALSRDRGVPLSSVWRRVHPRHRVPANAVWLCAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(51054, .51064,52665, .52692,52912, .52939,
53215, .53309,54838, .54993,55148, .55507))
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59872 ..59939,60259 ..60326,66423 ..60509,61006 ..61080,
61169 ..61246,61374 ..61478,62143 ..62229)
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45284. .45403,46511. .46693,47014. .47094))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(51054. .55507)
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db_xref="GI:21741209"
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db_xref="GI:21741210".
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Jene-"OSJNBb0086G13.5"
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                                                                                                                                      'db_xref="GI:21741208"
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.91339
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MSDAKESATGKVFGAVKRCKDRLCGAAREAEBGAKDKASAGEHGAEEAARGAEEALSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKEIAEDKVFDAASKVKETAVGAKDKVSEAAGKAKERASHVQHGAAETVRNAKDKVSH
AARHARESARERAMDAKDRVSDVAERAEQCTEDAAGRAAQKAARAEEAVKAKAGEAAS
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AKETQKHNHSELQEEYRPSQVEEATCCGTDSCGACTCSDAAQQCNPGPERSENSTPQS
CGDATHQEAVQSKLVRRNVEGAVKSSESDTAKQVGEIQRLNVAARRFPDVDTILWGGL
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LISKCKSANKPLVVAGCVPQGSRDLKELEGISVIGVQQIDRVVEVVEETLKGHEVRLL
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LFHNYTSQAMNREYTVSEFRRVVDTLCELVPGMQIATDIICGFPGETDEDFSGTVNLV
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TEDHTESPLKSQVLLQAAEIENLKILDKLRLAEEKDGLEIHSQKLAEESSYAKELAAAA
AVELKNLAEEVTRLSYENAKLNADLAAAKDQTRSSIQSDTKRRDQENGIFVEELQKEL
                                                       VASCQREAVLEDTLSQRARRESELLKVIEDĀKCHEHDLENELANĀMLVAELKKENSQ
EDLFQFKATQNGYHSSKSDTGRAMSGMEASDNRNWDGVSVSTYEEAKAAYNVQRRRCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLSDIARRARDVASDAAAHLLGGGPREAARTATAVMHLLGFAAAYGASLWVTFVSSYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEMEDIEDVLGPAGIAGGGAAPGLRLPLAAVAVKPKRPRSSRVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHLVHLARRLOIASVC"
89836. .93186
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91425. .91500,91886. .92038,92176. .92268,92361. .92521,
92629. .93186)
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                         complement(join(87600. .87950,88030. .89253))
/gene="OSJNBb0086G13.7"
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join(99664...99827.100088. .101258)
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Deleershijder, W., Wiegers, R. and Weske, M.
Human enzymes of the metalloprocease family
Patent: WO 0136610-A 1 25-MAY-2001;
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53;
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                                                                                                                                                    complement(87600. 89253)
/gene="OSJNBb0086G13.7"
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99664. .101258
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Sequence 1 from Patent W00136610.
AX146976 AX146976.1 GI:14346247
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                 complement (87600.
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19; Conservative
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Search completed: July 8, 2003, 03:34:47
Job time: 245.107 secs
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 AX146980.1 GI:14346251
                                                Homo sapiens
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                                                                                                                                                                                                                                                                          ETLDELGWMDEESKKKAQEKAMSIREQIGHPDYILLEEMNRRLDEEYSNLNFSEDLYFE
                                                                                                                                                                                                                                                                                                                     YGNY SWDLADEONVNGFNTLGENIADNGGVRQAYRAYLKWMAEGGKDQOLPGLDLTHE
QLFFINYAQVWCGSYRPEFALQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPM
HPKERCRVW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plowman, G.D., Whyte, D., Sudarsanam, S., Manning, G., Caenepeel, S. and
                                                                                                                                                              /translation-"CTTPGCVIAAARILQNMDPTTEPCDDFYOFACGGWLRRHVIPET
                                                                                                                                                                           NSRYSIFDVLRDELEVILKAVLENSTAKDRPAVEKARTLYRSCMNOSVIEKRGSOPLL
                                                                                                                                                                                                                                                         RKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMYRELIDKVRTVFV
                                                                                                                                                                                                                                                                                                          <u>EQPQALNFGGIGMVIGHEITHGFDDNGRNFDKNGNMMDWWSNFSTQHFREQSECMIYQ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 08-JUN-2001
                                                                                                                                                                                                           IYIDQPTLGMPSREYYFNGGSNRKVREAYLQFMVSVATLLREDANLPRDSCLVQEDMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 14-DEC-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                             /note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18.8; DB
Pred. No. 64;
0; Mismatches
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Pred. No. 64;
0; Mismatches
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Patent: WO 0183782-A 28 08-NOV-2001;
Sugen, Inc. (US)
Location/Qualifiers
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Sequence 28 from Patent W00183782..
AX319864
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/db_xref="taxon:9606"
620 c 705 g 39
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Sequence 5 from Patent WO0136610.
AX146980
                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
Solvay Pharmaceuticals B.V. (NL)
Location/Qualifiers
                                                                                                                                             /db_xref="GI:14346248"
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1 Similarity 90.9%;
20; Conservative
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1 Similarity 90.9%;
20; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 20; Conserv
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ORIGIN
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DEFINITION
ACCESSION
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AX319864/c
LOCUS
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ORIGIN
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AX146980/c
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VERSION
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
             FEATURES
                                                                              CDS
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MIYQYGNYSWDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWMAEGGKDQQLPGLD
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2262)
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                                                                                                                                   Human enzymes of the metalloprotease family Patent: WO 0136510-A 5 25-MAY-2001; Solvay Pharmaceuticals B.V. (NL) Location/Qualifiers
                                                                                                        Deleersnijder, W., Wiegers, R. and Weske, M.

    .2262
    /note="unnamed protein product"

                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 90.9%;
Matches 20; Conservative
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Sequence 3 Sequence 1 Sequence 3 Sequence 1 Sequence 3 Sequence 3

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Synthetic DNA Sequences Having Enhanced Expression in Monocotyledonous Plants and Method For Preparation Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Synthetic DNA Sequences Having TITLE OF INVENTION: Expression in Monocotyledonous TITLE OF INVENTION: Preparation Thereof NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS: ADDRESSE: Dennis R. Hoerner, Jr., Monsanto Co. STREET: 700 Chesterfield Parkway No. 5689052th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,492
                                              US-08-463-092B-3
US-08-462-109A-1
US-08-462-109A-3
                                JS-08-463-092B-1
                                                                                                                                             US-08-463-179A-3
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Pred. No. 20;
                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/172,333
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 106, Application US/08530492
Patent No. 5689052
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sanders, Patricia R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown, Sherri M.
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86.4%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Dean, Duff A. : Fromm, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1919 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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OPERATING SYSTEM:
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CITY: St. Louis
STATE: Missouri
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               -08-530-492-106/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63198
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                                                   Appl
                                                                                                                              (without alignments)
222.151 Million cell updates/sec
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                                                                                                             8, 2003, 01:24:03; Search time 30.3707 Seconds
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/cgn2_6/ptodata/1/ina/BE_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
             5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/ina/5A_COMB.seq:*/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-09-004-838-116
US-09-263-933-22
5310729-3
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US-08-254-338-1
US-08-775-391-1
US-08-709-609-1
US-08-07118-1
US-09-770-315-3
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US-08-991-953A-1
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US-09-851-896-3
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                                                                                                                                                                                                                                                                                              441362 seqs, 153338381 residues
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             GenCore version
Copyright (c) 1993 - 2003
                                                                            nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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22
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Maximum DB seq length: 200000000
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Match Length DB
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Post-processing:

Database

Result Š

Title: Perfect score:

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scoring table:

Searched:

us-09-647-780a-12.rni

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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,089A
                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 600-1-198 CIP TELECOMMUNICATION INFORMATION:
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Best Local Similarity 86.4%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches
                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: mouse
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGTCATCATTCCAGATGAAGAG 22
                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                          FILING DATE: 31-Mar-1998
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Patent No. 6429001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1975 base pairs
                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
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Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                         COMPUTER READABLE FORM:
                                               STATE: New Jersey
                    CITY: Hackensack
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                                                                USA
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                                                                                       ZIP: 07601
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                                                                                                                                                                                                                                                                                                                                                                    cotyledonous Plants and Method For
    Gaps.
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TITLE OF INVENTION: SIGNAL TRANSDUCER FOR THE INF RECEPTOR SUPER NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 1919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1:30
URRENT APPLICATION DATA: US/08/906,517
APPLICATION WUMBER: US/08/906,517
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
TREERENDE.ZPOCKET NUMBER: MOBT:170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1315 GGTCTTCATTCCTGATGACGAG 1294
                                                                                1315 GGTCTTCATTCCTGATGACGAG 1294
                                        1 GGTCATCATTCCAGATGAAGAG 22
                                                                                                                                                                                         Sequence 106, Application US/08906517 Patent No. 6180774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              · 1 GGTCATCATTCCAGATGAAGAG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 106:
                                                                                                                                                                                                                                                                                                                         Sanders, Patricia
                                                                                                                                                                                                                                                          Brown, Sherri M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTORNEY / AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lee, SOO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 86.4
Matches 19; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512-474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houston
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                                                                                                                                                                     us-08-906-517-106/c
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19;
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Matches
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Gaps

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DB 4; Length 1975;

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                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Chiron Corporation.
TITLE OF INVENTION: Recombinant AAV Packaging Systems:
FITLE REFERENCE: 20263-501
CURRENT APPLICATION NUMBER: US/09/770,315
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,536
PRIOR APPLICATION NUMBER: US 60/178,536
PRIOR APPLICATION NUMBER: US 60/178,536
SOFTWARE: FASTESQ for Windows Version 3.0
SOFTWARE: FASTESQ for Windows Version 3.0
LENGTH: 4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.2; E
Pred. No. 23;
0; Mismatches
1294 GGACACCATTCCGGATGAAGAG 1273
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DB 1; Length 4680;
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Patent No. 5858775
GENERAL INFORMATION:
APPLICANT: JOHNSON, Philip R.
TITLE OF INVENTION: Adeno-Associated Virus Materials and
TITLE OF INVENTION: Methods
. NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: GJOG Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: 1111nois
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.2; DB
Pred. No. 23;
0; Mismatches
               APPLICATION NUMBER: US/08/475,391
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3870 GGTCATGATTACAGACGAAGAG 3891
                                                                        PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/254,358
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: NO. 5786211and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID: NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGTCATCATTCCAGATGAAGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435.
ATTORNEY/AGENT INFORMATION:
NAME: No. 5858/75and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : (312) 474-6300
(312) 474-0448
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LENGTH: 4680 base pairs
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INFORMATION FOR SEQ ID NO:
URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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US-08-709-609-1
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                                                    Sequence 1, Application US/08254358
Patent No. 5658785
GENERAL INFORMATION:
APPLICANT: Joinson, Philip R.
TITLE OF INVENTION: Adeno-Associated Virus Materials and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08475391
Fatent No. 5786211
GENERAL INFORMATION:
APPLICANT: JOHNSON, Philip R.
TITLE OF INVENTION: Methods
ITLE OF INVENTION: Methods
NUMBER OF SEQUENCES:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREPT: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/254,35
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5658785and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
FELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATENTIN Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-254-358-1
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Best Local Similarity 86.4%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                 90909
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                                   US-08-254-358-1
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          RESULT 5
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Gaps

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Query Match

Matches

RESULT 8

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Length 7557;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chiron Corporation
TITLE OF INVENTION: Recombinant AAV Packaging Systems
TITLE REFERENCE: 20263-501
CURRENT APPLICATION NUMBER: US/09/770,315
CURRENT FILING DATE: 2001-01-26
PRIOR PLILICATION NUMBER: US 60/178,536
PRIOR FILING DATE: 2000-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
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Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                  Score 17.2; E
Pred. No. 25;
0; Mismatches
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 8698
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: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGTCATCATTCCAGATGAAGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: recombinant DNA US-09-770-315-2
                                                                                                                                                       ; OTHER INFORMATION: recombinant DNA US-09-770-315-3
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09770315 Patent No. 6429001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08652971
Patent No. 5814507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                  78.2%;
ilarity 86.4%;
Conservative
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: United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cheng, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
STREET: 460 Point Sa
CITY: South San Fran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                           TYPE: DNA
ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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ORGANISM: Unknown
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                                                                          7557
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                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-770-315-2
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                                                                          LENGTH:
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                                                     Length 4680;
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                                                                                                                                                                                                                                                                                                                                                                                             AUURESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                      Adeno-Associated Virus Materials and
Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Chiron Corporation
TITLE OF INVENTION: Recombinant AAV Packaging Systems
FILE REFERENCE: 20263-501
CURREMT APPLICATION NUMBER: US/09/770,315
CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07178
                                                       DB 2;
                                                   Score 17.2; DI
Pred: No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.2; DI
Pred. No. 23;
0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/178,536
PRIOR FILING DATE: 2000-01-26
                                                                                                                                                                          3870 GGTCATGATTACAGACGAAGAG 3891
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                                                                                                                                                                                                                                                                        Sequence 1, Application PC/TUS9507178
GENERAL INFORMATION:
APPLICANT: JOHNSON, PHILIP R.
TITLE OF INVENTION: Adeno-Associat
TITLE OF INVENTION: Methods
                                                                                                                                  1 GGTCATCATTCCAGATGAAGAG 22
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Patent No. 6429001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                 78.2%;
ilarity 86.4%;
Conservative
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4680 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                      Local Similarity
les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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          US-08-709-609-1
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APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
WUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                    Length 5769;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB 2;
Pred. No. 30;
1; Mismatches
                                                                                                                                                                                          1; Mismatches
                                                                                                                                                     Score 17;
                                                                                                                                                                       Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 460 Point San Bruno Blvd. CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   4735 CATCATCCCAGATGARGAG 4753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4735 CATCATCCCAGATGARGAG 4753
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Patent No. 5976852
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TELEFAX: (415) 225-3216
TELEFAX: (415) 952-9881
TELEX: 910 371-7168
NFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                    77.3%;
89.5%;
                                        MOLECULE TYPE: DNA (genomic)
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89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5769 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER
                                                                                                                                                    Query Match 77.3 Best Local Similarity 89.5 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
     single
                                                                                               379..4686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
US-08-769-399-1
                                                                           ; NAME/KEY:
; LOCATION:
US-08-991-258A-1
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                                                                                                                                                                                                                                                                                                                         RESULT 13
US-08-769-399-1
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ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08991258A
Patent No. 592887
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 5769;
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COMPUTER: Floppy disk
COMPUTER: SID FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NATA:
RIGHT NAMER: US/08/991,258A
FILING DATE: 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                    77.3%; Score 17;
89.5%; Pred. No.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAX-1996
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/652,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CATCATTCCAGATGAAGAG 22
                                                                                             33,055
                                                                        NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: PIELECOMMUNICATION INFORMATION:
                                                                                                                                                TELEPHONE: (415) 225-3216
TELERAX: (415) 925-9881
TELEX: 910 371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5769 base pairs
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                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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(415) 398-3249
                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5769 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                            CDS
379..4686
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Best Local Similarity
Watches 17; Conserv
                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-652-971-1
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ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                         GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5769;
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ACETYL-COA CARBOXYLASE AND USES
THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version.#1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,953A
FILING DATE: 16-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 3;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/08611107
Patent No. 5801233
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: GOINICKI, PLOIT
TITLE OF INVENTION: NUCLEIC ACID COTTILE OF INVENTION: THERFOR TITLE OF INVENTION: THERFOR NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING-SYSTEM: PC-DOS/MS-DOS
                 Sequence 1, Application US/08991953A Patent No. 6083748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4735 CATCATCCCAGATGARGAG 4753
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.3%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 5769 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                        STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 781-19
TELEFAX: (415) 398-3249
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379..4686
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; LOCATION:
US-08-991-953A-1
US-08-991-953A-1
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STATE:
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                                   COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
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COMPUTER: Floppy disk
CLASIFICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
PRIOR APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 14-APR-1995
APPLICATION NUMBER: US SN 08/422,560
FILING DATE: 14-APR-1995
ATPORNEY/AGENT INFORMATION:
NAMME: KITChell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: ARCD:221
TELECOMMUNICATION NUMBER: ARCD:221
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0; Mismatches
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10950 GATCATCTTTCCAGGTGAAGA 10930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: July 8, 2003, 09:31:47
Job time : 31.4207 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (512) 418-3000
TELEFAX: (512) 447-7577
INFORMATION FOR SEQ ID NO: 30
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 11748 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.73
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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US-08-611-107-30
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

8, 2003, 00:43:28; Search time 138.224 Seconds (without alignments) 358.431 Million cell updates/sec July Run on:

US-09-647-780A-12 22 Title: Perfect score:

1 ggtcatcattccagatgaagag 22 Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

2185239 segs, 1125999159 residues Searched:

4370478 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

#### SUMMARIES

No. Score   Match Length DB   ID   Description			æ						
Score Match Length DB ID  22 100 0 2765 20 AA228818 22 100 0 2765 20 AA228810 20.4 92.7 2286 24 AAD28130 20.4 92.7 2285 21 AAA63763 18.8 85.5 2076 22 AAF89737 18.8 85.5 2232 24 AAS97186 18.8 85.5 2332 24 AAS97186 18.8 85.5 2340 22 AAF89739 18.8 85.5 2340 22 AAF89739	Result		Query			,			
100.0 22 20 AA228818 100.0 2765 20 AA228810 92.7 2286 24 AAD28130 85.5 2076 22 AAA63763 85.5 2232 24 AAS97186 85.5 2218 24 AAS97186 85.5 2318 24 AAS97186 85.5 2318 24 AAS9738	NO.	Score	Match	Length	DB	ID		Description	
100.0 2765 20 AAZ28810 92.7 2286 24 AAD28130 85.5 2076 22 AAK69773 85.5 2232 24 AAS97186 85.5 2232 22 AAK89739 85.5 2218 24 AAD30580 85.5 2318 24 AAD30580	7	22	100.0	22	20	AAZ28818	t 1 1 1 1 1 1 1 1 1	Rat membrane metal	
92.7 2286 24 AAD28130 85.5 2076 22 AAA63763 85.5 2076 22 AAF89737 85.5 2262 22 AAF89739 85.5 2362 22 AAF89739 85.5 2340 22 AAF89739	c 0	22	100.0		20	AAZ28810		Rat membrane metal	
92.7 2925 21 AAA63763 85.5 2076 22 AAF89737 85.5 2232 24 AAS97186 85.5 2262 22 AAF89739 85.5 2318 24 AAD30580 85.5 2340 22 AAF89738	о С	20.4	92.7		24	AAD28130		Soluble secreted e	
85.5 2076 22 AAF89737 85.5 2232 24 AAS97186 85.5 226.2 22 AAF89739 85.5 2318 24 AAD30580 85.5 2340 22 AAF89738	0	20.4	92.7	2925	21	AAA63763		cDNA encoding neut	٠.
85.5 2232 24 AAS97186 85.5 226 22 AAR89739 85.5 2318 24 AAD30580 85.5 2340 22 AAR89738	c S	18.8	85.5	2076	22	AAF89737		Nucleotide sequenc	
85.5 2262 22 AAF89739 P 85.5 2318 24 AAD30580 F 85.5 2340 22 AAF89738 P	9 0	18.8	85.5	2232	24	AAS97186		Human metalloprote	
85.5 2318 24 AAD30580 F 85.5 2340 22 AAF89738 N	c 7	18.8	85.5	2262	22	AAF89739		Nucleotide sequenc	
85.5 2340 22 AAF89738	დ ე	18.8	85.5	2318	24	AAD30580		Human protease, PR	
	თ	18.8	85.5	2340	22	AAF89738		Nucleotide sequenc	

endopept	neprilysin-1	neprilysin-l	encoding neut	neprilysin-l	SEP endopept	le secr	ng nove	cDNA inc	g novel	m codin		ns buen	B.t.k. P	thuringie	Cry2Aa delta-endot	l gene	CryIIA insecticida	t cell	1 liver	for ge	expres		for ge		used t	genome-deriv	receptor	helper	iated v	Nucleotide sequenc	iated v	iated v	DNA sequence.	Wild-type adeno-as	Adeno-associated v
SEP e	nepri	nepri	encodi	nepri	SEP e	soluble	encoding	SEP	encoding	c glutamicum	Streptococcus	Streptococcus	etic B	lus th	a delt	nsecticidal	4 inse	Human breast	foetal	#3972	brain	pone	#4038	#4172	#3949	genom	TNF r	/irus	Adeno-associated	otide	Adeno-associated	Adeno-associated	ONA se	type a	-assoc
Human	Human	Human	CDNA 6	Human	Human	Human	CDNA 6	Human	DNA er	C glut	Strept	Strept	Synthetic	Bacillus	Cry2A	Insect	CryII	Human	Human	Probe	Human	Human	Probe	Probe	Probe	Human	Mouse	Adenovirus	Adeno.	Nucle	Adeno	Adeno.	AAV2 I	Wild-t	Adeno
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4280	0996	1996	3764	9659	4279	8544	8251	8547	3029	6892	5940	5941	5798	8952.	5561	9680	3312	5341	5830	5506	4048	9533	4105	5486	3958	4084	1619	6327	1481	9931	2989	6974	3750	8006	6326
ABN8428	AAF5966	AAF59661	AAA63764	AAF5965	ABN8427	AAD2854	ABK4825	AAD2854	ABK33029	AAH6689	AAZ3594	AAZ35941	AAQ05798	AAS0895	AAA1556	AAV00396	AAF7331	<b>ABA453</b>	ABA5583	ABA25506	AAK0404	AAK2	AAI14105	AA135486	AAI03958	ABS04084	AAD3161	AAH2632	AAH41481	AAF8993	ABA0298	AA16697	AAF2375	AAT09008	AAH2632
24	22	22	21.	22	24	24	- 24	24	24	22	20	20	11	22	21	19	22	22	22	22	22	22	22	22	22	24	24	22	22	22	24	22	22	17	22
2580	2636	2663	2676	2714	2893	2893	2953	2975	645	528	1260	1260	1905.	1905	1907	1919	1919	1969	1969	1969	1969	1969	1969	1969	1969	1969	1975	4072	4675	4675	4675	4679	4679	4680	7557
5.5	. 5.5	5.5	5.5	5.5	5.5	5.5	5	5.5	8.1	٠.	3.2	٠.	•	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2		2.2						•	8.2	3.2
8	85	8	80	8	8	86	80	86	8	78	78	.78	7	7	78	78	7	78	78	78	78	78	. 4	7	78	7	7	7.	7	7	7	7	7	7	7
18.8		18.8	œ			18.8	18.8	18.8	18	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2
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10	11	12	13	14	15	16	17	18	19	. 20	21		. 2	~	7	~	~	28	29	30	31	32	33	34	35	36	ω	38	39	40	41	42	43	44	45
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#### ALIGNMENTS

AAZ28818 standard; DNA; 22 BP

AAZ28818;

01-FEB-2000 (first entry)

Rat membrane metalloprotease NEPII gene probe #8.

Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; ss; neuron; hormone; pepilde messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; probe; hybridsation. Rat; membrane metalloprotease; neprilysine II; NEPII; neuron; hormone; peptide messenger; inhibitor; detecticardiovascular disease; neurodegenerative disease; gro

Synthetic. Rattus rattus.

15-0CT-1999,

FR2777291-A1

98FR-0004389. 08-APR-1998;

98FR-0004389. 08-APR-1998; (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

Haret C, Bonhomme MC, Facchinetti P; Ouimet T, Gros C, Schwartz JC;

WPI; 1999-593429/51

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membrane metalloprotease designated neprilysine II (NEPII) gene. (AAZ28810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; neurou; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds
                                                                                                                                                                                                neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine
                                                                                                    for detecting the rat
                involved in proteolysis of
                                                                                                                                                                                                                                                                                                                     ö
                            to screen for inhibitors,
           New membrane metalloprotease NEP II, involved in proteolysis neuronal and hormonal peptides, used to screen for inhibitors potentially useful for treating e.g. cardiovascular disease
                                                                                                                                                                                                                                                                                       Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonhomme MC, Facchinetti P;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                     Score 22; DB 20;
Pred. No. 0.33;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
                                                                                                                                                                                                                                                           Sequence 22 BP; 7 A; 4 C; 6 G; 5 T; 0 other;
                                                                                               Sequences AAZ28811-Z28827 represent probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat membrane metalloprotease NEPII gene.
                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                             1 GGTCATCATCCAGATGAAGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                             1 GGTCATCATTCCAGATGAAGAG
                                                                                                                                                                                                                                                                                                                   0
                                                                    Claim 3; Page 22; 29pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA228810 standard; cDNA; 2765
                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haret C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98FR-0004389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98FR-0004389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gros C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR2777291-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouimet T, G
Schwartz JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-0CT-1999
                                                                                                                                                                                                                                disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ28810;
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
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This sequence represents the gene for the rat membrane metalloprotease designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in calls and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of

New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardiovascular disease

WPI; 1999-593429/51.

P-PSDB; AAY44177

Claim 2; Page 12-16; 29pp; French

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Gaps

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(e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such as premature ejaculation, anorgasmia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is SEP consensus DNA sequence found in human, mouse and rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as female sexual arousal disorder -
  disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phillips SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD)
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analgesic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme; gynaecological; antisense-therapy; male erectile dysfunction
MED; female sexual dysfunction; FSD; female sexual arousal disorder;
FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds.
                                                                                                                                                                                                                     ö
                                                                                                                                                                     Length 2765;
in which NEPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endocrine; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wayman CP, Wayman CP,
                                                                                                                                                                                                                        Indels
                                                                                                                        Sequence 2765 BP; 684 A; 735 C; 787 G; 559 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soluble secreted endopeptidase (SEP) consensus DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1664..2286
/*tag- a
/note- "Encodes catalytic domain"
                                                                                                                                                                   20;
                                                                                                                                                                                            0.69;
                                                                                                                                                                        DB
                                                                                                                                                                Query Match
100.0%; Score 22; DB
Best Local Similarity 100.0%; Pred. No. 0.6
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEP;
                                                                                                                                                                                                                                                                                            818 GGTCATCATTCCAGATGAAGAG 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 6; 167pp; English.
                                                                                                                                                                                                                                                                  1 GGTCATCATTCCAGATGAAGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walsh RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD28130 standard; DNA; 2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUL-2001; 2001WO-IB01263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000GB-0017387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                        endocrine disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-155042/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PFIZ ) PFIZER LTD. (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200206492-A1
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD28130;
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endopeptidase metallopeptidase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   psychlatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and psychiatric disorders. NL enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of neurological diseases such as Alzheimer's disease, pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;
                                                                    Length 2286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEP-like enzyme; protein production; protein secretion;
neurological disease; Alzhelmer's disease; pain; psychiatric
fertility; bone disease; abnormal phosphate metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence encodes a murine neutral endopeptidase
                                                                                                                    Indels
                   Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2925 BP; 710 A; 797 C; 836 G; 582 T; 0 other;
                                                                      DB 24;
                                                                 Score 20.4; DE
Pred. No. 4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
332..2629
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "neutral
                                                                                                                                                                                                          694 GGTCGTCATTCCAGATGAAGAG 673
                                                                                                                                                                1 GGTCATCATTCCAGATGAAGAG 22
                                                                                                                                                                                                                                                                                                                          CDNA; 2925 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 3; 59pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boileau G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-CA00147.
                                                                 92.7%;
llarity 95.5%;
Conservative
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P-PSDB; AAB08130.
                                                                      Local Similarity
les 21; Consorr
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AAA63763 standard;
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                                                                 Query Match
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urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peripheral vascular disease; Raynaud's disease; motility disorder; gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion;
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                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; anglaa pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New IGS5 polypeptides useful for treating infections, pain, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
                                                 ;
  Length 2925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mental retardation; dyskinesia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inilammation; chemotherapy induced injury; tumour invasion; immune disorder; arthritis; endotoxin shock; sepsis; diabet
                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of a human metalloprotease enzyme IGS5.
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "metalloprotease enzyme IGS5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infections, pain, cancer, diabetes, obesity, anorexia, Parkinson's disease, acute heart failure, hypotension,
  21;
  DB
                                                    Mismatches
Score 20.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de la Tourette's syndrome; ss
                                                                                                                                                  1013 GGTCGTCATTCCAGATGAAGAG 992
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                                                                                                     1 GGTCATCATTCCAGATGAAGAG 22
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                                                                                                                                                                                                                                                                             AAF89737 standard; DNA; 2076 BP
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99NL-1013616.
2000EP-0201937.
2000NL-1015356.
92.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000; 2000WO-EP11532
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                               21; Conservative
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                       Similarity
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  Query Match
Best Local
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                                               Matches
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The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vasotropic; antimigrafie; analgesic; endocrine; nootropic; tranquiliser; hypotensive; neuroleptic; neuroprotective; anabolic; antilnflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; chaematopoietic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; hamner-related disease; cardiovascular disease; neuronal disease; migralne; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder;
                                                                                                     infarction, peripheral vascular disease, Rapaud's disease, kidney diseases, gastrointestinal disorders, motility disorders and conditions of delayed gastric emptying, post-operative or diabetic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, andotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
                                                                                   cerebral ischemia, cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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y, cardiovascular diseases, sleep subarachnoid hemorrhage, cerebial ischemin lerdi Voscular diseases, arteriosclerosis, neral Voscular diseases, cerebial ischemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                              Sequence 2076 BP; 493 A; 578 C; 636 G; 369.T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human metalloprotease partial DNA sequence #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.8; DE
Pred. No. 24;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 GGTCGTCGTTCCAGATGAAGAG 439
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90.9%;
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Best Local Similarity 90.9
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                                             disorder, epilepsy,
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                                                                                   cerebrovasospasm,
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haematopoietic origin, of the breast, colon, lung, prostrate, cervical, blain, ovarian, blaider or kidney); immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases sexual dysfunction, moded disorders, attention disorders, confittion alsorders, and appropriation, moded disorders, attention disorders, contribution disorders, hypotension, hypertension, psychotic disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a dispnostic tool for a disease or disorders such as those above AAS97159-AAS97195 represent human protease coding sequences and primers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metalloprotease, IGS5, infection, pain, cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension, uthary retention; osteoprosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple sclerogis; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
mental retardation; dyskinesia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
inflammation; chemotherapy induced injury; tumour invasion;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peripheral vascular disease; Raynaud's disease; motility disorder;
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                                                                                                                                                                                                                                                                                                                            Length 2232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of a human metalloprotease enzyme IGS5.
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                                                                                                                                                                                                                                                                           Sequence 2232 BP; 512 A; 620 C; 705 G; 395 T; 0 other;
                                                                                                                                                                                                                                                                                                                         Match 85.5%; Score 18.8; DB 24; Local Similarity 90.9%; Pred. No. 24; es 20; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weske M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGTCATCATTCCAGATGAAGAG
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99NL-1013616.
2000EP-0201937.
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/*tag=
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P-PSDB; AABB3842.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200136610-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-NOV-1999;
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Matches
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The present sequence encodes a human metalloprotease enzyme designated 1GS5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hyperension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulicers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis, Alzheimer's disease, and other neurodegenerative diseases, sleep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases, gastrointestinal disorders, motility disorders and conditions of delayed gastrointestinal disorders, motility disorders and conditions of delayed gastric emptying, post-operative or diabetic gastroparesis, of delayed gastric emptying, cost-operative or diabetic gastroparesis, immune disorders, archititis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such
                                                                                                                                                                                                                                                                                                                                                                                                                            disorder, epilepsy, cardiovascular diseases, arteriosclerosis, cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney
   New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bullmia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as Huntington's disease or Gilles de la Tourette's syndrome
                                                                                                                       Claim 11; Page 8-9; 115pp; English.
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Score 18.8; DB 22; Length 2262; Pred. No. 24; Indels Ouery Match
Best Local Similarity 90...
20; Conservative ò

RESULT 8
AAD30580/c
ID AAD30580 standard; cDNA; 2318 21-MAY-2002 (first entry) 셤

Human protease, PRTS-13 cDNA

Human; protease; PRTS-13; enzyme; gastritis; cirrhosis; Crohn's disease; gastrointestinal disorder; autoimmune; inflammatory; cell proliferative; cardiovascular; developmental; epithelial; neurological; reproductive; AIDS; Acquired Immune Deficiency Syndrome; allergy; rheumatoid arthritis; hepatitis, cancer; psoriasis; Cushing's syndrome; hypothyroidism; eczema; epilepsy; Alzheimer's disease; Huntington's disease; Parkinson's disease; Pick's disease; infertility; vitiligo; drug screening; gene therapy; ss. asthma; atherosclerosis; hypertension; myocardial infarction; epilepsy; anaemia;

/*tag= b 428..1648 338..1651 338..427 /*tag= WO200208396-A2 Homo sapiens sig_peptide mat_peptide 

17-JUL-2001; 2001WO-US22397 31-JAN-2002

benign prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple sclerosis; Alzheimer's disease;

angina pectoris; myocardial infarction; stroke; ulcer; allergy;

neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm;

Subarachnoid hemorrhage; cerebral ischemia; cerebral infarction; peripheral vascular disease; Raynaud's disease; motility disorder;

Metalloprotease, IGS5, infection, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis,

Nucleotide sequence of a human metalloprotease enzyme IGS5.

23-JUL-2001 (first entry)

XX DX DX

AAF89738;

21-JUL-2000; 2000US-220063P

520 A; 628 C; 716 G; 398 T; 0 other; /product= "Mature PRTS-13 protein" 'product- "Human 'PRTS-13 protein" 85.5%; Scor. 90.9%; Pred. No. ... 0; Mismatches 646 GGTCGTCGTTCCAGATGAAGAG 625 Location/Qualifiers 1 GGTCATCATTCCAGATGAAGAG 22 Sequence 2262 BP;

0

Indels

Length 2318;

DB 24;

Score 18.8; DF Pred. No. 24; 0; Mismatches

Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative

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AAF89738/c ID AAF89738 standard; DNA; 2340

RESULT 9

g

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22

1 GGTCATCATTCCAGATGAAGAG

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anaemia, asthma), cardiovascular disorder (atherosclerosis, hypertension, myocardial infarction), cell proliferative disorders (hepatitis, cancer, psortasis), developmental disorders (cushing's syndrome, hypothyroidism), epithelial disorder (vitiligo, keloid, eczema), neurological disorders (epilepsy, Alzheimer's disease, pick's disease, Huntington's disease, Parkinson's disease,), and reproductive disorders (infertility). PRTS
                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                New human protease polypeptide, useful in diagnosis, prevention and treatment of gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated human protease polypeptide (PRTS). PRTS protein and DNA are useful for diagnosing, treating and preventing gastrointestinal disorders (gastritis, cirrhosis, Crohn's disease), autoimmune/inflammatory disorders (AIDS, allergy, rheumatoid arthritis,
                                                                                                                                                                                                                                                  Todd
                                                                                                                                  AR, Hafalia AJA, Lu Dww,
Kallick DA, Nguyen DB, Lee EA, Khan ra,
riffin JA, Policky JL, Ramkumar J, Yang J;
riffin JA, Policky JL, Borowsky ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PRTS DNA is useful creating knockin humanised animals or transgenic animals to model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases, in somatic or germline gene therapy and in microarrays utilising fluids or tissues from patients to detect altered PKIN expression. The present sequence is human PKTS-13 cDNA.
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                                                                                                                                                                                                                        L, Baughn MR, I
1 N, Walia NK, I
Azimzai Y, Lu Y;
                                                                                                                                                                                                                                                                        Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 174-175; 182pp; English.
                                                                                                                                                                                                   Griffin JA,
                                                                                                                                                                           Tribouley CM, Das D, Kallick I
Yue H, Au-Young J, Griffin Ja,
Thangavelu K, Ding L, Kearney
Sanjanwala MS, Yao MG, Burford
                                                                                                                                                                                                                                                                   Elliott VS,
2000US-223544P
2000US-224717P
                                                                                                           (INCY-) INCYTE GENOMICS INC
                                          2000US-225988P
                                                                2000US-227568P
                                                                                                                                                        Gandhi AR,
                                                                                                                                                                                                                                                                                                              WPI; 2002-206082/26.
P-PSDB; AAE19176.
                                                                                                                                                                                                                                                                   Lo TP, Tang YT,
                                                                                                                                                        Delegeane AM,
Tribouley CM;
                                                             23-AUG-2000;
                     1-AUG-2000;
                                             6-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders
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SEP; endopeptidase; enzyme; human; neuropeptide Y1; receptor; male sexual dysfunction; male erectile dysfunction; obesity; anorexia; bullmia; vasotropic; anorectic; therapy; inhibitor; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of an inhibitor of neuropeptide Y in the preparation of \mathfrak m for the treatment or prevention of male erectile dysfunction
                   Human SEP endopeptidase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Naylor AM, Van Der Graaf PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-2001; 2001WO-IB02399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-547828/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2001;
13-JUL-2001;
24-AUG-2001;
                                                                                                                                        Homo sapiens
                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2001;
23-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2001;
                                                                                                                                                                                                                                                CDS
       The present sequence encodes a human metalloprotease enzyme designated 1GS5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, arkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, uleers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis, alzahimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis, cerebral ischemia, cerebral infarction, peripheral vascular disease, maying diseases, kidney diseases, gastrointestinal disorders, motility disorders and conditions of delayed gastric emptying, post-operative or diabetic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, munume disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2340;
gastrointestinal disorder; gastric emptying; gastroparesis; inflammation; chemotherapy induced injury; tumour invasion; immune disorder; arthritis; endotoxin shock; sepsis; diabete; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New IGS5 polypeptides useful for treating infections, pain, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as Huntington's disease or Gilles de la Tourette's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                            /product= "metalloprotease enzyme IGS5"
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Pred. No. 24;
0; Mismatches
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                                                                                                                                        Location/Qualifiers
1..2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deleersnijder W, Wiegers R,
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90.9%;
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31-MAY-2000; 2000EP-0201937.
31-MAY-2000; 2000NL-1015356.
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Best Local Similarity 90.9%
Matches 20; Conservative
                                                                                                                                                                          /*tag- a
                                                                                                                                                                                                                                                                                                                                                                                                                       (SOLV ) SOLVAY PHARM BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-343815/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAB83841
                                                                                                                                                                                                                            WO200136610-A1
                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                   19-NOV-1999;
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                                                                                                                                          Key
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2001GB-0008730. 2001GB-0009910.

2001GB-0011037 001US-0895367

2000GB-0030647

2001US-0905846 2001GB-0020679

note= "the CDS does not include a stop codon"

/product- "SEP"

/partial

.ute= "5' p. 258..2580 /*tag= '

partial vector sequence"

Location/Qualifiers

1..65 /*tag=

/*tag= c /note= "the 3' end of the sequence is missing from Figure 8 of the specification"

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                                                   The present sequence is a nucleotide sequence coding for human SEP, a soluble secreted endopeptidase, with an additional 5' octor partial sequence. The invention relates to the use of an inhibitor of NPY, or an inhibitor of NPY is receptor, especially an inhibitor selective for an NPY or NPY II receptor, especially an inhibitor selective for an NPY or NPY II receptor, especially an endequent of prevention of male sexual dysfunction, especially male crectile dysfunction (MED). The NPY inhibitor may be used with an auxiliary active agent such as an SEP inhibitor. The invention contained as a SEP assay that can be used to detect candidate inhibitors of SEP. In addition to treatment of MED, NPY inhibitors can also be used to treatment of MED, NPY inhibitors can also be used to treat and metabolic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18.8; DB 24;
Pred. No. 25;
0; Mismatches 2;
Disclosure, Fig 8; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGTCATCATTCCAGATGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 85.5%; Sc
Best Local Similarity 90.9%; Pr
Matches 20; Conservative 0;
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medicament

Wayman CP;

2580

RESULT 10 ABN84280/c ID ABN84280 standard; cDNA;

23-SEP-2002 (first entry

ABN84280;

SXXXE

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GGTCGTCGTTCCAGATGAAGAG 952
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Human neprilysin-like membrane metallopeptidase SNEPb cDNA,
                                     AAF59660 standard; cDNA; 2636 BP
                                                                                                                   (first entry)
                                                                                                                   27-APR-2001
                                                                             AAF59660;
RESULT 11
AAF59660/
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respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic; cerebroprotective; hypotensive; cytostatic; antiinflammatory; Human; SNEDb; neprilysin-like membrane metallopeptidase; splice variant; alternative splicing; zinc endopeptidase family; neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia; pain; hypertension; cancer; inflammation; cardiovascular disease; neuronal disease; pancreatic disease; prostatic disease; cardiovascular; hepatotropic; ss.

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99EP-0401767.
                                   99EP-0401767
                                         (SNFI ) SANOFI-SYNTHELABO
                                   5-JUL-1999;
                          Homo sapiens
                                      15-JUL-1999;
                             EP1069188-A1
                                17-JAN-2001.
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New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal Culouscou J; Jagerschmidt A, Agnel M, WPI; 2001-212582/22. P-PSDB; AAB60562.

Claim 5; Page 30-33; 72pp; English.

and hepatic ischemia

WPI; 2001-212582/22. P-PSDB; AAB60563.

The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and the CDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SNEP concletides may be used as hybridisation probes for CDNA and genomic nucleotides may be used as hybridisation probes for CDNA and genomic SNEP or SNEP; to isolate full-length CDNAs and genomic clones encoding SNEPa, SNEP or SNEP or SNEP; to isolate CDNA and genomic clones of SNEP homologues; as research reagents and material for the discovery of treatments and diagnostics for animal and human diseases; and for chromosome identification. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPa, SNEP or SNEP. Such protein, or to purify the proteins by affinity chromatography.

SNEP proteins may also be used in screening for compounds which modulate SNEP endopeptidase activity, and to assess enzymatic cleavage of small molecule substrates in cells, cell-free preparations, chemical libraries and product mixtures. The SNEP proteins (as vaccine compositions), disorder related to abnormal respiratory or hepatic diseases, they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnorm ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, well as cardiovascular, neuronal, pancreatic, prostatic, renal, Proceedings, and SNEP activators or inhibitors may used treat acute and chronic renal insufficiency, renal and hepatic well as cardiovascular, SNEP

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                                                                                                                                                                                                                                                                                                                                             respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic; cerebroprotective; hypotensive; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                         Human; SNEPc; neprilysin-like membrane metallopeptidase;
splice variant; alternative splicing; zinc endopeptidase family;
neuropeptide; peptide hormone; processing, metabolism; oxectine;
drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
                                                                             Gaps
  sequence represents
                                                                           ö
                                                      Length 2636;
                                                                                                                                                                                                                                                                                                                      cardiovascular disease;
                                                                                                                                                                                                                                                   Human neprilysin-like membrane metallopeptidase SNEPc cDNA.
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                  neuronal disease; pancreatic disease; prostatic disease;
                                 Sequence 2636 BP; 601 A; 759 C; 813 G; 462 T; 1 other;
 present
                                                       DB 22;
                                                                             5
                                             Score 18.8; D
                                                                 Pred. No. 25;
0; Mismatches
SNEPb or SNEPc. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agnel M, Culouscou J;
                                                                                                               hypertension; cancer; inflammation;
                                                                                                   1 GGTCATCATTCCAGATGAAGAG 22
                                                                                                                                                                                                                                                                                                                                                                    cardiovascular; hepatotropic; ss.
                                                                                                                                                                                AAF59661 standard; cDNA; 2663 BP
                                                       85.5%;
ilarity 90.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-0401767
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                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SNFI ) SANOFI-SYNTHELABO
expression of SNEPa, CDNA encoding SNEPb.
                                                                  Local Similarity
es 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jagerschmidt A,
                                                                                                                                                                                                                                                                                                                                                                                                                EP1069188-A1.
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                             27-APR-2001
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                                                                                                                                                                                                        AAF59661;
                                                          Query Match
                                                                                                                                                           RESULT 12
                                                                                                                                                                       AAF59661,
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The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SNEP nucleotides may be used as hybridisation probes for CDNA and genomic DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa, as research reagents and material for the discovery of treatments and diagnostics for animal and human diseases; and for chromosome polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal identification. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPa. SNEPD. or SNEPc. Such antibodies are used to isolate or identify clones expressing the protein, or to purify the proteins by affinity chromatography. membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc Claim 5; Page 35-38; 72pp; English. and hepatic ischemia

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SNEP proteins may also be used in screening for compounds which modulate SNEP endopeptidase activity, and to assess enzymatic cleavage of small molecule substrates in cells, cell-free preparations, chemical libraries and product mixtures. The SNEP proteins (as vaccine compositions), SNEP nucleotides, and SNEP activators or inhibitors may used to treat acute and chronic renal insufficiency, renal and hepatic ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as well as cardiovascular, neuronal, pancreatic, prostatic, renal, respiratory or hepatic diseases, they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "neutral endopeptidase metallopeptidase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEP-like enzyme; protein production; protein secretion;
neurological disease; Alzheimer's disease; pain; psychiatric disorder;
fertility; bone disease; abnormal phosphate metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-2
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                              another organ, or to diagnose or treat any disorder related to abnorn expression of SNEPa, SNEPb or SNEPc. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;
                                                                                                                                                                                                                                                                              DB 22; Length 2663;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                            Sequence 2663 BP; 609 A; 769 C; 816 G; 468 T; 1 other;
                                                                                                                                                                                                                                                                                                            ;
;
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                          Score 18.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme NL-2"
                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            1 GGTCATCATTCCAGATGAAGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA63764 standard; cDNA; 2676 BP
                                                                                                                                                                                                                                                                          sh 85.5%;
L Similarity 90.9%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-FEB-2000; 2000WO-CA00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boilean
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P-PSDB; AAB08131.
                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desgroseillers L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200047750-A2
                                                                                                                                                                                                                cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .7-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA63764;
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
AAA63764/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ношо
                                                                                                                                                                                                                                                                                                            Matches
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The present sequence encodes a human neutral endopeptidase metallopeptidase-like enzyme, designated NL-2. The specification also describes NL-1 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used

Disclosure; Fig 4; 59pp; English.

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SNEP
to promote production and secretion of foreign proteins and active biopeptides, using chimeric constructs containing the foreign protein downstream from and in phase with the N-terminal region. The NL enzymes are have been localised to the brain, and may be useful in the treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders. NL enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide processing by the NL-3 enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like membrane metallopeptidases and are the products of alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; SNEPa; neprilysin-like membrane metallopeptidase;
splice variant; alternative splicing; znc endopeptidase family;
neuropeptide; peptide hormone; processing; metabolism; vaccine;
drug screening; renal ingufficiency; hepatic disease; ischaemia; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                         Length 2676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuronal disease; pancreatic disease; prostatic disease; respiratory disease; gene therapy; nephrotropic; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human neprilysin-like membrane metallopeptidase SNEPa cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertension; cancer; inflammation; cardiovascular disease;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                     Sequence 2676 BP; 608 A; 771 C; 823 G; 474 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotides may be used as hybridisation probes for
                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                            Pred. No. 25;
0; Mismatches
                                                                                                                                                                                                                                                           Score 18.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Culouscou J;
                                                                                                                                                                                                                                                                                                                                                          703 GGTCGTCGTCCAGATGAAGAG 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 25-28; 72pp; English.
                                                                                                                                                                                                                                                                                                                                    1 GGTCATTCCAGATGAAGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular; hepatotropic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF59659 standard; cDNA; 2714 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerebroprotective; hypotensive;
                                                                                                                                                                                                                                                           85.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agnel M,
                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-212582/22.
                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                           Query Match
Best Local S
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AAF59659/C
                                                                                                                                                                                                                                                                                                  Matches
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Use of an inhibitor of neuropeptide  $\Upsilon$  in the preparation of medicament for the treatment or prevention of male erectile dysfunction

WPI; 2002-547828/58. P-PSDB; ABB79521.

Disclosure; Fig 7; 179pp; English.

NAME OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART O

The present sequence is a nucleotide sequence coding for human SEP, a soluble secreted endopeptidase. The invention relates to the use of an inhibitor, of NPY II receptor, especially an inhibitor selective for an NPY or NPY II receptor associated with male genitalia, in the preparation of a medicament for the treatment or prevention of male sexual dysfunction, especially male erectile dysfunction (MED). The NPY inhibitor may be used with an auxiliary active agent such as an SEP inhibitor. The invention provides a SEP assay that can be used to detect candidate inhibitors of SEP. In addition to treatment of MED, NPY inhibitors can also be used to treat abnormal drink and food intake disorders, such as obesity, bulimia, anorexia and

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SMEPP or SNEPC; to isolate cDNA and genomic clones of SNEP homologues; as research reagents and material for the discovery of treatments and dagnostics for animal and human diseases; and for chromosome identification. The SNEP proteins may be used as immunogens to produce antibodies mmunospecific for SNEPa, SNEPD or SNEPC. Such protein, or to purify the proteins by affinity chromatography. SNEP endopeptidase activity, and to assess enzymatic cleavage of small molecule substrates in cells, cell-free preparations, chemical libraries and product mixtures. The SNEP proteins (as vaccine compositions), SNEP nucleotides, and SNEP proteins (as vaccine compositions), to treat acute and chronic renal insufficiency, renal and hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                   propulate activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnormal expression of SNEPa, SNEPb or SNEPc. The present sequence represents cDNA encoding SNEPa.
                                                                                                                                                                                                                                                                                                                                                  ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as well as cardiovascular, neuronal, pancreatic, prostatic, renal, respiratory or hepatic diseases. they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
  to isolate full-length cDNAs and genomic clones encoding SNEPa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEP; endopeptidase; enzyme; human; neuropeptide Y1; receptor; male sexual dysfunction; male erectile dysfunction; obesity; anorexia; bulimla; vasotropic; anorectic; therapy; inhibitor; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.5%; Score 18.8; DB 22; Length 2714; 90.9%; Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2714 BP; 621 A; 780 C; 836 G; 476 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   731 GGTCGTCGTTCCAGATGAAGAG 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGTCATCATTCCAGATGAAGAG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN84279 standard; cDNA; 2893 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 90.99
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Matches
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Wayman CP;

Van Der Graaf PH,

Naylor AM,

(PFIZ ) PFIZER LTD. (PFIZ ) PFIZER INC.

2001GB-0011037. 2001US-0895367. 2001US-0905846. 2001GB-0008730 2001GB-0009910

> **04-MAY-2001** 3-JUL-2001

2001GB-0020679

24-AUG-2001;

10-DEC-2001; 2001WO-IB02399

2000GB-0030647

15-DEC-2000;

**06-APR-2001** 23-APR-2001 39-JUN-2001

.ocation/Qualifiers 185..2524

Homo sapiens.

/*tag= a /product= "SEP"

WO200247670-A1

20-JUN-2002.

/*tag=

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Gaps
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85.5%; Score 18.8; DB 24; Length 2893; 90:9%; Pred. No. 25; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                 Search completed: July 8, 2003, 02:18:59
Job time : 139.224 secs
                                                                                               908 GGTCGTCGTTCCAGATGAAGAG 887
                                                                          1 GGTCATCATTCCAGATGAAGAG 22
                                      20; Conservative
                       Best Local Similarity
   Query Match
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Sequence 2893 BP; 658 A; 854 C; 876 G; 505 T; 0 other;

metabolic disorders. ,

us-09-647-780a-12.rnpb

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(without alignments) 273.390 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                          1105431 seqs, 789497651 residues
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Maximum DB seq length: 200000000
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Perfect score:
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Published Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

40. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed derived by analysis of the total score distribution. Pred. N score g and is

# SUMMARIES

ì	Description	Seguence 4 Appli	Sequence 1, Appli	i.	'n	Sequence 79, Appl	Sequence 1927, Ap	Sequence 3972, Ap	Seguence 1, Appli			7	Sequence 1, Appli	Sequence 10, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appl1	Sequence 1, Appli	Sequence 67, Appl
	QI	US-10-017-273A-4	US-09-905-846-1	US-10-017-273A-5	US-09-905-846-5	US-09-893-737-79	US-09-738-626-1927	US-09-864-761-3972	US-10-240-198-1	US-09-782-378A-1	US-09-782-378A-2	US-10-038-972A-12	US-09-804-898-1	US-09-945-681-10	US-10-077-294-1	US-10-163-886-1	US-10-263-127-1	US-10-205-942-2	US-09-738-626-1	US-10-175-523-67
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ф	Query Match	85.5	85.5	85.5	85.5	81.8	78.2	78.2	78.2	78.2	78.2	78.2	78.2	78.2	78.2	78.2	78.2	78.2	78.2	76.4
•	Score	18.8	18.8	18.8	18.8	18	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	16.8
	Result No.	c 1	c 2	ი ი	Ω 4	o 2	9	7	æ	6	10	11	12	13	14	15	16	17	18	c. 19

Sequence 34768, A	Sequence 9815, Ap	Sequence 52, Appl	Sequence 89, Appl	Sequence 7460, Ap	Sequence 3467, Ap	Sequence 3466, Ap	Sequence 824, App	Sequence 825, App	Sequence 823, App	Sequence 12, Appl	Sequence 12, Appl	Sequence 3933, Ap	Sequence 1, Appli		Sequence 12144, A	Sequence 2, Appli	Sequence 1, Appli	Sequence 60, Appl	S,	Sequence 1, Appli	.5.	Sequence 6, Appli	Sequence 16, Appl	Sequence 7, Appli	-
US-09-918-995-34768	US-09-864-761-9815	US-09-774-639-52	US-09-969-130-89	US-09-815-242-7460	US-09-764-877-3467	US-09-764-877-3466	US-09-764-872-824	US-09-764-872-825	US-09-764-872-823	US-10-060-763-12	US-10-063-763-12	US-09-764-877-3933	US-10-041-856-1	US-09-960-352-12444	US-09-918-995-12144	US-09-745-605-2	US-10-105-989-1	US-09-070-927A-60	US-10-175-523-75	US-10-329-960-1	US-09-931-732-15	US-10-142-566-6	US-09-931-732-16	US-10-142-566-7	US-09-878-574-14461
481 9	550 10	865 9	865 9	1575 10	2673 10	3538 10	3656 9	9551 9	15558 9	31124 9	31124 12	32220 10	66479 9	408 10	422 9	1516 10	4398 9	9927 10	85548 9	1830121 9	6 94	6 92	100	103 9	165 10
74.5	74.5	73.6	73.6	73.6	73.6	73.6	73.6	73.6	73.6	73.6	73.6	72.7	72.7	71.8	71.8	71.8	71.8	71.8	71.8	71.8	70.9	. 70.9	70.9	70.9	70.9
16.4	16.4	16,2	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16.2	16	16	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.6	15.6	15.6	15.6	15.6
c 20	c 21	c 22	c 23	24	c 25	c 26	27	28	29	30	31	c 32	33	34	c 35	c 36	c 37	c. 38 :	c 39	c 40	c 41	c 42	43	44	c 45
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## ALIGNMENTS

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Valor, Alasdair M.
Van Der Graaf, Pieter H
Wayman, Christopher P.
FENTION: Treatment of Male Sexual Dysfunction
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                                                                                             LICATION NUMBER: US/10/017,2732
                                                                                                              DATE: 2001-12-12
ION NUMBER: US 60/265,358
ATE: 2001-01-31
ION NUMBER: GB 0030647.2
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/291,722
FILING DATE: 2001-05-17
                                                                                                                                                                                                                                                                           LICATION NUMBER: US 09/905,846
                                                                                                                                                                                                                 LING DATE: 2001-04-06
LICATION NUMBER: GB 0120679.6
ING DATE: 2001-08-24
                                                                                                                                                                                 ATE: 2000-12-15
ION NUMBER: GB 0108730.3
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Best Local Similarity 90.9%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
JS-10-017-273A-4
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1 GGTCATCCAGATGAAGAG 22

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Gaps

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Gaps
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APPLICANT: Roderick Thomas Walsh
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
FILE REFERENCE: PCS10926APME
CURRENT APPLICATION NUMBER: US/09/905,846
CURRENT FILING DATE: 2001-07-13
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red. No. 34;
Mismatches 0; Indels
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APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pred. No. 1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2975
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 79
                                         973 GGTCGTCGTTCCAGATGAAGAG 952
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PRIOR APPLICATION NUMBER: 0017387.2
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/220,908
PRIOR FILING DATE: 2000-07-26
1 GGTCATCCAGATGAAGAG 22
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Patent No. US20020110855A1
                                                                                                                                                    Sequence 5, Application US/09905846 Patent No. US20020102707A1
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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Best Local Similarity 90.9%;
Matches 20; Conservative
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APPLICANT: Ian Dennis Harrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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US-09-893-737-79
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APPLICANT: Roderick Thomas Walsh
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
FILE REFERENCE: PCS10926Apms
CURRENT APPLICATION NUMBER: US/09/905,846
CURRENT APPLICATION NUMBER: 0201-07-13
PRIOR APPLICATION NUMBER: 02001-07-14
PRIOR FILING DATE: 2000-07-14
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PPLICANT: Van Der Graaf, Pieter H
PPLICANT: Wayman, Christopher P.
ITLE OF INVENTION: Treatment of Male Sexual Dysfunction
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Pred. No. 17;
0; Mismatches
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Pred. No. 17;
0; Mismatches
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LOR APPLICATION NUMBER: US 60/265,358

LIOR FILING DATE: 2001-01-31
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IOR APPLICATION NUMBER: US 09/905,846
IOR FILING DATE: 2001-07-13
IOR APPLICATION NUMBER: US 60/291,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 09/895,367
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 2975
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IOR FILING DATE: 2000-12-15
IOR APPLICATION NUMBER: GB 0108730.3
IOR FILING DATE: 2001-04-06
IOR APPLICATION NUMBER: GB 0120679.6
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PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 8
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                                                                Sequence 1, Application US/09905846
Patent No. US20020102707A1
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illarity 90.9%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.5%;
Best Local Similarity 90.9%;
Matches 20; Conservative
                                                                                                          GENERAL INFORMATION:
APPLICANT: Ian Dennis Harrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-846-1
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; ORGANISM: Homo sapiens
US-10-017-273A-5
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Best Local Similarity
Matches 20; Conserv
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Pred. No. 1.1e+02;
0; Mismatches 3; Indels 0
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Pred. No. 98;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/240,198
                                                          FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
PCT/US01/00665
                                          PCT/US01/00668
                                                                                                      FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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APPLICANT: BEARD DR, PETER
APPLICANT: RAJ DR, KENNETH
TITLE OF INVENTION: CYTOTOXIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGTCATCATTCCAGATGAAGAG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 86.4%;
Matches 19; Conservative
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86.4%;
                                                                                                                                                     FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 19; Conserv
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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US-09-864-761-3972
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LENGTH: 4675
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Pred. No. 8:
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PRICH DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/23,366
PRIOR PLILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                         INVENTION: NOVEL POLYNUCLEOTIDES SRENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
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PRIOR FILING DATE: 1999-12-16
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           , Application US/09738626
5. US20020197605A1
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Patent No. US20020048763A1
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                                                                                                      MIZOGUCHI, HIROSHI
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Best Local Similarity 86.4%;
Matches 19; Conservative
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                                                                               NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
                                                                                                                       ANDO, SEIKO
HAYASHI, MIKIRO
                                                                                                                                                                                                                TATEISHI, NAOKO SENOH, AKIHIRO
                                                                                                                                                                                             OKOI, HARUHIKO
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SOFTWARE: Patentin ver. 3.0
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LENGTH: 528
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78.2%; Score 17.2; DB 9; Length 4679; ilarity 86.4%; Pred. No. 1.1e+02; Conservative 0; Mismatches 3: Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: XIAO, WEIDONG
TITLE OF INVENTION: PRODUCTION OF CHIMERIC CAPSID VECTORS
FILL REFERENCE: 102182-14
CURRENT APPLICATION NUMBER: US/09/804,898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . DB 10;
L.1e+02;
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                  TITLE OF INVENTION: AAV VECTORS AND METHODS FILE REFERENCE: 28335/36996US CURRENT APPLICATION NUMBER: US/10/038,972A
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PRIOR APPLICATION NUMBER: PCT/EP 00/01854
PRIOR FILING DATE: 2000-03-05
                                                                                CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SED ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
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Patent No. US20020064878A1
                                                                                                                                                                                                                                              TYPE: DNA
CRCANISM: adeno-associated virus 2
US-10-038-972A-12
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APPLICANT: UNIVERSITE DE NANTES
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SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 4679
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Best Local Similarity 86.4%;
Matches 19; Conservative
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APPLICANT: DURING, MATHEW
XIAO, WEIDONG
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SEQ ID NO 10
LENGTH: 4679
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Matches 19; Conserv
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Pred. No. 1.1e+02;
0; Mismatches 3; Indels 0;
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86.4%; Pred. No. 1.1e+02;
tive 0; Mismatches 3;
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APPLICANT: Sandalon, Ziv
APPLICANT: Gnatenko, Dmitri
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04970
CURRENT APPLICATION NUMBER: US/09/782,378A
                                                                                                                                                                                                                                          APPLICANT: Sandalon, Ziv
APPLICANT: Gnatenko, Dmitri
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04970
CURRENT APPLICATION NUMBER: US/09/782,378A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/237,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Human adeno-associated virus 2
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3865 GGTCATGATTACAGACGAAGAG 3886
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PRIOR FILING DATE: 2000-10-02
                                                                                                                             Sequence 1, Application US/09782378A Patent No. US20020102731A1
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
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Best Local Similarity 86.4%;
Matches 19; Conservative
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                                                                                                                                                                                                    : Hearing, Patrick
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Best Local Similarity
Matches 19; Conserv
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SEQ ID NO 2
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TITLE OF INVENTION: Adeno-Associated Virus Materials and
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TITLE OF INVENTION: Adeno-Associated Virus Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SE: Marshall, O'Toole, Gerstein, Murray 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                         Query Match 78.2%; Score 17.2; DB 10; Best Local Similarity 86.4%; Pred. No. 1.1e+02; Matches 19; Conservative 0; Mismatches 3;
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Pred. No. 1.1e+02;
0; Mismatches 3;
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FILING DATE: 15-Feb-2002
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REFERENCE/DOCKET NUMBER: 31975
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-077-294-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                            1 GGTCATCCAGATGAAGAG :22
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; ORGANISM: adeno-associated virus 2 US-09-945-681-10
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                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10077294
Patent No. US20020159979A1
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Publication No. US20020187129A1
GENERAL INFORMATION:
APPLICANT: Johnson, Philip R
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
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1 Similarity 86.4%;
19; Conservative
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STATE: Illinois
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Best Local Similarity
Matches 19; Conserva
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
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1.1e+02;
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Pred. No. 1.1e+
0; Mismatches
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/292,703 FILING DATE: <Unknown>
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 31975
                                                                                                                                                                                                                                                                                                                                                                          NAME: No. US20020187129Alan
REGISTRATION NUMBER: 35,302
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CLASSIFICATION: <Unknown>
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INFORMATION FOR SEQ ID NO: 1:
                                                                                           ZIP: 60606
COMPUTER READABLE FORM:
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                                                                          COUNTRY: USA
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Matches 19; Conserv
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600 bp mRNA linear EST 20-DEC-2001 4044-75 Mouse E14.5 retina lambda ZAP II Library Mus musculus CDNA, BI989738
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BF186831 EST443118
BE455509 HVSME9001
A7039556 421 PLIEG
AN739556 421 PLIEG
BM110208 EST557744
BQ118381 EST603957
BG476576 602224536
AN702998 TGEST2280
BG406112 SAC34C08.
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AUG60271 AUG60271
AQ655598 HS_2160_A
AQ459342 HS_5062_B
BJ325350 BJ325350
BJ325377 BJ325377
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BH485426 BOGME10TF
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
Gene expression in the developing mouse retina by EST sequencing
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Fax: 713 790 0329
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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/db_xref="taxon:10090"
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AQ060271
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A0568304 HS_5237_B
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Copyright (c) 1993 - 2003
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Tetraodon

the cultivar IR36

etiolated leaf sheath from

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                                    /dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dT. NRA Isolation: cytoplasmic RNA preps
(Manniatis); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb,
Insertion site: TACGTCCACTGAATTCTGAGTG---> Other
information regarding entire library may be found at
http://pga.swmed.edu/bata/Libraries/microarray_cdna_librar
ies.htm."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Straffcornell.edu Cloning and mapping was performed in the Plant Breeding Dept. at Cornell University. DNA Sequencing was done by the Advanced Genetic Analysis Center (ARGAC) at the University of Minnesota. Informatics was done at the Computational Biology Centers (CBC) at University of Minnesota. For mapping information, additional citations and other related information concerning this probe, please refer to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases I to 388)

Causse, M.A., Fulton, T.M., Cho, Y.G., Ahn, S.N., Chunwongse, J., Wu, K., Xiao, J., Yu, Z., Konald, P.C., Harrington, S.E., Second, G., McCouch, S.R. and Tanks, Ley, S.D.
Saturated molecular map of the rice genome based on an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 19-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ars-genome.cornell.edu/cg1%2Dbin/WebAce/webace?db=r1cegenes&class=Marker&object-R2565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
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/note="Vector: pBLUESCRIPT; Derived from mRNA extracted
clone_lib⇒"Mouse E14.5 retina lambda ZAP II Library"
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                       /tissue_type="neural retina"
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Pred. No. 39;
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Senetics 138 (4), 1251-1274 (1994)
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/cultivar="IR36"
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/clone="RZ565"
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Seg primer: M13 Reverse
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ilarity 95.5%;
Conservative
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Dept Plant Breeding
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Fax: 607 255 6683
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682 bp DNA linear GSS 29-SEP-2000 1M065L20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0065L20 R, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
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Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                Length 388;
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University of Utah
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'clone="UUGC1M0065L20"
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                                                                                                      86.4.,
100.0%; Pre
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(O.sativa).
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Mammalia; Eutheria;
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Dunn, D., Aoyagi, A.,
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Contact: Robert B.
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Fax: 801 585 7177
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Query Match 83.6
Best Local Similarity 95.0
Matches 19; Conservative
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KEYWORDS
                                           RESULT 5
AQ568304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/Inde="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NDHM, pregnant uterus
NDHEU, and fettal heart NDHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A. 6.E. clones 260232-265223,
340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                 436 bp mRNA linear EST 02-MAR-1998 af73a01.rl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047624 AA644490
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhin; Hominidae; Homo.
1 (bases I to 436)
Hillier,L., Allen,M., Boyles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kuchan,T., Lary,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., WashG-XI; Watlerston,R. and Wilson,R.
chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance." 135 c 141 g 219 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares_NHHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length: 658 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                             Length 682;
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                                                                                                                                      Indels
                                                                                               Score 18.8; DB 17;
Pred. No. 2.3e+02;
0; Mismatches 2;
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Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:9606
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                                                                                                                                                                                             337 GGGCATCATTCCAGATGAAGTG 316
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90.9%;
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95.0%;
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20; Conserv
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Best Local Similarity
Matches 19; Conserv
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                                         187
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Matches 2
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JOURNAL
COMMENT
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SOURCE
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Email: jwallaceu, washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 813 row: D column: 15
Seq primer: T7
Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 Vector at EcoRI sites 117 g 178 t 6 others
GSS 01-JUN-1999
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602324955F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4413133 5',
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 605)
                                                                                                                                                                                                                                                                                                         Mahairas, G.G.; Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                         S_5237_B1_B08_T7A RPCI-11 Human Male BAC Library Homo sapiens enomic clone Plate=813 Col=15 Row=D, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High Throughput Sequencing Center
University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 3.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=813 Col=15 Row=D"
  DNA
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Location/Qualifiers
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                                                                                                                AQ568304.1 GI:4961524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.68;
95.08;
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AI558754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 22-JAN-2001
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PMO-NN1171-181000-001-h12 NN1171 Homo sapiens CDNA, mRNA sequence.
BF944641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="lorgan: liver; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb Library enriched for full-length clones and constructed by Life Technologies.
this is a NIH_MGC Library."
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                             NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution MGC clone distribution for Clone distribution for Clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 3.6e+02;
); Mismatches 1
                                                                                                                                                                                                                                                                                                               http://image.llnl.gov
Plate: LLAM10138 row: n column: 14
                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 569.
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                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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95.0%;
                                            (bases 1 to 740)
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                                                                                                            Unpublished (1999)
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BF944641/c
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AUTHORS
TITLE
JOURNAL
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profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Clark,M., Johnson,S.L., Lehrach, H., Lee,R., Li,F., Marra,M., Eddy,S.H., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                PCR (U.S. Letters Patent application Institute for Cancer Research)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-NN1171-
181000-001-h12&t3=2000-10-18&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research.Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ь
Б
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI558754 520 bp mRNA linear EST 07-3
fb80b01.y1 Zebráfish WashU MPIMG EST Danio rerio cDNA clone
IMAGE:3718153 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                          Vector: puc18; Site was made by cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ore 18; DB 12;
red. No. 4.5e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Stephen L. Johnson
Washington University School of Medicine
                                                                                                                                                                                                                                                                                           /dev_stage="Adult"
//note="Organ: nervous_normal; V
Site_2: Smarl: A mini-library wa
derived from ORESTES PCR (U.S.
No. 196,716 - Ludwig Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         low stringency conditions.
75 c 94 g 117
                                                                                                                                                                                                               /db_xref="taxon:9606"
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Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /ordanism="Danio rerio"
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                                                                               Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 38
Location/Qualiflers
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                                                                                                                                                                                                                                                                          /clone_lib="NN117]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.00,
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 ATCATTCCAGATGAAGAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: T3 ET from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 81.8
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zebrafish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLYA-No.
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VERSION
KEYWORDS
SOURCE
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In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones
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EST43118 potato stolon, Cornell University Solanum tuberosum cDNN clone cSTA37C3 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asteridae, eusterids I: Solanales; Solanaceae; Solanum.

(bases 1 to 586)
van der Hoeven, R., Bezzerides, J., Bachem, C., Horvath, B.; Visser, R., Holt, I.E., Liang, F., Hansen, T.S., Utterback, T., Bowman, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Tanksley, S.D. and Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For clone information, please contact Research Genetics, Libraries Division, tel# 1-800-711-6195, email- cdna@resgen.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
                                                                                                     'note="Vector: pSPORT1; Site_1: Not1; Site_2: SalI; 1st
                                                                                                                                                                                                                                                                                                                                                                                  single cDNA from each cluster was chosen for sequencing
                                                                                                                                                                                                                                                                                                                                                            data were used to computationally cluster cDNAs, and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     swelling
                                     /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 were sequenced additional times to assess quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="axillary buds of stem explants, stolons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation of ESTs from potato swelling stolons Unpublished (1999)
clone_lib="Zebrafish Washu MPIMG EST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.8; DB 9;
Pred. No. 6.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/potato/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Solanum tuberosum"
/cultivar="Bintje"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="potato.stolon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research Rockville, MD 20850, USA Tel: (301)838-0200
                                                                                 'lab_host="XL1-blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4113"
/clone="cSTA37C3"
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90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Conservative
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Best Local 9
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ORIGIN
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COMMENT
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BF186831
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae, Pooldeae
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                                                                                                                                                                                                            described in Bachem et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wing, R., Close, T.J., Kleinhofs, A., Wise, R.; Begum, D., Frisch, D., Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Close, S.J., Oates, R. and Main, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Development of a genetically and physically anchored EST resource for barley genomics: Morex pre-anthesis spike cDNA library
                                                                                                  Horvath(Laboratory of Plant Breeding, Dept. of Plant Sciences, Wageningen University, The Netherlands). Total RNA was isolated from developing axillary buds of potato nodal stem cuttings cultured on medium for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     combined, poly(A) RNA was purified from the mixture, one
                                              /note="Wector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Khol; RNA was supplied by Christian Bachem & Beatrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                                                                                                                                                                                                               al. (Plant Journal 1996). Tissue samples were taken stages corresponding to growing stolons and the early stages of tuber formation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVSNEg0017115f Hordeum vulgare pre-anthesis spike EST ilbrary HVcDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone HVSNEg0017115f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jul 26, 2000 this sequence version replaced gi:9465256 Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                              Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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/tissue_type="pre-anthesis spike"
                                                                                                                                                                                                            Introduction of tuber formation as
                                                                                                                                                                                                                                                                                                                                                                                           Score 17.8; DB 12;
Pred. No. 6.5e+02;
0; Mismatches 2;
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/dev_stage="1 to 3 days".
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4513"
/clone="HVSMEg0017115f"
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Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 556.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE455509.2 GI:13154820
                                                                                                                                                                                                                                                                                                                                                                                              80.9%;
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Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                            Xho1;
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Best Local Similarity 90.5%;
Matches 19; Conservative
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                     19; Conservative
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Fax: 5105596440
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BM110208.1
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primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close lab (Choi) at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing) Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu. Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or abbove. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 16-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 637)
Man, C.-H., Yu, Y., Sasinowski, M. and Wing, R.A.
Cotton EST Database: Sequence Analysis of 2000 cDNA Clones from an Abscission Zone Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tracheophyta;
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/note="Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI055512 637 bp mRNA linear EST 16-JUL-coau0004D05 Cotton Boll Abscission Zone cDNA Library Gossypium hirsutum cDNA clone coau0004D05 5', mRNA sequence.
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Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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Pred. No. 6.5e+02;
0; Mismatches 2;
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Pred. No. 6.6e+02;
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Seq primer: SPO30 (AACAGGTATGACCATGATTA)
High quality sequence stop: 363.
Location/Qualifiers
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100 Jordan Hall, Clemson, SC 29634, USA
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90.5%;
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Best Local Similarity
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Best Local Simi
Matches 19;
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The tissue source for this library is xylem. The xylem tissue was harvested in spring and summer from branches of seed orchard trees which are clones of the same genotype. Branches were 4-6 inches in diameter. The CDNAS were directionally cloned into Lambda 2ap and were rescued as a Bluescript derivative in the EcoRI and XhoI
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EST557744 potato roots Solanum tuberosum cDNA clone cPR07M1 5' end,
                                                                                                                                                                                                        EST 15-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                  ukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ipermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus;
(bases_1 to 642)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: csk@s27w007.pswfs.gov
The sequence entry for this EST has been reverse complimented and
is being submitted in the sense orientation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="xylem"
//issue_type="xylem"
//note="vector: lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
//note="vector: lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
//note="vector: lambda zarvested" in spring and summer from brancher tissue was harvested in spring and summer from brancher
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                                                                                                                                                                                                     AA739656 642 bp mRNA linear EST 15
421 PtIFG2 Pinus taeda cDNA clone 8707M 3', mRNA sequence.
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Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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Pred. No. 6.7e+02;
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/clone="8707M"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Claire S. Kinlaw USDA IFG Dendrome Project
                                                                                                                                                                                                                                                                                                                                                                                                          dukaryota; Viridiplantae;
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                                 41 GGTCTTCATCCCAGATGAAGA
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1 GGTCATCATTCCAGATGAAGA
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/clone_lib="mixed potato tissues"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Wetcor: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University, Tanksley lab.; Sequencing: The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium: Roots were isolated two weeks after placing the stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST603957 mixed potato tissues Solanum tuberosum cDNA clone STMEA47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: potatofilgr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta. Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum. I (bases I to 766) Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation of a set of potato cDNA clones for microarray analyses
              l (bases 1 to 689)
van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
ימו מאר האיזייה א Bougri,O., Buell,C.R., Ronning,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                     For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cuttings from in vitro grown plants on medium.
142 c 137 g 191 t.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                      'dev_stage="in vitro grown stem cuttings"
|lab_host="SOLR"
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9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                    Generation of ESTs from potato roots
Unpublished (2001)
Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
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/cultivar="Kennebec or Binjte"
                                                      Utterback, T., Chlemingo, A., Bougri, O., Tanksley, S. and Baker, B.
                                                                                                                                                                                                                                                                     1. 689
/organism="Solanum tuberosum"
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/clone="STMEA47"
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                                                                                                                                                                                                                                                                                                                                              clone="cPR07M1"
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                                                                                                                                                                           Email: cdna@resgen.com
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BQ118381
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90.5%;
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Contact: Robin Buell
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BG476576 869 bp mRNA linear EST 21-MAR-2001
602524536F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642976 5',
                                          /note-"vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
tubers, or cots."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /issue_type="melanotic melanoma"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by Oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 7.4e+02;
); Mismatches 2;
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Pred. No. 7.1e+02;
): Mismatches 2;
'tissue_type="mixed tissues"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:4642976"
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                                                                                                                                                                                                                                                                                                                                                               2 GTCATCCAGATGAAGAG 22
                                  /lab_host-"SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BG476576
BG476576.1 GI:13408855
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Best Local Similarity 90.5%;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Search completed: July 8, 2003, 09:21:43 Job time: 1120.5 secs

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 00:45:53; Search time 220.098 Seconds

(without alignments)
2644.537 Million cell updates/sec
Title: US-09-647-780A-13*

Sequence: 1 cgatgaggacgcctgttg 20
Sequence: 1 cgatgaggacgcctgttg 20
Scoring table: IDBNTINY_NUC
Gapop 10.0, Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : GenEmbl:*

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1 90_bas:*

2 9b_htg:*

4 9b_om:*

5 9b_ln:*

6 9b_ov:*

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11 9b_pr:*

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12 9b_vr:*

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18 em_hum:*

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40: em_htgo_mus:*
41: em_htgo_other:*
Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	DNA					•				Rose, C.		ase and	•	
	20 bp	WO9953077.				•				Ouimet, T.,		talloprote	rapy	
	AX014713 .	Sequence 13 from Patent W09953077.	AX014713	AX014713.1 GI:10040986		synthetic construct.	synthetic construct	artificial sequences.	1 (bases 1 to 20)	Schwartz, J.C., Gros, C., Ouimet, T., Rose, C., Bonhomme, M.C. and	Facchinetti, P.	Novel nep 11 membrane metalloprotease and its use for screening	inhibitors useful in therapy	
AX014713	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS		TITLE		

PAT 14-DEC-2001

linear

DNA

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Payne, V
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ETLDELGWMDEESKKKAQEKAMSIREQIGHPDYILEEMNRRLDEEYSNLNFSEDLYFE
                                                                                                                                                                                                                                                                                                                                                                                      PAT 08-JUN-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2076)
Patent: WO 9953077-A 13 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
LOCATION/Qualifiers
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                                                                                                     /organism="synthetic construct"
/db_xref="taxon:32630"
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Sequence 1 from Patent W00136610.
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                                                                                                                                    /note="oligonucleotide"
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llarity 100.0%;
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RESULT 3 . AX319864/c

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Plowman, G.D., Whyte, D., Sudarsanam, S., Manning, G., Caenepeel, S. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2262)
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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17;
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Mismatches
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AX319864 2232 bp
Sequence 28 from Patent WO0183782.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
. 620 c 705 g 399
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AX146980
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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Patent: WO 0183782-A
Sugen, Inc. (US)
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ORIGIN
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Human neprilysin protease
Patent: WO 02505958-A 3 04-APR-2002;
MILLENNIUM PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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| Similarity 100.0%;
20; Conservative 0
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Best Local S
Matches 20
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NFDKRGNADWWSNPSTOHFREQSECHIYQYGNYSWDLADEQNVNGFNTLGENIADNG
ROYQAYRAYLKWMAEGGRDQQLPGLDITHEQLFFINYAQVWCGSYRPEFAIQSIKTDV
HSPLKYRVLGSLQNLARHCARGTPMHFKERCRVW"
649 c 139 g 413 t
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QLALMNSQFNRRVLIDLFIWNDDQNSSRHIIYIDQPTLGMPSREYYFNGGSNRKVREA
YLQFWVSVATLLREDANLPRDSCLVQEDMMQVLELETQLAKATVPQEERHDVIALYHR
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GHPDYILEEMNRRLDEEYSNLNFSEDLYFENSLQNLKVGAQRSLRKLREKVDPNLMII
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Mammalia, Eutheria, Primates, Caterrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DB 6; Length 2262;
17;
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Deleersnijder,W., Wiegers,R. and Weske,M.
Human enzymes of the metalloprotease family
Patent: WO 0136610-A 3 25-MAY 2001;
Solvay Pharmaceuticals B.V. (NL)
Location/Qualifiers
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                                      0; Mismatches
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Sequence 3 from Patent W00226958.
AX473102
AX473102.1 GI:22207836
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Sequence 3 from Patent W00136610.
AX146978
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/db_xref="taxon:9606"
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     Score 20;
Pred. No.
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                                                                                           622 CGATGAGGACGCGCCTGTTG 603
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100.0%;
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Best Local Similarity 100.
Matches 20; Conservative
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     Query Match
Best Local Similarity
Matches 20; Conserv
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AX473102/c
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ACCESSION
VERSION
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AX146978/c
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GTPMHPKERCRVW"
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                                                                                                        Score 20; DB 6;
Pred. No. 17;
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Pred. No. 17;
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Sequence 3 from Patent EP1069188.
AX139743.
AX139743.1 GI:14275325
/organism="Homo sapiens"
/db_xref="taxon:9606"
a 647 c 740 g 413
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/db_xref="taxon:9606"
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/db_xref="GI:14275326"
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Mammalia; Eutheria; Primates;
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db_xref="GI:14275324
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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KEYWORDS
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Patent: WO 0047750-A 14 17-AUG-2000;
BOILEAU GUY (CA) ; DESGROSEILLERS LUC (CA) ; UNIVERSIIE DE MONTREAL
               PAT 30-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORPAVEKARTLYRSCMNQSVIEKRGSQPLLDILEVVGGWPVAMDRWNETVVQQARPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /RELIDKVRTVFVETLDELGWMDEESKKKAOEKAMSIREO1GHPDYTLEETNRRLDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SNLNFSEDLYFENSLQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIV
                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Boileau, G. and Desgroseillers, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2663;
                 linear
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                 DNA
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Sequence 14 from Patent W00047750.
                                                                                                                                                                                                                                                                              organism="Homo sapiens"
'db_xref="taxon:9606"
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1. 2676
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                 AX139745 2663 bp
Sequence 5 from Patent EP1069188
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PAT 30-MAY-2001
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                                                                                                                                                                                                                         TLYRSCMNQSV1EKRGSQPLLD1LEVVGGWPVAMDRWNETVGLEWELERQLALMNSQF
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17;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2714)
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                                                                                                                         translation="MVESAGRAGOKRPGFLEGGLLLL"
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/note="unnamed protein product"
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; Pred. No. 17;
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1. 2714
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Sequence 1 from Patent EP1069188
AX139741
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                                                           /protein_id="CAC09978
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AK093058
KEYWORDS
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YKAYLQWLAEGGRDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAIQSIKTDVHSPLK
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Homo sapiens neprilysin-like metallopeptidase 2 mRNA, complete cds.
AF336981 AF336981.1 GI:15811370
                                                                                                                                                                                                                                                                                                                                                                   Novel nep ii membrane metalloprotease and its use for screening
                                                                                                                                                                                                                                                                                                                                                                                                       INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
LOCATION/QUALIFIES
                                                       Gaps
                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 2765)
Schwartz,J.C., Gros,C., Ouimet,T., Rose,C., Bonhomme,M.C. and
Facchinetti,P.
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Sciurognathi; Muridae; Murinae;
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Pred. No. 17;
; Mismatches 0
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                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                               inhibitors useful in therapy
Patent: WO 9953077-A 1 21-OCT-1999;
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/db_xref="taxon:10117"
                          Score 20;
Pred. No. 1
                                                                                                                                                                           Sequence 1 from Patent W09953077.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                             Molecular cloning, tissue distribution, and chromosomal localization of MWEL2, a gene coding for a novel human member of the neutral endopeptidase-24 11 family DNA Cell Biol. 20 (8), 493-498 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-JAN-2001) Biochemistry, University of Montreal, P. Box 6128, Station Centre Ville, Montreal, Quebec H3C 3J7, Canada Location/Qualifiers
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Homo sapiens cDNA FLJ35739 fis, clone TEST12003824, moderately
similar to Mus musculus neprilysin-like metallopeptidase I (N11)
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                                                                                                                                                                                                                                                                                                                                                                                     Lemieux, N., Crine, P., Boileau, G. and
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Homo sapiens testis cDNA to mRNA, clone_lib:TESTI2
clone:TESTI2003824.
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                                                                                                  Lemleux, N., Crine, P., Bolleau, G.
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Mismatches 0
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789 c 841 q 485 t
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/db_xref="taxon:9606"
/chromosome="1"
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Matches 20; Conservative 0;
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                                                                                           Bonvouloir, N.,
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AX463057.1
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AX463057/c
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                                                                                                                                                                                                                                                                                                               (E-mail:genomics&trico.jp, Tel:81-948-52-3935, Far:81-438-52-3986)
(E-mail:genomics&trico.jp, Tel:81-948-52-3935, Far:81-438-52-3986)
MEDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA full insert sequencing: Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-6 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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ted (04-JUL-2002) Takao Isogal, FLJ Project(HRI Team); 2-6-7
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Ishlbashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiquchi,S., Kusano,J., Watanabe,M., Fujimori,K., Tanai;H., Ishiqa,M., Yamashita,H., Ishida,M., Yamanoto,J., Isnoo,Y., Kawai-Hio,Y., Sato,H., Wakamatish,A., Ishii,S., Yamamoto,J., Isnoo,Y., Kawai-Hio,Y., Satio,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y. Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A., Nagahari,K., Masuho,Y., Nagai,K., and Isogai,T., Sugano,S., NEDO human cDNA sequencing project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="TESTI2"
/note="cloning vector; pME18SFL3"
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Pred. No. 17;
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Patent: WO 0206492-A 1 24-JAN-2002;
Location/Qualifiers
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/db_xref="taxon:9606"
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PAT 15-JUL-2002
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 17;
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                                                                                                                                  Sequence 4 from Patent W00247670.
AX463057
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/db_xref="taxon:9606"
854 c 876 g 501
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Job time: 222.098 secs
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CGATGAGGACGCGCCTGTTG 20
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Best Local Similarity 100.0%;
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Bacillus lichenifo Bacillus lichenifo

Human adenylyl and Drosophila melanog

Drosophila melano

Human soluble secr CDNA encoding nove Human SEP CDNA inc

Rat membrane meta Human SEP endopept

Human neprilysin

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Drosophila melanog Neisseria meningi

Neisseria meningi

Gene #2168 used to Drosophila melanog

Propionibacterium

N. meningitidis pa Neisseria meningit N. meningitidis pa Sequence of the 5'

Human brain expres

Human bone marrow Human foetal live Probe #13460 for

N. meningitidis p Human breast cell

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Probe Probe Probe

genome-der1

Perfect score:

Title:

Sequence:

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Run on:

Scoring table:

Total number

Database

Searched:

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Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; ss neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; probe; hybridsation
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Schwartz JC;
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/genesegn-embl/NA1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gcgdata/geneseq/geneseqn-embl/NA1980.
                                                                                                                                                                                                                                                                                                                                                        4370478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/genesegn-embl/NA1982
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                        nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF89737
AAS97186
AAF89739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF89738
ABN84280
AAF59660
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                                                                                                                                                                                                                           cgatgaggacgcgcctgttg 20
                                                                                                           2003, 00:43:28
                                                                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                US-09-647-780A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing; Minimum Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2232
2262
2286
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Match
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Score

Result No.

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(SOLV ) SOLVAY PHARM BV.

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membrane metalloprotease designated metallysine II (NEBII) gene (AA228810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic- hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune disorder; arthritis, endotoxin shock; sepsis; diabetes mellitus; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple solerosis; Alzheimer's disease; neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
peripheral vascular disease; Raynaud's disease; motility disorder;
gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea;
                                                                                                                          represent probes for detecting the rat
                  proteolysis of
                                     to screen for inhibitors
cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of a human metalloprotease enzyme IGS5.
                                                                                                                                                                                                                                                                                                                                                          Score 20; DB 20; Length 20;
Pred: No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour invasion;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "metalloprotease enzyme IGS5"
                    involved in
                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
              New membrane metalloprotease NEP II,
neuronal and hormonal peptides, used
potentially useful for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGATGAGGACGCCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                       22; 29pp; French.
                                                                                                                                                                                                                                                                                                                                                        100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                          Sequences AAZ28811-Z28827
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             Matches 20;
                                                                                                                                                                                                                                                                                   disorders
                                                                                     Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
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vasotropic; antinigraties; analgesic; endocrine; nootropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; antinifalmmatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoletic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infarction, peripheral vascular disease, Raymand's disease, kidney diseases, gastrointestinal disorders, motility disorders and conditions of delayed gastric emptying, post-operative or diabetic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or dilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urinary retention, osteoporosis, angina perforis, myocardial infarction stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis, Alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma,
Parkinson's disease, acute heart failure, hypotension, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes a human metalloprotease enzyme designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGS5 polynucleotides and polypeptides are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; psychotic disorder disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 22; Length 2076; Pred. No. 2.1;
                                                                                                                                                                                                                      diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia,
                                                                                                                                                                                  New IGS5 polypeptides useful for treating infections, pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2076 BP; 493 A; 578 C; 636 G; 369 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human metalloprotease partial DNA sequence #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dyskinesia; metabolic disorder; inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
Weske M;
                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 5-6; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 CGATGAGGACGCGCCTGTTG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS97186 standard; cDNA; 2232 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2000; 2000US-201879P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                       WPI; 2001-343815/36.
P-PSDB; AAB83840.
Deleersnijder W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200183782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
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enzyme IGS5'

/product= "metalloprotease

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Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
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                                                                                                                                                                                                                                                                                      The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or beamaropoletic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), brain or neuronal associated diseases disorders, cardiovascular disease, brain or neuronal associated diseases sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dysfunction, metabolic disorders and infamatory disorders and disorders and infamatory disorders and disorders and infamatory disorders.
                                                                                                                                                      Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders. (1) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAS97159-AAS97195 represent human protease coding sequences and primers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angina pectoris; myocardial infarction; stroke; ulcer; allergy;
benign prostatic hypertrophy; migraine; psychotic disorder;
neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus severe mental retardation; dyskinesia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metalloprotease, IGS5; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subarachnoid hemorrhage, cerebral ischemia; cerebral infarction; peripheral vascular disease; Raynaud's disease; motility disorder;
                                         Caenepeel S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 24; Length 2232; Conservative 0; Mismatche.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a human metalloprotease enzyme IGS5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2232 BP; 512 A; 620 C; 705 G; 395 T; 0 other;
                                         Manning G,
                                                                                                                                                                                                                                                     Claim 30; Figure 1R-S; 232pp; English.
                                       Sudarsanam S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tourette's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..2262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 CGATGAGGACGCCTGTTG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF89739/c
ID AAF89739 standard; DNA; 2262 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGATGAGGACGCGCCTGTTG
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                                     Whyte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-041502/05.
P-PSDB; AAU72903.
(SUGE-) SUGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                       Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUL-2001
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                                                         Payne V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Silles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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IGSS. IGSS polynucleotides and polypetides are useful for treating the froctions, pain, cancer, diabetes, obssity, anoraxia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, uninary retention, osteoporosis, anion pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autitism, multiple solerosis, Alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis, errebroasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney diseases, gastrointestinal disorders, motility disorders and conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Buntinoton's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted endopeptidase; SEP; endocrine; vasotropic; analgesic enzyme; gynaecological; antisense-therapy; male erectile dysfunction MED; female sexual dysfunction; FSD; female sexual arousal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSAD; premature ejaculation; anorgasmia; vaqinismus; mouse; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New IGS5 polypeptides useful for treating infections, pain, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence encodes a human metalloprotease enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2262 BP; 520 A; 628 C; 716 G; 398 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble secreted endopeptidase (SEP) consensus DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 22;
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Weske M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 8-9; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        622 CGATGAGGACGCGCTGTTG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGATGAGGACGCGCCTGTTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                      Deleersnijder W, Wiegers R,
                                                                                                                                                                                          19-NOV-1999; 99EP-0203862.
19-NOV-1999; 99NL-1013616.
31-MAX-2000; 2000EP-0201937.
31-MAX-2000; 2000NL-1015356.
                                                                                                                           17-NOV-2000; 2000WO-EP11532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                      (SOLV ) SOLVAY PHARM BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-343815/36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAB83842
WO200136610-A1.
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                                                               25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD28130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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AAD28130/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal disorder; autoimmune; inflammatory; cell proliferative; cardiovascular; developmental; epithelial; neurological; reproductive; AIDS; Acquired Immune Deficiency Syndrome; allergy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction in particular and exertile dysfunction (MED) or female sexual dysfunction in particular (e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such say premature e)aculation, anorgasmia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is SEP consensus DNA sequence found in human, mouse and rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anaemia; asthma; atherosclerosis; hypertension; myocardial infarction; pepatitis; cancer; psoriasis; Cushing's syndrome; hypothyroidism; eczema; epilepsy; Alzheimer's disease; Huntington's disease; Parkinson's disease; Pick's disease; infertility; vitiligo; drug screening; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; protease; PRTS-13; enzyme; gastritis; cirrhosis; Crohn's disease;
                                                                                                                                                                                                                                                                                                               An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as female sexual arousal disorder -
                                                                                                                                                                                                                                                        Phillips SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2286;
                                                                                                                                                                                                                                                          Wayman CP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
                                              /*tag= a
/note= "Encodes catalytic domain".
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Pred. No. 2.1;
Mismatches 0;
                                                                                                                                                                                                                                                          Wayman CP,
                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 6; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                670 CGATGAGGACGCCCTGTTG 651
                                                                                                                                                                                                                                                          Walsh RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD30580 standard; cDNA; 2318 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Silarity 100.0%; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protease, PRTS-13 cDNA
                                                                                                                                                 16-JUL-2001; 2001WO-IB01263
                                                                                                                                                                                14-JUL-2000; 2000GB-0017387
                            1664..2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                          Stacey P,
                                                                                                                                                                                                                                                                                      WPI; 2002-155042/20
                                                                                                                                                                                                            (PFIZ ) PFIZER LTD (PFIZ ) PFIZER INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                       WO200206492-A1
               Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                     24-JAN-2002.
                                                                                                                                                                                                                                                        Harrow ID,
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XX
FT
FT
FT
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PD
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Location/Qualifiers

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The invention relates to an isolated human protease polypeptide (PRTS). PRTS protein and DNA are useful for diagnosing, treating and preventing quastrointestinal disorders (gastriits, cirrhosis, Crohn's disease), autoimmune/inflammatory disorders (AIDS, integry, rheumatoid arthrits, anaemia, asthma), cardiovascular disorder (altergy, rheumatoid arthritis, anaemia, asthma), cardiovascular disorder (altergosclerosis, hypertension, myocardial infarction), cell proliferative disorders (hepatitis, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  psoriasis), developmental disorders (Cushing's syndrome, hypothyroidism) epithalial disorder (vitiligo, keloid, eczema), neurological disorders (epilepsy, Alzheimer's disease, Ptck's disease, Huntington's disease, Parkinson's disease, Parkinson's disease, Protein is useful in a number of drug sorreening techniques and to protein is useful in a number of drug sorreening techniques and to analyse the proteome of a tissue or cell type. PRTS DNA is useful for creating knockin humanised animals or transgenic animals to model human diseases, in sometic or germline gene therapy and in microarrays utilising fluids or tissues from patients to detect altered PKIN expression. The present sequence is human PRTS-13 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human protease polypeptide, useful in diagnosis, prevention and treatment of gastrointestinal, cardiovascular, autoimmune/inflammatory cell proliferative, developmental, epithelial and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yue H, Au-Young J, Griffin JA, Policky JL, Ramkumar J, Yang J; Thangavelu K, Ding L, Rearney L, Baughn MR, Borowsky ML; Sanjanwala MS, Yao MG, Burford N, Walla NK, Lal P, Lee S, Todd Lo TP, Tang YT, Ellict VS, Azimzal Y, Lu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                     "Human PRTS-13 protein"
                                                                                                                                                                                             "Mature PRTS-13 protein
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Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AR, Hafalia AJA, Lu DAM
Kallick DA, Nguyen DB,
iriffin JA, Policky JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 174-175; 182pp; English.
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                                                                                                                                                                                                                                                                                                                                                                      2001WO-US22397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-225988P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC
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Das D, Kal
                                                     /product=
338..427
/*tag= b
                                                                                                                                        428..1648
/*tag= c
                                                                                                                                                                                                   /product=
338..1651
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Matches 20: Conservative
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Tribouley CM,
                                                                                                                                                                                                                                                                                                                                                                         17-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6-AUG-2000
                                                                                      sig_peptide
                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                    31-JAN-2002
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AAF89738/C
ID AAF8973
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Length 2340;

DB 22;

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Metalloprotease; IGS5; Infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypotension; urinary retention; osteoporosis; angina pectoris; myocardial infraction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder; allergy; neurological disorder; autism; multiple sclerosis; Alzheimer's disease; neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arterlosclerosis; cerebrovasospasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a human metalloprotease enzyme designated IGS5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulinia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis, Alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
                                                                                                                                                                                                                                                 subarachnoid hemorrhage; cerebral ischemia; cerebral infarction; peripheral vascular disease; Raynaud's disease; motility disorder; gastrointestinal disorder; gastrointestinal disorder; gastrio emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion; immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus; severe mental retardation; dyskinesia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bullmia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                    Nucleotide sequence of a human metalloprotease enzyme IGS5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product- "metalloprotease enzyme IGS5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weske M;
                                                                                                                                                                                                                                                                                                                                                         de la Tourette's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 6-7; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99EP-0203862.
99NL-1013616.
2000EP-0201937.
2000NL-1015356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000; 2000WO-EP11532.
                                   (first entry)
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P-PSDB; AAB83841.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200136610-A1.
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31-MAY-2000;
31-MAY-2000;
                                   23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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AAF89738;
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cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney disease, gastrointestinal disorders, motility disorders and conditions of delayed gastric emptying, post-operative or diabetic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetics mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.

Sequence 2340 BP; 539 A; 649 C; 739 G; 413 T; 0 other;

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medicament
                                Gaps
                                                                                                                                                                                                                                                                                                    male sexual dysfunction; male erectile dysfunction; obesity; anorexia; bulimia; vasotropic; anorectic; therapy; inhibitor; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a nucleotide sequence coding for human SEP, a soluble secreted endopeptidase, with an additional 5' vector partial sequence. The invention relates to the use of an inhibitor of NPY, or an inhibitor of NPY II receptor, especially a inhibitor selective for an NPY or NPY YI receptor associated with male genitalia, in the preparation of a medicament for the
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /partial
/note= "the CDS does not include a stop codon"
2580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c "the 3' end of the sequence is missing from Figure 8 of the specification"
                                                                                                                                                                                                                                                                                    SEP; endopeptidase; enzyme; human; neuropeptide Y1; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of an inhibitor of neuropeptide Y in the preparation of mase the treatment or prevention of male erectile dysfunction
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            partial vector sequence"
                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Der Graaf PH, Wayman CP;
 Score 20;
Pred. No.
                                                                                                                                                                                                                                                        Human SEP endopeptidase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 8; 179pp; English.
                                                                           700 CGATGAGGACGCCCTGTTG 681
                                                                                                                               RESULT 8
ABN84280/c
ID ABN84280 standard; cDNA; 2580 BP.
                                                           1 CGATGAGGACGCGCCTGTTG 20
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/product= "SEP"
                               ö
 100.0%;
100.0%;
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2001GB-0011037
2001US-0895367.
2001US-0905846.
2001GB-0020679.
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                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "5'
258..2580
                                                                                                                                                                                                                          23-SEP-2002 (first entry)
                               Conservative
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/note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-547828/58
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               Similarity
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(PFIZ ) PFIZER
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                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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Query Match
Best Local Simi
Matches 20;
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06-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-2001
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13-JUL-2001
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                                                                                                                                                                                            ABN84280;
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membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc and specificates play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splice variant, alternative splicing; zinc endopeptidase family; neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia; pain; hypertension; cancer; inflammation; cardiovascular disease; neptraconal disease; pancreatic disease; prostatic disease; respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic; cerebroprotective; hypotensive; cytostatic; antilnflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNEPa, SNEPb and SNEPc
for treating e.g. acute and
e, cancer, inflammation, renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNEP homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotides may be used as hybridisation probes for cDNA and genomic DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa, SNEPD or SNEPC; to isolate cDNA and genomic clones of SNEP homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    research reagents and material for the discovery of treatments and
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the human SNEPa, SNEPb and SNEPc proteins, the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like
treatment or prevention of male sexual dysfunction, especially male erectile dysfunction (MED). The NPY inhibitor may be used with an auxiliary active agent such as an SEP inhibitor. The invention provides a SEP sexust can be used to detect candidate inhibitors of SEP. In addition to treatment of MED, NPY inhibitors can also be used to treat abnormal drink and food intake disorders,
                                                                                                                                                                                               Score 20; DB 24; Length 2580; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neprilysin-like membrane metallopeptidase SNEPb cDNA.
                                                                                                                    such as obesity, bulimia, anorexia and metabolic disorders.
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNEPb; neprilysin-like membrane metallopeptidase;
                                                                                                                                                           Sequence 2580 BP; 587 A; 741 C; 794 G; 458 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New membrane-associated metallopeptidase SNEPa, polypeptides and polynucleotides, useful for tre chronic renal insufficiency, pain, stroke, cance
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Culouscou J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 30-33; 72pp; English.
                                                                                                                                                                                                                                                                                               CGATGAGGACGCGCTGTTG 930
                                                                                                                                                                                                                                                                                                                                                                                                                AAF59660 standard; cDNA; 2636 BP.
                                                                                                                                                                                                                                                                             1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular; hepatotropic; ss
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                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-0401767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jagerschmidt A; Agnel M,
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and hepatic ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-212582/22.
                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAB60562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF59660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                                                              AAF59660/c
ID AAF596
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diagnostics for animal and human diseases; and for chromosome identification. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPa. SNEPb or SNEPc. Such antibodies are used to isolate or identify clones expressing the protein, or to purify the proteins by affinity chromatography. SNEP proteins may also be used in screening for compounds which modulate SNEP endopeptidase activity, and to assess enzymatic cleavage of small amplecule substrates in cells, cell-free preparations, chemical libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analgesic;
                                                                                                                                                                                                                                                                                                                                                                                       disorder related to abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; SNEPC; neprilysin-like membrane metallopeptidase; splice variant; alternative splicing; zonc endopeptidase family; neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
                                                                                                                                                                                                                                                                                   ischemia, pain, ströke, hypertensive disease, cancer, inflammation, well as cardiovascular, neuronal, pancreatic, prostatic, renal, respiratory or hepatic diseases. they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnorm expression of SNEPa, SNEPb or SNEPc. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                            and product mixtures. The SNEP proteins (as vaccine compositions), SNEP nucleotides, and SNEP activators or inhibitors may used to treat acute and chronic renal insufficiency, renal and hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory disease, gene therapy, nephrotropic; vasotropic; cerebroprotective; hypotensive; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypertension, cancer; inflammation; cardiovascular disease; neuronal disease; pancreatic disease; prostatic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neprilysin-like membrane metallopeptidase SNEPc cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2636 BP; 601 A; 759 C; 813 G; 462 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 2.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Culouscou J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661/c
AAF59661 standard; cDNA; 2663 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular; hepatotropic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629 CGATGAGGACGCGCCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jagerschmidt A, Agnel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNFI ) SANOFI-SYNTHELABO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and hepatic ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA encoding SNEPb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001.
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               $$$$$$$$$$$$$$$$$$$$$$$$$$$
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Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders

Boilean G;

Desgroseillers L,

WPI; 2000-549148/50

P-PSDB; AAB08131

Disclosure, Fig.4; 59pp; English.

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diagnostics for animal and human diseases, and for chromosome identification. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPa, SNEPb or SNEPc. Such antibodies are used to isolate or identify clones expressing the protein, or to purify the proteins by affinity chromatography.

SNEP proteins may also be used in screening for compounds which modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                      molecule substrates in cells, cell-free preparations, chemical libraries and product mixtures. The SNEP proteins (as vaccine compositions), SNEP nucleotides, and SNEP activators or inhibitors may used to treat acute and chronic renal insufficiency, renal and hepatic
                      The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and the CDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SNEP nucleotides may be used as hybridisation probes for CDNA and genomic DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa, SNEPb or SNEPc; to isolate cDNAs and genomic clones encoding SNEPa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tschaemia, pain, stroke, hypertensive disease, cancer, inflammation, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           another organ, or to diagnose or treat any disorder related to abnormal expression of SNEPa, SNEPb or SNEPc. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "neutral endopeptidase metallopeptidase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEP-like enzyme; protein production; protein secretion;
neurological disease; Alzheimer's disease; pain; psychiatric disorder;
fertility; bone disease; abnormal phosphate metabolism; ss.
                                                                                                                                                                                                                                             as research reagents and material for the discovery of treatments and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     well as cardiovascular, neuronal, pancreatic, prostatic, renal, respiratory or hepatic diseases. they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  SNEP endopeptidase activity, and to assess enzymatic cleavage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2663;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2663 BP; 609 A; 769 C; 816 G; 468 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; llarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzyme NL-2
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                    invention relates to the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660 CGATGAGGACGCCCTGTTG 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
ses 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200047750-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo saptens.
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metallopeptidase-like enzyme, designated NL-2. The specification also describes NL-1 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimeric constructs containing the foreign protein downstream from and in phase with the N-terminal region. The NL enzymes are have been localised to the brain, and may be useful in the treatment of neurological diseases such as Alzheimer's disease, pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splice variant; alternative splicing; zinc endopeptidase family; neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia; pain; hypertension; cancer; inflammation; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                       and psychlatric disorders. M. enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide processing by the NL-3 enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal disease; pancreatic disease; prostatic disease; respiratory disease; gene therapy; nephrotropic yasotropic; exerbioprotective, hypotensive; cytostatic; antiinflammatory;
                                                                                                                                                                                              sequence encodes a human neutral endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human neprilysin-like membrane metallopeptidase SNEPa cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNEPa; neprilysin-like membrane metallopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2676 BP; 608 A; 771 C; 823 G; 474 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB;
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease; pancreatic disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF59659 standard; cDNA; 2714 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNFI ) SANOFI-SYNTHELABO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-212582/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jagerschmidt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1069188-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999;
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The invention relates to the human SNEPA, SNEPB and SNEPC proteins, and the cDNAs encoding them. SNEPA, SNEPB and SNEPC are neprilysin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptidase and peptide hormones. SNEP nucleotides may be used as hybridisation probes for cDNA and genomic SNEPP or SNEPP or SNEPP or SNEPP or SNEPP.

SNEPP or SNEPP; to isolate collastion probes for cDNA and genomic SNEPP or SNEPP; to isolate collassion and isometical for the discovery of treatments and diagnostics for animal and human diseases; and for chromosome identification. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPP, SNEPP or SNEPC. Such antibodies immunospecific for SNEPP, SNEPP or to purify the proteins by a affinity chromatography.

SNEP protein, or to purify the proteins by a fifinity chromatography.

SNEP proteins may also be used in screening for compounds which modulate snep endopeptidase activity, and to assess enzymatic cleavage of small and product mixtures. The SNEP proteins compounds compositions), considered so the snep activators or inhibitors may used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnormal
                                     New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, well as cardiovascular, neuronal, pancreatic, prostatic, renal, respiratory or hepatic diseases. they may also be used in modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNEPc. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; deuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treat acute and chronic renal insufficiency, renal and hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 20; DB 22; Length 2714; 100.0%; Pred. No. 2.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2714 BP; 621 A; 780 C; 836 G; 476 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat membrane metalloprotease NEPII gene.
                                                                                                                                              Claim 5; Page 25-28; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression of SNEPa, SNEPb or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98FR-0004389
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ID AAZ28810 standard; cDNA;
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                                                                                                        and hepatic ischemia
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Best Local Similarity
Matches 20; Conserv
P-PSDB; AAB60561.
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This sequence represents the gene for the rat membrane metalloprotease designated neprilysine II (NEPII), which is involved in (In)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved. e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                male sexual dysfunction; male erectile dysfunction; obesity;
anorexia; bulimia; vasotropic; anorectic; therapy; inhibitor; gene;
                                                                                                                                        proteolysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                     New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endopeptidase; enzyme; human; neuropeptide Y1; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2765;
                                           Bonhomme MC, Facchinetti P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 2.1;
           (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
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185. 2524
/*tag= a
/product= "SEP"
                                                                                                                                                                                               Claim 2; Page 12-16; 29pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN84279 standard; cDNA; 2893
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Best Local Similarity 100.0%;
Matches 20; Conservative C
                                             Haret C,
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                                                                                        WPI; 1999-593429/51.
P-PSDB; AAY44177.
                                             Gros C,
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                                                           Schwartz JC;
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                                             Ouimet T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN84279;
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An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as female sexual arousal disorder -
                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD) (e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such as premature ejaculation, an organia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is human SEP
  Phillips SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 2.1;
Wayman CP,
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  Wayman CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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  Walsh RT,
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                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 167pp; English
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ilarity 100.0%;
Conservative 0
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  Stacey P,
                                                  WPI; 2002-155042/20.
P-PSDB; AAE17779.
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  Harrow ID,
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Best Local S
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Job time :
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                                                                                                                                                                                    of an inhibitor of neuropeptide Y in the preparation of medicament the treatment or prevention of male erectile dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ne; gynaecological; antisense-therapy; male erectile dysfunction female sexual dysfunction; FSD; female sexual arousal disorder; premature ejaculation; anorgasmia; vaginismus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                associated with male genitalia, in the preparation of a medicament for the treatment or prevention of male sexual dysfunction, especially male erectile dysfunction (MED). The NPY inhibitor may be used with an auxiliary active agent such as an SEP inhibitor. The invention provides a SEP assay that can be used to detect candidate inhibitors of SEP. In addition to treatment of MED, NPY inhibitors can also be used to treat abnormal drink and
                                                                                                                                                                                                                                                                                                                           The present sequence is a nucleotide sequence coding for human SEP, a soluble secreted endopeptidase. The invention relates to the use of an inhibitor of NPY, or an inhibitor of NPY XI receptor especially an inhibitor selective for an NPY or NPY XI receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intake disorders, such as obesity, bulimia, anorexia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2893 BP; 658 A; 854 C; 876 G; 505 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/note= "Encodes catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 24;
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human soluble secreted endopeptidase (SEP) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted endopeptidase; SEP; endocrine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human SEP protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                        Wayman CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                     Disclosure; Fig 7; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD28544 standard; cDNA; 2893 BP
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                                                        PH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= 'a
/product= "]
1711..2893
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                                                        Van Der Graaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185..2524
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                                                                                                        2002-547828/58
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  (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 20, Conserv
                                                                                                                                       P-PSDB; ABB79521
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                                                        Naylor AM,
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Sequence 1685, Ap

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Sequence 1 Sequence 3 Sequence 3 Sequence 5 Sequence 5 Sequence 6 Sequence 6

Sequence Sequence (Sequence us-09-647-780a-13.rni

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APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Armitage, Richard J.
APPLICANT: Armitage, Richard J.
APPLICANT: Armitage, Richard J.
APPLICANT: No. 5480981el Cytokine That Binds CD30 NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seese, Immunex Corporation
Street
                                                                                                                                                                               US-09-134-001C-1685
                                                                                                                                               US-09-134-001C-1515
                                                                                                                                                                                                    US-09-199-637A-404
US-09-134-001C-1626
                                                                       US-09-380-420C-1
US-09-311-924-3
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                                                                                                                                                              US-08-030-096-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
PPPLICATION NUMBER: US/08/225,989
FILLING DATE: 12 APRIL 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 12 APRIL 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-U1-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 997,600
APPLICATION NUMBER: US 999,600
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Patent No. 5480981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seese, Kathryn A. REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 86
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51 University
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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APPLICANT: GOODWIN
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222.151 Million cell updates/sec
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Sequence 19, A
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Sequence 9,
Sequence 1,
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Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-125-468-1

US-08-125-468-1

US-08-279-600D-1

US-09-122-632-1

US-09-122-632-1

US-09-240-179-11

US-09-240-179-12

US-09-387-800-1

US-09-199-637A-400
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US-09-221-017B-545
US-09-215-694-19
                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                            441362 seqs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                       - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_NA:*
                                                                                                                                                                        US-09-647-780A-13
                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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5633 4
31328 4
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Perfect score:
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                                                                     OM nucleic
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Gaps

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APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Armitage, Richard J.
APPLICANT: Armitage, Richard J.
APPLICANT: Gruss, Hans-Jurgen
TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                 76.0%; Score 15.2; DB 1; Length 39; 85.0%; Pred. No. 63; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Kathryn A. Seese, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
FILING DATE: 20-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNDBER: US/08/225,989
FILING DATE: 1994
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27.0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
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APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
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FILING DATE: 02-JUN 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 889,71
FILING DATE: 26-MAY-1992
ATTORNEY,AGENT INFORMATION:
NAME: Seese, KALHYN A
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-580-014-9/c; Sequence 9, Application US/08580014; Patent No. 5753203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 26
ELECOMMUNICATION INFORMATION:
TELEX: 756822 .
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     Ouery Match 76.0
Best Local Similarity 85.0
Matches 17; Conservative
                                                              : 39 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                ; IMMEDIATE SOURCE:
; CLONE: 5' PCR Primer
US-08-570-923-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seattle
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                                                                                  TYPE: nucleic STRANDEDNESS:
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                                                              LENGTH:
                                                                                                                                                                                                                                                                                                Gaps
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APPLICANT: Smith, Craig A.
APPLICANT: Armitage, Richard J.
APPLICANT: Gruss, Hans-Jurgen
TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                       Length 39;
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Kathryn A. Seese, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Apple Machicosh
COMBOTER: Apple Machicosh
CORENTING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
FILLING DATE: 12-DEC-1995
                                                                                                                                                                                                                                                     Score 15.2; DB
Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 530
CLASSIFFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRL 1994
APPLICATION NUMBER: US 07/966,775
TITING DATE: 27-027-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: US 892,459
FILING DATE: 02-JUN-1992
PRIOR APPLICATION NUMBER: US 892,459
PRIOR APPLICATION NUMBER: US 892,459
APPLICATION NUMBER: US 892
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FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
                                                                                                                                                                                                                                                                                                                                                             31 CGAGGAGGACGCGCATGGTG 12
                                                                                                                                                                                                                                                                                                                                        1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-08-570-923-9/c
Sequence 9, Application US/08570923
Patent No. 5677430
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seese, Kathryn A. seese, Transfer 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 28 FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     76.0%;
ilarity 85.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
  TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                              LENGTH: 39 base pairs.
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: 5' PCR Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98101
                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                            US-08-225-989-9
                                                                                                                                                                                                                                                                                                Matches
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Gaps

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. LOCATION: (939]..(1014)
. OTHER INFORMATION: Shares partial identity with the promoter region
. OTHER INFORMATION: of the rice anther-specific gene (RTS2)
US-09-587-700-1
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Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1434;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Puthigae, Sathish
APPLICANT: Skadsen, Ronald W.
TITLE OF INVENTION: Spike Tissue Specific Promoter
FILE REFERENCE: 960296.97231
CURRENT APPLICATION NUMBER: US/09/587,700
PRIOR APPLICATION NUMBER: 60\2007
PRIOR APPLICATION NUMBER: 60\2007
PRIOR FILING DATE: 2000-05-12
                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                   Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.2; Di
Pred. No. 82;
0; Mismatches
                                                                                                                                                                                                                                               Score 15.2;
Pred. No. 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 CGCTGACGACGTGCCTGTTG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: MORRISON & FOERSTER 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                31 CGAGGAGGACGCGCATGGTG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-587-700-1; Sequence 1, Application US/09587700; Patent No. 6291666
                                                                                                                                                                                                                                                                                                                          1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                               76.0%;
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Best Local Similarity 85.0%;
Matches 17; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 39 has
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Hordeum vulgare
                                                                                                                                              MOLECULE TYPE: DNA
IMMEDIATE SOURCE:
CLONE: 5' PCR Primer
US-09-079-785-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1187)..(1237)
NAME/KEY: misc_feature
                                                                                            nucleic acid
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SOFTWARE: PatentIn Ve
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TTY: Palo Alto
                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                            STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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ov
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Armitage, Richard J.
APPLICANT: Armitage, Richard J.
APPLICANT: Armitage, Bids Jurgen
TITLE OF INVENTION: NO. 6143869el Cytokine That Binds CD30
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                 Length 39;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Kathryn A. Seese, Immunex Corporation
51 University Street
                                                                                                                                                                                                                                               Score 15.2; D
Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US 899,660
15-JUN-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 889,717
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                31 CGAGGAGGACGCGCATGGTG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09079785
Patent No. 6143869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Seese, Kathryn A. REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
                 TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 39 base pairs
                                                                           : 39 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                MOLECULE TYPE: DNA
IMMEDIATE SOURCE:
CLONE: 5' PCR Primer
US-08-580-014-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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Washington
                                                                                                                                  linear
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                                                                                                          STRANDEDNESS:
TOPOLOGY: lir
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Gaps

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OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FRASER, CLUAR M.
APPLICANT: FRASER, CLUAR M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007, 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FRASER, Claire M. APPLICANT: VENTER, ODIN C. TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4403765;
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                                                                        ; DB 4; Length 31328;
1e+02;
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                                                                                                                    Indels
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Pred. No. 61;
                                                                        Score 15.2; DE
Pred. No. 1e+02
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.2; D)
Pred. No. 61;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2233178 CGATGACGACGGGCCGGTTG 2233197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                  28294 CGAAGATGACGCGCCTATTG 28313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                            1 CGATGAGGACGCGCCTGTTG 20
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APPLICANT: FLEISCHMAN, ROBERT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D
                                                                        76.0%;
illarity 85.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%;
85.0%;
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85.0%;
              ; ORGANISM: Aspergillus terreus
US-09-215-694-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.0
Matches 17; Conservative
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SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHITE, Owen R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: H37RV US-09-103-840A-1
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                                                                        Query Match
Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 4403765
                                                                                                                                                                                                                                                            RESULT 8
US-09-103-840A-2,
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US-09-103-840A-1
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TYPE: DNA
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QC
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APPLICANT: Kennedy, Jonathan n.m.i
APPLICANT: Rennedy, Jonathan n.m.i
APPLICANT: Park, Cheonseok n.m.i
TITLE OF INVENTION: METHOD OF PRODUCING ANTIHYPERCHOLESTEROLEMIC AGENTS
TITLE REFERENCE: 960296,95718
CURRENT APPLICATION UMBER: 08.2/09/215,694B
CURRENT FILING DATE: 1999-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 5633;
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                                                                                                   OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
JURENT APPLICATION DATA:
PAPPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.0%; Score 15.2; 85.0%; Pred. No. 91
                                                                                                                                                                                                                                       PAPELICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
APPLICATION DATE: 4PPLICATION DATE: APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA: APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/09215694B Patent No. 6391583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 27. ELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 706141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: double
                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                      OMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 17; Conserva
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SOFTWARE: Patentin Ve
SEQ ID NO 19
LENGTH: 31328
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APPLICANT: Wiscons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE
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JS-09-221-017B-545
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                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-215-694-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
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Cloning of the biosynthetic pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning of the biosynthetic pathway for chlortetracycline and tetracyline Formation and cosmids useful therein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 30001;
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                                chlortetracycline and tetracyline useful therein
                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.8; DB 1;
Pred. No. 1.6e+02;
); Mismatches 2;
                                                                                                  American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 American Cyanamid Company
                                                                                                                                                                                                                                                                                                 FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/474,933
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08474933
Patent No. 5866410
                                                                                        STREET: One Cyanamid Plaza CITY: Wayne STATE: New Jersey
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: American Cyanam
STREET: One Cyanamid Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 30001 base pairs
nucleic acid
EDNESS: single
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Best Local Similarity 88.9*
- 16: Conservative
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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          TITLE OF INVENTION: CLONTITLE OF INVENTION: ChloTITLE OF INVENTION: usef NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Jersey
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US-08-474-933-1/C
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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              Gaps
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       Indels
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                                                                                                                                                                                                                                                                                    ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.8; DB 2;
Pred. No. 1.4e+02;
          Mismatches
                                                                                                                                                        Sequence 1, Application US/08635121
Patent No. 5910442
GENERAL INFORMATION:
APPLICANT: Gelman, Irwin H.
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                             2235879 CGATGACGACGGCCGGTTG 2235898
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FILING DATE: 19-APRIL-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
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Patent No. 5589385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Clark, Richard S
REGISTRATION NUMBER: 26,154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: A3
FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5134 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
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Lotvin, Jason A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: ATTORNEY/AGENT INFORMATION:
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 88.99
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
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                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10112-0228
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                            STREET: 50 TTTY: New York
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                                                                                                                                                                                                                                                                                                                                                           USA
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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US-08-125-468-1/c
       17;
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APPLICANT:
APPLICANT:
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APPLICANT: NAMBA, KENING
TITLE OF INVENTION: FINE MAGNETIC PARTICLES CONTAINING USEFUL PROTEINS
TITLE OF INVENTION: FINE MAGNETIC PROCESS FOR PRODUCING THE SAME, AND USE
TITLE OF INVENTION: HEREOF
FILE REPERRENCE: MATSUNAGA
CURRENT APPLICATION NUMBER: US/08/973,275B
CURRENT APPLICATION NUMBER: US/08/973,275B
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1996-03-27
EARLIER PLICATION NUMBER: UP 8-7536
EARLIER FILING DATE: 1996-03-28
EARLIER FILING DATE: 1996-03-28
EARLIER FILING DATE: 1996-03-28
EARLIER FILING DATE: 1996-03-16
EARLIER FILING DATE: 1996-03-16
NUMBER OF SEQ ID NOS: 6
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APPLICANT: Tadashi MATSUNAGA
TITLE OF INVENTION: PROTEIN-BOUND MAGNETIC PARTICLES AND
TITLE OF INVENTION: PROCESS OF PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 2e+02;
0; Mismatches 1;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/529,600
                                                                                                                                                                                                                         Sequence 5, Application US/08973275B Patent No. 5558706 GENERAL INFORMATION: APPLICANT: MATSUNAGA, Tadashi APPLICANT: KAMIYA, Shinji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09122632
Patent No. 6033878
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2 GATGAGGACGCGCCTG 17
                                         Query Match 72.0%;
Best Local Similarity 93.8%;
Matches 15; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09
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SEQ ID NO 5
LENGTH: 1302
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MEDIUM TYPE: Diskett
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ZIP: 20005-3918
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                                                                                                                                                                                                 US-08-973-275-5
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VENTION: PROTEIN-BOUND MAGNETIC PARTICLES AND
VENTION: PROCESS OF PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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Pred. No. 2e+0;
0; Mismatches
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                                                       APPLICAL.
APPLICAL.
ATING DATE:
ATTORNEY/AGENT INFORMATICAL.
NAME: TSEVIGS, ESTELLE J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
TELECOMMUICATION INFORMATION:
TELEFAX: (201)831-324
TELEFAX: (201)831-336
INFORMATION: FOR EGD ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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APPLICATION NUMBER: US/08/529,600D
FILING DATE: 18-SEP-1995
CLASSIFICATION: 435
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PRIOR APPLICATION NUMBER: JP 6-248700
FILING DATE: 16-5EP-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: J30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,468
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.0%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
Matches 15, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-08-529-600D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-08-529-600D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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δ

Gaps

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FILING DATE: 18-SEP-1995

APPLICATION NUMBER: JP 6-248700

FILING DATE: 16-SEP-1994

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs

TYPE: nucleic acid
STRANDEDNES: double

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

LOCATION: 1.1302.
US-09-122-632-1
```

 Query Match
 72.0%; Score 14.4; DB 3; Length 1302;

 Best Local Similarity
 93.8%; Pred. No. 2e+02;

 Matches
 15; Conservative
 0; Mismatches
 1; Indels
 0;

 Qy
 2 GATGAGGACGCTG
 17
 1111111111111111
 Db
 69 GATGATGACGCCCTG
 84

0; Gaps

Search completed: July 8, 2003, 09:31:59 Job time: 39.6598 secs Sequence 7102, Ap Sequence 216, App Sequence 69, Appl Sequence 117, Appl Sequence 76, Appl

Sequence 27, Sequence 76, Sequence 333

000000

Sequence 1 Sequence 8 Sequence 5

Sequence 333, Apples gequence 134, Apples gequence 1, Appl. Sequence 1362, Apples gequence 58, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. S

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(without alignments) 273.390 Million cell updates/sec
                                                                                                      8, 2003, 19:09:54 ; Search time 115.512 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                      1105431 seqs, 789497651 residues
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                             1 cgatgaggacgcctgttg 20
                                                                                                                                                                                                                                                 IDENTITY_NUC Gapov 10.0 , Gapext 1.0
                                                                                                                                                                        US-09-647-780A-13
                                                                                                                                                                                                                                                                                                                                                                           length: 0
length: 2000000000
                                                                                                                                                                          Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                      Run on:
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score greater than or equal to the score of the result bei and is derived by analysis of the total score distribution is the number of Pred. No.

'USO8_NEW_PUB.seq:* 'USO8_PUBCOMB.seq:*

Database

ubpna/US09_NEW_PUB.seq

O_NEW_PUB.seq

		dP	•		SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	08	ID	Description
υ.	20	100.0	2893	6	US-10-017-273A-4	Section 4 experimes
O.	20	100.0	2893	10	US-09-905-846-1	
3	20	100.0	2975	6	US-10-017-273A-5	۸,
Ω	20	100.0	2975	10	US-09-905-846-5	٠.
S	18.4	92.0	300	6	US-09-990-03	
9	15.8	79.0	351	10	US-09-960-352-14675	7
7	15.8	79.0	1860	10	US-09-974-300-2780	Sequence 2780
80	15.8	79.0	1908	10	US-09-974-300-2714	Sequence 2714
ο Ο	15.8	79.0	10144	10	US-09-880-107-2168	Segment of 168
10	15.4	77.0	447	10	US-09-983-965-3946	
11	15.2	76.0	207	10	US-09-864-761-20314	Seguence 20314
12	15.2	76.0	437	10	US-09-864-761-3544	Segmence 3544
c 13	15.2	76.0	639	6	US-09-938-842A-126	26.
c 14	15.2	76.0	639	6	US-09-938-842A-481	
15	15.2	76.0	814	6	US-09-989-643-127	Sequence 127 Apr
° 0	15.2	76.0	846	<u>о</u>	US-10-156-761-2628	. α
17	15.2	76.0	891	6	US-09-989-643-160	Segmented 160 Apr
c 18	15.2	76.0	954	Φ	US-10-156-761-2747	2747
19	15.2	76.0	968	10	115-09-770-445-293	** (00 00000000

DB 9; Length 2893;

100.0%; Score 20; DB 9, 100.0%; Pred. No. 0.74;

20; Conservative

Query Match Best Local Similarity Matches 20; Conserv

												-			-					
CINTENDITO	273A-4/c	<pre>; Sequence 4, Application US/10017273A ; Publication No. US20030119714A1</pre>	; GENERAL INFORMATION: ; APPLICANT: Pfizer Inc	Christopher P.	; FILE OF INVENTION: Treatment of Male Sexual Dystunction ; FILE REFERENCE: PC22013	; CURRENT APPLICATION NUMBER: US/10/017,273A ; CURRENT FILING DATE: 2001-12-12	Ų	; PRIOR APPLICATION NUMBER: GB 0030647.2 ; PRIOR FILING DATE: 2000-12-15	APPLICATION N	; PRIOR FILING DATE: 2001-04-06	 APPLICATION N	FILING DATE:	; PRIOR APPLICATION NUMBER: US.60/291,722 ; PRIOR FILING DATE: 2001-05-17	APPLICATION N	; PRIOR FILING DATE: 2001-06-29	; SOFTWARE: PatentIn version 3.1 : SEO ID NO 4	LENGTH: 2893	; TYPE: DNA	; ORGANISM: Homo sapiens US-10-017-273A-4	
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TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction CURRENT APPLICATION UNDER: US/09/905,846
CURRENT APPLICATION UNDER: US/09/905,846
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 0017387.2
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 00/220,908
PRIOR FILING DATE: 2000-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2975;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lesley, Scott A.
APPLICANT: Enuth, Mark
TITLE OF INVENTION: Solubility Reporter Gene Constructs
FILE REPERENCE: P00120520
CURRENT APPLICATION NUMBER: U5/09/990,099
CURRENT APPLICATION NUMBER: U5 09/721,340
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2000-11-21
PRIOR FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 300
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Pred. No. 5.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20;
Pred. No. C
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  949 CGATGAGGACGCGCCTGTTG 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09990099 Publication No. US20030119094A1
949 CGATGAGGACGCGCCTGTTG 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                     Sequence 5, Application US/09905846
Patent No. US20020102707A1
                                                                                                                                                                                        APPLICANT: Ian Dennis Harrow
APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; Escherichia coli
US-09-990-099-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens US-09-905-846-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-960-352-14675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
                                                                                                                            APPLICANT: Peter Stacey
APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh
TILE OF INVENTION: Compounds for the treatment of sexual dysfunction
FILE REFERENCE: PCS10926APME
CURRENT APPLICATION NUMBER: US/09/905,846
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 0017387.2
PRIOR APPLICATION NUMBER: 0017387.2
PRIOR APPLICATION NUMBER: 000-07-26
PRIOR FILING DATE: 2000-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 2893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LICANT: Naylor, Alasdair M.
PLICANT: Van Der Graaf, Pieter H
PLICANT: Wayman, Christopher P.
TE OF INVENTON: Treatment of Male Sexual Dysfunction
P. REFERENCE: PC22013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; Dinlarity 100.0%; Pred. No. 0.7 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRENT APPLICATION NUMBER: US/10/017,273A RRENT FILING DATE: 2001-12-12
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: GB 0108730.3
FILING DATE: 2010-04-06
APPLICATION NUMBER: GB 0120679.6
FILING DATE: 2001-08-24
APPLICATION NUMBER: US 09/905,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRENT FILING DATE: 2001-12-12
IOR APPLICATION NUMBER: US 60/265,358
IOR FILING DATE: 2001-01-31
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S: £
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APPLICATION NUMBER: US 60/291,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 0030647.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  984 CGATGAGGACGCGCCTGTTG 865
                                       Sequence 1, Application US/09905846 Patent No. US20020102707A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
ilarity 100.0%;
Conservative C
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SOFTWARE: PatentIn version 3.1
                                                                                     GENERAL INFORMATION:
APPLICANT: Ian Dennis Harrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserva
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Matches 20; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 2893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-905-846-1
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Gaps

Gaps

Indels

Mismatches

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TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE REFERENCE: 37-21(10297)C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10144;
                                                                                                                                                                                                                                                                                                     Length 1908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Genbank Accession No. US20020142981A1 L17131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                     DB 10;
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                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8;
Pred. No. 87
                                                                                                                                                                                                                                                                                                   Score 15.8;
Pred. No. 9
                                            PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1). (10144)
OTHER INFORMATION: n = a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/211,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3946, Application US/09983965
Patent No. US20020137160A1
                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1013 CGCTGAGGACGCGCCTGCT 995
                                                                                                                                                                                                                      ; ORGANISM: Bacillus licheniformis US-09-974-300-2714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGATGAGGACGCCCTGTT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.0%;
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.5*
                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-880-107-2168/c
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                                                                                                                                                            SEQ ID NO 2714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2168
                                                                                                                                                                                                          TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                     LENGIH:
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                                                                                                                                                       ID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: BOS taurus
; OTHER INFORMATION: Clone ID: 63-LIB188-003-Q1-E1-H4
US-09-960-352-14675
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.8; DB 1
Pred. No. 1e+02;
0; Mismatches
                                                                               APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLE
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2780
LENGTH: 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/974,300
Sequence 14675, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2780, Application US/09974300 Patent No. US20020146721A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1158 CCATGAGGACGCGTCTGTT 1176
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US-09-974-300-2780
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
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Matches 17; Conservative
                                                                                                                                                                                                                                                             NUMBER OF SEQ II
SEQ ID NO 14675
LENGTH: 351
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US-09-974-300-2714
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TILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL.
TILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20314
LENGTH: 207
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pred. No. 2e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICATION NUMBER: PCT/US01/00666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-02-04
APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
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APPLICATION NUMBER: US 60/236,359
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illarity 85.0%;
Conservative
                                                                                                                                            ORGANISM: Homo sapiens
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Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION US-09-864-761-20314
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                                                                                                                                                                                                                                                                                                                                                               Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                       Score 15.4; DB 10;
Pred. No. 1.6e+02;
0; Mismatches 1;
         CURRENT APPLICATION NUMBER: US/09/983,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00661
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                                              PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 3946
LENGTH: 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JICATION NUMBER: US 60/234,687 ING DATE: 2000-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                          Ouery Match 77.0%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Bos taurus
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us-09-647-780a-13.rnpb

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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAIL
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Roy, Paul H.
TITLE.OF INVENTION: Species-Specific, Genus-Specific and Universal DNA
TITLE OF INVENTION: Probes and Amplification Primers to Rapidly Detect and
TITLE OF INVENTION: Identify "Common Bacterial and Fungal Pathogens and
TITLE OF INVENTION: Associated Antibiotic Resistance Genes from
FILE REFERENCE: 12287.29
CURRENT APPLICATION NUMBER: US/09/989,643
CURRENT FILING DATE: 2001-11-20
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Pred. No. 1.9e+02;
0; Mismatches 3; Indels
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Pred. No. 1.9e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION UNDBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR PLING DATE: 2001-01-01
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-06-22
                                                                JS-09-938-842A-481/c
Sequence 481, Application US/09938842A
Patent No. US20020160378A1
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Publication No. US20030049636A1
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Best Local Similarity 85.0%;
Matches 17; Conservative
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                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM:
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SOFTWARE:
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PPLICANT: Zhu, Tong
ITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
ITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 2e+02;
0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    N: EXPRESSED IN BT474, SIGNAL = 7
N: EXPRESSED IN FETAL LIVER, SIGNAL = 9
N: EXPRESSED IN LUNG, SIGNAL = 7.6
N: EXPRESSED IN HELA, SIGNAL = 6.4
N: EXPRESSED IN HEART, SIGNAL = 6.2
N: EXPRESSED IN HEAL100, SIGNAL = 5.8
N: EXPRESSED IN ADULT LIVER, SIGNAL = 8.4
N: EXPRESSED IN BADIT SIGNAL = 6.9
N: EXPRESSED IN BONE MARROW, SIGNAL = 6.1
N: EXPRESSED IN PLACENTA, SIGNAL = 6.1
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                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/938,842A.
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PELING DATE: 2000-06-30
PRIOR PFLICE DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 CGGTGAGGACGCAGCTGTTG 334
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Best Local Similarity 85.0%;
Matches 17; Conservative
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nilarity 85.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo saplens
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Best Local Similarity
Matches 17; Conserv
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US-09-864-761-3544
                                                                                                                                                                                                                                                                                                                                                                                                                               THER INFORMATION:
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                                                                                                                                                                                                                                                                SOFTWARE: Anno
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Search completed: July 9, 2003, 02:22:19 Job time: 126.562 secs

7 18:4 92.0 422 14 BQ703364 8 18.4 92.0 436 12 BG837021	18:4 92.0 444 10 AW202460 18:4 92.0 464 14 BQ635402 18 4 02.0 466 14 BD037440	18.4 92.0 481 13 BI431034	13 18.4 92.0 489 10 14 18.4 92.0 494 14 15 18.4 92.0 498 14	16 18.4 92.0 506 9 AI668369 17 18.4 92.0 528 9 AI834379	18 18.4 92.0 537 9 AIG65885.	20 18:4 92.0 54/ 10 AW56252 21 18:4 92.0 549 10 AW67236	18.4 92.0 550 10 AW181220 18.4 92.0 552 9 AI691236	24 18.4 92.0 555 10 AN352676 25 18.4 92.0 556 12 BG833132	26 18.4 92.0 563 12 BG833131 27 18.4 92.0 565 10 AW062014	18.4 92.0 572 9 18.4 92.0 583 10	30 18.4 92.0 587 9 AIG91181	18.4 92.0 588 10 AW256209 18.4 92.0 600 13 BI989738	34 18.4 92.0 608 9 AI691299 6 35 18.4 92.0 621 9 AI691802 AI691802 6	18.4 92.0 642 10 BE553003 BE55300 18.4 92.0 675 14 BQ529205 BO559200	18.4 92.0 821 12 BG837038 BG837038	4 92.0 2534 11. ATIU3538 AY103538 4.4 87.0 341 D BB701995 BB701995 7.7 15 15 15 15 15 15 15 15 15 15 15 15 15	42 17.4 87.0 464 17 AZ180792 AZ180792	43 16.8 84.0 236 12 BF991788 BF991788 MR 44 16.8 84.0 251 13 BM645820 BM645820 170	10.8 84.0 285 10 AW061907 AW061907	ALIGNMENTS		RESULT 1.	BQ668192 141 bp mRNA linear EST 1 946103H11 x1 946 tassel primordium proparada hy cohmidae	mays cDNA, mRNA sequence.	z	Zea	ltae: Streptophyta: Embryophyta		do min		JOURNAL Unpublished (1999) COMMENT Contact: Walbot V		Cord	Tel: 550 723 2227 Fax: 650 725 8221	Email: walbot@stanford.edu
GenCore version 5.1.6 Convright (r) 1993 - 2003 Communes 143		OM nucleic – nucleic search, using sw model			Title: US-09-647-780A-13 Perfect score: 20 Sequence: 1 cataaqaccccctattg 20	able: IDENTITY NUC		Searched: 16154066 seqs, 8097743376 residues.	Total number of hits satisfying chosen parameters: 32308132	Minimum DB seq length: 0 Maximum DB seq length: 200000000	cessino	Maximum Match	16111	1: 1:	2: em_estnum:* 3: em_estn:*	4: em_estmu:* 5: em_estov:*	6: em_estpl:* 7: em_estro.*	8: em_htc:* 9: ab est1:*	10: gb_est2:*	11: gp_ntc:* 12: gb_est3:*	14: gb_est4:*	15: em_estfun:* 16: em_estom:*	ssb_dp/:		em_gss	3: em_gss	em_gss	20: em_gss_pro:* 27: em_gss_rod:*	No. is the number of results predicted by chance	score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query	No. Score Match Length DB ID Description	1 18.4 92.0 2 18.4 92.0	O International Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Contr

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Query Match

Best Local Similarity 95.0%;
Matches 19; Conservative
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AI691198.1
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AW600514/c
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A1691198/c
LOCUS
DEFINITION
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TITLE
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/tissue_trype="embryo" can's our
/dev_stage="14, 21, 28, and 35 days after pollination"
/dev_stage="14, 21, 28, and 35 days after pollination"
/dev_stage="14, 21, 28, and 35 days after pollination"
/dev_stage="15" coil solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, solf, s
                                                                                                                                                                                                         /note-"Organ: tassels; Vector: HybrizAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybrizAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 bp mRNA. linear EST 30-MAR-2000 embryo from Delaware Zea mays CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC
                                                                                                                     /dev_stage="lust after the transition from vegetative to
Inflorescence development"
/lab_host="XLOLR"
                                    clone_lib="946 - tassel primordium prepared by Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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/cultivar="111inois High Oil"
/ob.xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 141;
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855 California Ave, Palo Alto, CA 94304, USA
723 227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.4; DB 14;
Pred. No. 1.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnollophyta; Lillopsid
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: walbot@stanford.edu
Plate: 687076 row: D column: 03.
Location/Qualifiers
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                                                                                             'tissue_type="tassels"
            'db_xref="taxon:4577"
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ilarity 95.0%;
Conservative
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Unpublished (1999)
Contact: Walbot V
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Best Local Similarity
Matches 19; Conserv
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COMMENT
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82

BASE COUNT. ORIGIN

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mRNA linear EST 23-MAR-2000 of anther and pollen Zea mays CDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XLOLR (Stratagene)"
/note="Organ: immature ear; Vector: pBK-CMV; Site_1: EcoRI
; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt
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clāde; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2017)
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yta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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/clone_lib="606 - Ear tissue cDNA library from Schmidt
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    Length 260;
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                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Bmail: walbot@stanford.edu
  ; DB 10;
1.9e+02;
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Pred. No. 2e+02;
0; Mismatches 1;
Score 18.4; Di
Pred. No. 1.9e4
0; Mismatches
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Plate: 606025 row: D column: 10.
Location/Qualifiers
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- Mixed stages
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Spermatophyta; Magnoliophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 CGATGAGGACGAGCCTGTTG 282
                                                                                                         247 CGATGAGGACGAGCCTGTTG 228
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                                                                                      1 CGATGAGGACGCGCCTGTTG 20
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Best Local Similarity 95.0%;
Matches 19; Conservative
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Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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mRNA sequence.
AW600514
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Zea mays
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Gaps

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/note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhOI; Anther and pollen cDNA library.
Directionally sequenced with 5' end at the EcoRI site.
Created by Amie Franklin."
                                                                                                                                                                                                                                                                                                                                                         660070D05.yl 660 - Mixed stages of anther and pollen Zea mays cDNA, mRNA.
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946108G07.x1 946 - tassel primordium prepared by Schmidt lab Zea
mays CDNA, mRNA sequence.
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Directionally sequenced with 5' end at the EcoRI site.
Created by Amle Franklin.
1 87 c 89 g 100 t
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clade; Panicoideae; Andropogoneae; 2ea
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/db_xref="taxon:4577"
/clone_lib="660 - Mixed stages of anther and pollen"
/tissue_type="whole premieotic anthers to pollen shed"
/dev_stage="premieotic anthers to pollen shed"
/lab_host="xLOLR"
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Pred. No. 2.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                                                                     Score 18.4; DB ]
Pred. No. 2e+02;
                                                                                                                                                                                            Mismatches
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Plate: 660070 row: D column: 05
Location/Qualifiers
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 /lab_host="XLOLR"
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Best Local Similarity 95.0%;
Matches 19; Conservative
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Best Local Similarity 95.0%;
Matches 19; Conservative
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Walbot V
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI; Anther and pollen cDNA library.
Directionally sequenced with 5' end at the EcoRI site.
Created by Amie Franklin."
90 c 86 g 66 t
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1 (bases 1 to 349)
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to pollen shed"
en shed"
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/tissue_type="whole premieotic anthers to pollen shed"
/dev_stage="premieotic anthers to pollen shed"
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                                               Maize ESTs from various cDNA libraries sequenced at Stanford
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Maize ESTs from various cDNA libraries sequenced at Stanford
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/db_xref="taxon:4577"
/clone_lib="660 - Mixed stages of anther
/tissue_type="whole premiectic anthers to
/dev_stage="premiectic anthers to pollen
/lab_host="XLDR"
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                                                                                                                                                            855 California Ave. Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotstanford.edu
Plate: 660070 row: D column: 05.
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Contact: Walbot V
Contact: Walbot V
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 725 8221
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Pred. No. 2e+02;
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Andropogoneae; Zea.
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Plate: 660065 row: H column: 10.
Location/Qualifiers
                                                                                                                           Department of Biological Sciences
Stanford University
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/clone_llb="660 - Mixed
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Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA OC6,
                                     Tel: (613) 759-1314
Fax: (613) 759-6566
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Fax: 650 725 8221
Email: walbot@stanf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A, Sprott
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cDNA clone Zm08_10d11, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Zea mays"
Coultivar="0H45"
(Ab_xref="taxon:4577"
/clone_lib="946 tassel primordium prepared by Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed Sequence Tags from Developing Maize Kernels Six Days after Silk Channel Inoculation with Fusarium graminearum Unpublished (2001)
                                                                                                               Poaceae; PACC
                                                                                                                                                                                     Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                             Liliopsida; Poales;
                                                                                                                                                                                                                                                                                              855 California Ave, Palo Alto, CA 94304, USA
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clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                            Department of Biological Sciences Stanford University
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                                                                                                                                                                                                                                                                                                                                                   Email: walbot@stanford.edu
Plate: 946108 row: G column
Location/Qualifiers
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Eastern Cereal and Oilseed
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                                                                                                                                                   (bases 1 to 422)
                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                             Contact: Walbot V
                                                                                                                                                                                                                                                                                                                 Tel: 650 723 2227
Fax: 650 725 8221
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/db_xref="taxon:4577"
/clone="Zm08_10d11"
/clone_lib="Zm08_AAFC_ECORC_Fusarium_graminearum_inoculate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 30-MAR-2000
                                                                                                                                                                                                                                                                              Tissue_type="Developing kernels (sibcrossed)"

/dev_stage="10-11 days post-silk emergence"

/dev_stage="10-11 days post-silk emergence"

/dev_stage="10-11" days post-silk emergence"

/note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;

Site_2: XhoI; Fleid-grown malize ears were silk

channel-inoculated in the morning (-10 am) with 1 ml of a

Fusarium graminearum macroconidial suspension (500,000

spores/ml) and whole ears were collected and immediately

frozen in liquid nitrogen 6 days later."

a 102 c 122 g 87 t 22 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW202460 11near EST 30-MAR-200
687030G10.x3 687 - Early embryo from Delaware Zea mays cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site_2: EcoRI: Library was prepared by Statagene using the Uni-TAP XR system (Stratagene BN93738-12). Clones were picked by a Q-bot after blue/white selection (ampicillin resistance - use 100 micrograms/microliter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28, and 35 days after pollination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="14, 21, 28, and 35 days after
/lab_host="E. coli SOLR"
/note="Organ: embryo; Vector: pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stanford University
855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18.4, DB 12;
Pred. No. 2.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cultivar="Illinois High Oil"
db_xref="taxon:4577"
clone_lib="687 - Early embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: walbot@stanford.edu
Plate: 687030 row: G column: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
                                                                                            /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 CGATGAGGACGAGCCTGTTG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGATGAGGACGCGCCTGTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae;
Email: harrislj@em.agr.ca
                                                                                                                         /cultivar="CO430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:6501087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.0%;
95.0%;
                                                                                                                                                                                                                                                          d_corn_ear"
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DEFINITION
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Developed from a pool of equal amounts of RNA from developing embryos sampled at 14, 21, 28 and 35 days after pollination of the Illinois High Oil Maize Strain Cycle. Of This closed strain has been selected for high Oil concentration for 90 generations and originates from the 1890s era open pollinated variety Burr's White"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pAD-GAL4; Site_1:
ry 606 was filtered for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptophyta; Embryophyta; Tracheophyta;
ta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4577"
/clone_lib="1091 - Immature ear with common ESTs screened
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                           screened by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Inflorescence meristem - floral organ
primordia"
                                                                                                                                                     Length 444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 464;
                                                                                                                                                                                                                                                                                                                                                           common ESTs
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sednenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Immature ear; Vector: pa
EcoRI; Site_2: XhoI; RNA from library
common ESTs found in 606."
119 c 109 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                     Score 18.4; DB 10;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             $core 18.4; DB 14;
Pred. No. 2.2e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                  1091070B04.x1 1091 - Immature ear with coscimidt lab Zea mays CDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize ESTs from various cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="0.5 cm to 2 cm"
/lab_host="Stratagene XLOLR"
                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: walbotestanford.edu
Plate: 1091070 row: B column: 04.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact; Walbot V
Department of Biological Sciences
Stanford University
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                                                                                                                                                                                                                                 280 CGATGAGGACGAGCCTGTTG 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cultivar="OH43"
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                                                                                                                                                  92.0%;
95.0%;
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ilarity 95.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 464)
                                                                                                                                              Ouery Match 92.0
Best Local Similarity 95.0
Matches 19; Conservative
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                   30635402
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                                                                                                  127
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                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                               RESULT 10
BQ635402/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                               DEFINITION
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ORIGIN
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KEYWORDS
SOURCE
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Matches
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BU037446
LOCUS
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EST 23-AUG-2002

linear

mRNA

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/note="Organ: tassels; Vector: HybrizAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between limm and 3mm. Sharon Stanfield prepared the cDNA tlbrary in HybrizAP. Sample insert size range was 350 bp to 3 Kb with a 1Kb average."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 20-AUG-2001
                                                                                                                                     Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="just after the transition from vegetative to inflorescence development"
         by Schmidt lab Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   one_lib="946 - tassel primordium prepared by Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steve Moose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophy
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoldeae, Andropogoneae, 2ea.
                                                                                                                                                                                                                              at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 bp mRNA linear E Juvenile leaf and shoot cDNA from
                                                                                                                                                                                                  Walbot,V.
Malze ESTs from various cDNA libraries sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
         prepared
                                                                                                                                                                                                                                                                                                                              855 California Ave; Palo Alto, CA 94304; USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                California Ave, Palo Alto, CA 94304, USA
                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.0%; Score 18.4; DB 14;
95.0%; Pred. No. 2.2e+02;
live 0; Mismatches 1;
946139A11.y1 946 - tassel primordium
                                                                                                                                                                                                                                                                                                                                           Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946139 row: A column: 11
Location/Qualifiers
                                                                                                                                                                                                                                                                                            Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="tassels"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/cultivar="OH43"
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                                                                                                                            Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host-"XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 CGATGAGGAGGCCTGTTG 235
                      mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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                                                        GI:22472966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:15214531
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                                                                                                                                                                               (bases 1 to 466)
                                                                                                                                                                                                                                                                                                           Stanford University
                                                                                                                                                                                                                                                        Jnpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 481)
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                                                                                                                                                                                                                                                                             Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
19; Conserve
                                                      BU037446.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI431034
BI431034.1
                                                                                              sea mays.
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                                                                           EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local §
                                                                                                         ORGANISM
                                                                                                                                                                                                   AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                   ACCESSION
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KEYWORDS
SOURCE
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ORGANISM
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                                                                                                                                                                                                                                                                         COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
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Site_1: EcoRI;

Length 489

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/note="Organ: anthers; vector: Lambda Zap; Site_1: Eco
Site_2: XhoI; Anther and pollen cDNA library.
Directionally sequenced with 5' end at the EcoRI site.
Created by Amie Franklin." 2 others
/dev_stage="premieotic anthers to pollen shed"
/lab_host="XLOLR"
                                                                                                                                             10;
                                                                                                                                            92.0%; Score 18.4; DB 10
95.0%; Pred. No. 2.2e+02;
iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library in HybrizaP. Sample to 3 Kb with a 1 Kb average.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946108 row: G colunn: 07.
Location/Qualifiers
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/organism="Zea mays"
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                                                                                                                                                                                                                           230 CGATGAGGACGAGCCTGTTG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar-"OH43"
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                                                                                                                                                                                                                                                                                                                                                       mays cDNA, mRNA sequence.
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illarity 95.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jnpublished (1999)
                                                                                                                                                                             Conservative
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Best Local Similarity
Matches 19; Conserv
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TITLE
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BQ744736
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660021C10.x1 660 - Mixed stages of anther and pollen Zea mays CDNA
                                                                                                                                               clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta;
poales; Poaceae; PACC
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to pollen shed"
                                                                                                                                                                                tissue_type="immature leaf primordium and vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                            dev_stage="4 stages from 3-13 days after imbibing"
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                                                                                                                                                                                                                                                                                                                                                                                                                    primordia, 9 days after sowing. 4. Partially e
greening leaves 4-5 at 13 days after sowing."
138 c 126 g 117 t
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/clone_lib="660 - Mixed stages of anthe
/tissue_type="whole premieotic anthers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.4; DB 13;
Pred. No. 2.2e+02;
0; Mismatches 1;
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Spermatophyta; Magnollophyta; Lillopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clade; Panicoideae; Andropogoneae; Zea
   Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotéstanford.edu
Plate: 949064 row: D column: 12.
Location/Qualifiers
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Location/Qualifiers
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                                                                                                                                  db_xref="taxon:4577"
                                                                                                      organism="Zea mays"
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/cultivar="Ohio43"
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                                                                                                                   cultivar-"W64A"
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1 Similarity 95.0%;
19; Conservative
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Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
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AW313130/c
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BQ744736 494 bp mRNA linear EST 17-JUL-2002 946108G07.yl 946 - tassel primordium prepared by Schmidt lab Zea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; 2ea.
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/clone_lib="946 - tassel primordium prepared by Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="tassels"
/dev_stage="just after the transition from vegetative
inflorescence development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 2.2e+02;
0; Mismatches 1;
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EST 15-MAY-2002
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EcoRI; Site_2: XhoI; RNA from library 606 was filtered for
common ESTs found in 606."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4577"
/clone_lib="1091 - Immature ear with common ESTs screened
by Schmidt lab"
                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Seprmatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 498)
            498 bp mRNA linear EST 15-MAY-Schmidt lab Zea mays cDNA, mRNA sequence.
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primordia"
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                                                                                                                                                                                                                                                                                                                                             Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA.94304, USA
Tel: 650 723 227
Fax: 650 725 8221
Email: Walbot@stanford.edu
Plate: 1091028 row: B column: 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="0.5 cm to 2 cm"
/lab_host="Stratagene XLOLR"
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                                                                                                      BQ294319.1 GI:20803269
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                                                                                                                                              Zea mays.
Zea mays
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SOURCE
ORGANISM
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Search completed: July 8, 2003, 09:21:47 Job time: 1018.1 secs

261 CGATGAGGACGAGCCTGTTG 242

Human immune/haema Human foetal liver Probe #17267 for g Human brain expres

Human bone marrow Probe #22642 used

DNA encoding novel Human secreted pro Human secreted pro Human genome-deriv

NKp46D2 (iso prostate exp prostate exp

Mouse secreted Human NKp46D2 (

Human nervous syst Human lung antigen Rat sequence diffe

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Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; ss; neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; probe; hybridsation.
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                                                                                                                                 AAS92643
AAX40291
AAC05013
                                                                                                                                                                        AAA44006
AAD30468
ABV14145
ABV14210
ABV35239
ABV35304
ABV4678
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Synthetic.
Rattus rattus
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358.431 Million cell updates/sec
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                                                                                      ; Search time 125.659 Seconds
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/ SIDSZ/gogdata/geneseqr-embl/Mal980.DAT:*
/ SIDSZ/gogdata/geneseqr-embl/Nal990.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/Na1999.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Human nerve differ Human T-box transc cDNA encoding neut Saccharomyces cere Colon tumour relat

AAD28130 AAZ28810 AAZ46480 AAZ90785 AAZ46477 AAA6477 AAA63763 AAV40294

2765 1529 2061 2494 2925 3323 402

100.0 100.0 100.0 92.0 92.0 92.0 92.0

AAZ28820

Score

Result No.

Rat membrane metal Soluble secreted e Rat membrane metal Human MTbx gene fr

WPI; 1999-593429/51.

INRM ) INSERM INST NAT SANTE & RECH MEDICALE

98FR-0004389

08-APR-1998;

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NKp46

Human Human

scramblase

bone marrow Probe #9680 used Human genome-deri

luman

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Disclosure; Fig 6; 167pp; English.
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   8 X C C C C C C C C C C X S
                                                                                                    Sequences AA228811-228827 represent probes for detecting the rat membrane metalloprotease designated neprilysine II.(NEPII) gene (AA228810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin, disturbances of the hypothalamic- hypophyseal axis or endocrine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phillips SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme; gynaecological; antisense-therapy; male erectile dysfunction; MED; female sexual dysfunction; FSD; female sexual arousal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted endopeptidase; SEP; endocrine; vasotropic; analgesic;
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds
                 involved in proteolysis of
                 New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardiovascular disease
                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                              Score 20; DB 20; Length 20;
Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soluble secreted endopeptidase (SEP) consensus DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "Encodes catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wayman CP,
                                                                                                                                                                                                                                                                      Sequence 20 BP; 4 A; 2 C; 8 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1664..2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walsh RT,
                                                                                                                                                                                                                                                                                                                                                                  1 TGCAGGAAAGGTTTGGTCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                1 TGCAGGAAAGGTTTGGTCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD28130 standard; DNA; 2286 BP
                                                                           Claim 3; Page 22; 29pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sexual arousal disorder
                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0%;
Watches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUL-2001; 2001WO-IB01263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-2000; 2000GB-0017387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stacey P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-155042/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PFIZ ) PFIZER LTD. (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200206492-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07.-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harrow ID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sb.
                                                                                                                                                                                                                                             lisorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD28130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
AAD28130
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The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD) (e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such as premature ejaculation, anorgasmia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is SEP consensus DNA sequence found in human, mouse and rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to 'screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the gene for the rat membrane metalloprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endocrine origin; disturbances of the hypothalamic-hypophyseal axis endocrine disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        involved in proteolysis of
to screen for inhibitors,
cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                             DB 24; Length 2286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                       Sequence 2286 BP; 565'A; 601 C; 674 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat membrane metalloprotease NEPII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New membrane metalloprotease NEP II, neuronal and hormonal peptides, used potentially useful for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        982 TGCAGGAAAGGTTTGGTCTG 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 12-16; '29pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TGCAGGAAAGGTTTGGTCTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ28810 standard; cDNA; 2765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haret C,
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98FR-0004389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gros C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY44177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FR2777291-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouimet T, G
Schwartz JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2000
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1 TGCAGGAAAGGTTTGGTCTG 20

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The invention relates to a human T-box transcription factor protein, MTbx. The polypeptide can be administered therapeutically, especially by expressing encoding polynucleotides, to treat disorders characterized by aberrant polypeptide expression or activity, e.g. immune system diseases (e.g. HIV, leukemia, etc.), chronic inflammatory diseases (e.g. asthma, theumatoid arthritis etc.), developmental disorders, cardiovascular disorders, or other disorders arising from improper transcriptional regulation. They are especially useful to treat conditions characterized by loss of tissue integrity relating to disease and/or injury e.g. HIV, diagnose related to polypeptide expression or activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-box transcription factor protein; MTbx; immune system disease; HIV; leukemia; inflammatory disease; asthma; rheumatoid arthritis; human; developmental disorder; cardiovascular; transcriptional regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     produce non-human transgenic animals
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and to produce probes useful to detect related sequences, or for gene mapping. The present sequence represents a fragment of the human Mtbx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotides encoding human T-box transcription factor protein, MTbx, useful to treat transcriptional regulation disorders
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                                                                          Length 2765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide may also be used to produce non-human trans
and to produce probes useful to detect related sequences,
                                                                                                                    Indels
                  Sequence 2765 BP; 684 A; 735 C; 787 G; 559 T; 0 other;
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Pred. No. 15;
0; Mismatches 1;
                                                                     DB 2
                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 148-150; 152pp; English.
                                                                     Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myocardial, ischemia; gene. mapping; ss.
                                                                                                                                                                                 1110 TGCAGGAAAGGTTTGGTCTG 1129
                                                                                                                                                         1 TGCAGGAAAGGTTTGGTCTG 20
                                                                                                                                                                                                                                                                                                          AAZ46480 standard; DNA; 1529 BP
                                                                                                                  ö
                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.0%;
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98US-0188811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I-box transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2000 (first entry)
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MTbx gene fragment.
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Best Local Similarity 95.0
Matches 19; Conservative
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P-PSDB; AAY49415.
                                                                                        Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9966025-A2
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09-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                           AAZ46480;
                                                                   Query Match
                                                                                                                                                                                                                                                                                         AA246480/C
                                                                                                                                                                                                                                                                       RESULT 4
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recombinant methodology. The nerve differentiation factor is useful for the treatment of nerve disorders such as senile dementia, and for the promotion of nerve regeneration after nerve injury. The present sequence represents a human Tbr-2 gene encoding the nerve differentiation factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                             nerve differentiation factor; brain; nerve disorder; human; dementia; nerve regeneration; nerve injury; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Tbr-2 highly expressed in fetal brain tissue encodes a nerve differentiation factor for treatment of nerve disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
92.0%; Score 18.4; DB 21; Length 2061;
Best Local Similarity 95.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                       Human nerve differentiation factor, Tbr-2 encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2061 BP; 465 A; 640 C; 557 G; 399 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                      senile dementia; nerve regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 75-82; 89pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..2061
404 TGCAGGAAAGGTTGGGTCTG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1713 TGCAGGAAAGCTTGGGTCTG 1694
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                                                                                                                         : AAZ90785 standard; DNA; 2061 BP
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/product=
                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dementia and nerve injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-237874/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kimura N, Taga T;
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                            23-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - 13-MAR-2000
                                                                                                                                                                   AAZ90785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ46477;
                                                                                RESULT 5
AAZ90785/c
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0;

Caps

Indels

/product= "neutral endopeptidase metallopeptidase-like

enzyme NL-1"

WO200047750-A2

Location/Qualifiers 332..2629

Mus sp

Key

Neprilysin; neutral endopeptidase metallopeptidase-like enzyme; NEP-like enzyme; prodeln production; protein secretion; neurological disease; Alzheimer's disease; pain; psychiatric disorder; fertility; bone disease; abnormal phosphate metabolism; ss

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This cDNA encodes a human T-box transcription factor protein, MTbx. The polypeptide can be administered therapeutically, especially by expressing encoding polynucleotides. to treat disorders characterized by aberrant polypeptide expression or activity, e.g. immune system diseases (e.g. HIV, leukemia, etc.), chronic inflammatory diseases (e.g. asthma, HIV, leukemia, etc.), developmental disorders, cardiovascular disorders, or other disorders arising from improper transcriptional regulation. They are especially useful to treat conditions characterized by loss of tissue integrity relating to disease and/or injury e.g. HIV, hibernating myocardium during myocardial ischemia etc. It can be used to diagnose diseases related to polypeptide expression or activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    produce non-human transgenic animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide may also be used to produce non-human transgenic animal and to produce probes useful to detect related sequences, or for gene mapping. The Mtbx gene was mapped to chromsome 3p23-p24.
                                                               disease; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein, MTbx,
                                                         T-box transcription factor protein; MTbx; immune system disease; HT leukemia; inflammatory disease; asthma; rheumatoid arthritis; human developmental disorder; cardiovascular; transcriptional regulation; myocardial ischemia; gene mapping; chromsome 3p23-p24; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.0%; Score 18.4; DB 21; Length 2494; Best Local Similarity 95.0%; Pred. No. 15; Matches 19; Conservative 0; Mismatches 1; Indels 0;
Human T-box transcription factor protein, MTbx encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2494 BP; 651 A; 639 C; 600 G; 594 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            es encoding human T-box transcription factor
treat transcriptional regulation disorders
                                                                                                                                                                                                                                                                   Location/Qualifiers
164..1717
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                  /product= "Mtbx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; F1g 1; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0089467.
98US-0163116.
98US-0188811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0189760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US13457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhodadoust M;
                                                                                                                                                                                                                                                                                                                                                                                                                              WO9966025-A2.
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-1998;
29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1998;
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Desgroseillers L, Boileau G;

WPI; 2000-549148/50. P-PSDB; AAB08130.

(UYMO-) UNIV MONTREAL.

99CA-2260376. 2000WO-CA00147

11-FEB-2000; 11-FEB-1999;

17-AUG-2000

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The present sequence encodes a murine neutral endopeptidase metallopeptidase-like enzyme, designated NL-1. The specification also describes NL-2 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimmeric constructs containing the foreign protein downstream from and in phase with the N-terminal region. The NL enzymes are have been localised to the brain, and may be useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA ligase IV; LIG4; cellular DNA repair; modulation; diagnosis; XRCC4; Ku-associated DNA repair pathway; cancer; retroviral infection;
                                                                                                                                                                                                                                                                                                   treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders. NL enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide processing by the NL-3 enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae LIG4 encoding nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2925 BP; 710 A; 797 C; 836 G; 582 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18.4; DI
Pred. No. 16;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1308 TACAGGAAAGGTTTGGTCTG 1327
                                                                                          Disclosure; Fig 3; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGCAGGAAAGGTTTGGTCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV40294 standard; DNA; 3323 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       llarity 95.0%;
Conservative
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nes 19; Conserv
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Gaps

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1 TGCAGGAAAGGTTTGGTCTG 20

AAA63763 standard; cDNA; 2925 BP.

RESULT 7 AAA63763

8

04-DEC-2000 (first entry)

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cDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-1.

(first entry)

12-OCT-2001

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A method has been developed of assaying for a compound able to modulate the interaction or binding between XRCC4 and any of DNA ligase IV and/or DNA-PRCs/Ku (DPK). The method comprises: (a) bringing into contact: (i) a substance including XRCC4 (or a fragment, derivative, variant or analogue able to bind DNA ligase IV or DPK); (ii) a substance including DNA ligase IV or DFK); (ii) a substance including bund xigore and/or (iii) DPK (or a fragment, derivative, variant or analogue able to bind XRCC4), and a test compound under conditions where, if the test compound is not an inhibitor of interaction or binding between the substances interact or bind; and (b) determining interaction or binding between the substances. Compounds which modulate the interaction between the substances. Compounds which modulate cellular DNA repair activity, e.g. in the treatment of proliferative disorders, cancers and tumours, disorders involving retroviruses such as AIDS, human adult T-cell leukaemia/lymphoma, Type I diabetes and multiple sclerosis, and also in radiotherapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemotherapy. They can also be used in the potentiation of gene targeting and gene therapy. They can also be used for the modulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune system function. The present sequence encodes Saccharomyces cerevisiae LIG4 which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulation of cellular DNA repair activity - using compounds identified as modulating the interaction of XRCC4, DNA ligase IV and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3323 BP; 1132 A; 543 C; 661 G; 987 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
                                                                                 Location/Qualifiers
                                                                                                292..3171
/*tag= a
/product= "LIG4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 6; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                        98WO-GB00095
                                                                                                                                                                                                                                                                                                                                                                                             97GB-0013131
97GB-0000574
immune system disorder; ds.
                                                                                                                                                                                       /*tag= b
337..3168
                                        cerevistae.
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                                                                                                                                                                                                                                  /*tag=
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P-PSDB; AAW69560.
                                      Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Critchlow SE,
                                                                                                                                                                                                                                                                    WO9830902-A1
                                                                                                                                                                                                                                                                                                                                                      13-JAN-1998;
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13-JAN-1997;
                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                               16-JUL-1998
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                                                                                                                                                                                                          mat_peptide
                                                                               Key
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Ouery Match 87.0%; Score 17.4; DB 19; Length 3323;
Best Local Similarity 94.7%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

B 5

RESULT 9
AA129107
ID AA129107 standard; cDNA; 402 BP
XX
XX
XX
XX
XX
XX
XX

The present invention describes colon tumour associated proteins.(I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as Colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and the presence of similar nucleic acids in samples, and immunosorbant assay (ELISA)). AAI28460 to AAI29512 herefore which patients may be in need of restorative therapy. (I) may lso be used as antigens in the production of antibodies against TCAPS Anti-(I) antibodies and antagonists may also be used to down regulate ICAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples and AAM24494 to AAM24523 represent nucleotide and amino acid sequences given in the exemplification of the present invention. in assays to identify modulators of TCAP expression and activity Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer -Colon tumour related determined cDNA sequence for clone CT2-75. Length 402; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer; ss. Meagher MJ, Sequence 402 BP; 105 A; 92 C; 109 G; 93 T; 3 other; Benson DR, Claim 25; Page 310; 472pp; English. 29-DEC-2000; 2000WO-US35596 2000US-0575251 2000US-0609448 2000US-0480321 2000US-0504629 Jiang Y; 2000US-0649813 20000S-051944 enzyme linked immunotherapy; WPI; 2001-441847/47. (CORI-) CORIXA CORP Wang T, Lodes MJ, WO200149716-A2 Homo sapiens 28-AUG-2000; 9-MAY-2000; 12-JUL-2001 30-DEC-1999 9-JUN-2000 5-FEB-2000 )6-MAR-2( King GE, 0-JAN-2 Human;

Ouery Match

84.0%; Score 16.8; DB 22; Length 402;
Best Local Similarity 90.0%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps

1 TGCAGGAAAGGTTTGGTCTG 20 ||||||| ||||||||| || 366 TGCAGGGAAGGTTTGGTTTG 385

g

RESULT 10 ABA19503

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2000US-0232399.
2000US-0232400.
2000US-0232401.
                                                                                            0000S-0232398
                                                                                                                                                                                  Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
                                                                                                                                                                                                                                                                                                                       infection; nephrotropic; gene therapy; vaccine;
                                                                                                                                                                                                                                                     antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal antiparasitic; cardiant; immune disorder; cardiovascular disorder
                                                                                                                                  Human nervous system related polynucleotide SEQ ID NO 11834.
ABA19503 standard; DNA; 14124 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US01334
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                          neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                               WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                          23-JAN-2002
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                                             ABA19503;
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cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; asstrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin ading; organ transplantation; food preservative; tissue regeneration; anti-infertility; food additive.
                                                                                                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01301
                                                                                                                                                                                                                              WO200155303-A2
                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2000;
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           The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemlytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative (d) wound healing; (e) neurological diseases such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; noctropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 11834; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.0%; Score 16.8; DB 22; Length 14124; 90.0%; Pred. No. 1.2e+02; 1ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14124 BP; 4411 A; 2767 C; 2750 G; 4196 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lung antigen genomic DNA #23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9679 TGCAGGTAAGGTTTGGTCAG 9698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGCAGGAAAGGTTTGGTCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                   05-JAN-2001; 2001US-0259678.
                                                                                                                2000US-0251988
                                                                                                                                             2000US-0256719
                                                                                                                                                                 2000US-0251479
                                                                                                                                                                                                 2000US-0251856
                                                                                                                                                                                                                           2000US-0251868
                                                                                                                                                                                                                                                  2000US-0251869
                                                                                                                                                                                                                                                                                  2000US-0251989
                                                                                                                                                                                                                                                                                                            2000US-0251990
                                                                                                                                                                                                                                                                                                                                         2000US-0254097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epilepsy; and (f) infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-541565/60.
                                                                                                          05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                            01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                                               08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                           08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA,
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AAS29953;

RESULT 11 AAS29953/

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the lung antigen polypeptides of the invention. Lung antigen polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a lung antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                             Sequences AAS29931-AAS30164 represent genomic DNA molecules, which encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat sequence differentially expressed in response to a hepatotoxin #1041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as premature labour and infertility, gastrointestinal disorders such as premature labour and infertility, gastrointestinal disorders such as crom's disease, renal disorders such as glomerulonephritis and respiratory disorders, such as astroma and pleuristy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn to maintain organs before transplantation; to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preservative to increase or decrease storage capabilities.
Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO at ftp wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperproliferative disorders such as neoplasms of the breast or liver,
                                                                                                                                                                                                                                Isolated polypeptide for treating, preventing and/or prognosing respiratory disorders related to the lung including lung cancers and also for testing and detection e.g. diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.8; DB 22; Length 16854;
Pred. No. 1.2e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differential expression; centrilobular necrosis; steatosis
                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 217; 507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5587 TGCAGGACAGGTTTGGTTTG 5568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGCAGGAAAGGTTTGGTCTG 20
                                                                                                                                               Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK63134 standard; cDNA; 656 BP
2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 90.0%;
Matches 18; Conservative
                                                               2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-222040P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-2002 (first entry)
                                                                                                                                               Barash SC,
                                                                                                                                                                                       WPI; 2001-457723/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200210453-A2.
08-DEC-2000;
11-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-NOV-2000;
                                                               05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-2002.
                                                                                                                                                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK63134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CCI-
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Gaps

Human; immune; haematopoletic; immune/haematopoletic antigen; cancer;

cytostatic; gene therapy; vaccine; metastasis; ds.

17-JAN-2001; 2001WO-US01354

WO200157182-A2 Homo sapiens.

09-AUG-2001

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The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxic and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or ceptession in a tissue or cell sample exposed to the compound of two or more genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic capturession. The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates to a coull. The method sufflises a set of at least two probes (on a solid support in kit form), where each of the probes comprises on a gene listed in the specification, a computer specifically hybridises to a gene listed in the specification, a capturer comprising at least two genes listed in the specification.

System comprising at least two genes listed in the specification of a set of genes comprising at least two genes listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in classic contaction or identification of the physiological state of tissue or cell exposed to a known toxin. The genes and gene expression information may be used as diagnostic markers for the prediction or identification or ident
                                                                                                                                                                                                                                                                                                                                                      Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a genewhich is differentially expressed in response to a hepatotoxic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     has been exposed to a compound or agent. Hepatotoxicity
                                                                                                                                                                                                                                                             Elashoff MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 656 BP; 151 A; 120 C; 206 G; 179 T; 0 other;
                                                                                                                                                                                                                                                          Castle AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Seq ID No 1041; 239pp; English.
                                                                                                                                                                                                                                                          Johnson KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.0%; Scc.
100.0%; Pre
0;
                                                                       20010S-295798P.
20010S-297457P.
20010S-298884P.
                                                                                              13-JUN-2001; 2001US-297457P
19-JUN-2001; 2001US-298884P
09-JUL-2001; 2001US-303459P
                                                                                                                                                                                                                                                                                                                                                                                                                                     unexposed tissues or cells .
                                                                                                                                                                                                                                                          Porter MW,
                                                                                                                                                                                                   (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity )
....hes 16; Conservat
                                                                                                                                                                                                                                                                                                         WPI; 2002-241625/29.
                       15-MAY-2001;
22-MAY-2001;
06-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                         Predicting teffects by c
                                                                                                                                                                                                                                                     Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ample that
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SEP-2000;
           -SEP-2000;
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Score 16; DB 24; Length 656; Pred. No. 2.1e+02;

Indels

Mismatches

Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25081

(first entry)

06-NOV-2001 AAK70269;

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0269/c AAK70269 standard; DNA; 1481 BP.

RESULT 13 AAK70269,

596 AGGAAGGTTTGGTCT 611

4 AGGAAAGGTTTGGTCT 19

ò g

Conservative

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PR 25-SEP-2000; 20000US-023498.
PR 25-SEP-2000; 20000US-023488.
PR 27-SEP-2000; 20000US-023488.
PR 29-SEP-2000; 20000US-023489.
PR 29-SEP-2000; 20000US-023480.
PR 29-SEP-2000; 20000US-023489.
PR 02-CCT-2000; 20000US-023493.
PR 13-CCT-2000; 20000US-023493.
PR 13-CCT-2000; 20000US-023493.
PR 13-CCT-2000; 20000US-024178.
PR 20-CCT-2000; 20000US-024178.
PR 20-CCT-2000; 20000US-024188.
PR 20-CCT-2000; 20000US-024188.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024188.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024188.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189.
PR 20-CCT-2000; 20000US-024189
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ARK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased carmple, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) cupplement the patients own production of (I). Additionally, (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54912 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 25081; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human foetal liver single exon nucleic acid probe #21823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 16; DB 22; 1 100.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                    Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA73518 standard; DNA; 200 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1205 GGAAGGTTTGGTCTG 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0%;
Matches 16; Conservative C
                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GGAAAGGTTTGGTCTG 20
05-JAN-2001; 2001US-0259678
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2000US-0608408
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                                                                                                                                                                                                                                  useful for preventing,
                                                                                                       Barash SC,
                                                                                                                                                        WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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21-SEP+2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
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                                                                                                                                                                                                                                                                  metastasis
                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA73518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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ABA73518/c
ID ABA73
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present sequence is one such probe. The probes may be used for predicting, mesuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system congenital heart disease. Hypertension, cardiac arrhythmias and Note: The sequence data for this patent did not form part of the printed appecification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                     Seguence 200 BP; 40 A; 54 C; 44 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                129 TGCAGAAAGGTTTGGCCT 111
                                                                                                                                                                                                                                                                                                                                                                                      1 TGCAGGAAAGGTTTGGTCT 19
                                                                                                                                                                                                                                                                                              Ouery Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative (
         888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                       measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                  The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.8; DB 22; Length 200;
Pred. No. 2.3e+02;
); Mismatches. 2; Indels 0
                                                                                                                                                      Claim 4; SEQ ID NO 21823; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 200 BP; 40 A; 54 C; 44 G; 62 T; 0 other;
    Chen W, Rank DR;
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                       genome-derived
      Hanzel DK,
                                           WPI; 2001-483447/52
    SG,
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8, 2003, 02:19:02
Search completed: July
Job time: 127.659 secs
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Probe #17267 for gene expression analysis in human heart cell sample Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;

(first entry)

23-JAN-2002

ABA38801;

congenital heart disease; ss

Human;

30-JAN-2001; 2001WO-US00666

WO200157274-A2

09-AUG-2001

Homo sapiens

2000US-0180312 000US-0207456 2000US-0608408 2000US-0632366 2000US-0234687 2000US-0236359 2000GB-0024263

04-FEB-2000;

BP.

ABA38801/c ID ABA38801 standard; DNA; 200

RESULT 15

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart.

Claim 4; SEQ ID No 17267; 530pp; English.

Single exon nucleic acid probes for analyzing gene expression in human hearts

Rank DR;

3

Chen

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Penn SG,

WPI; 2001-488899/53

MOLE-) MOLECULAR DYNAMICS INC.

04-OCT-2000;

-SEP-2000;

-SEP-2000;

-JUN-2000 3-AUG-2000 6-MAY-2000

Gaps

Indels 0; Length 200;

Score 15.8; DB 22; Pred. No. 2.3e+02; 0; Mismatches 2;

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
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US-09-453-702B-261
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                                                                                                                                                                                               441362 seqs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                          - nucleic search, using sw model
                                                                                                                                      1 tgcaggaaaggtttggtctg 20
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                           seq length: 0 seq length: 2000000000
                                                                                                           US-09-647-780A-14
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APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
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APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE OF INVENTION: THEREFOR
FILE REFERENCE: MNI-046CP
CURRENT APPLICATION NUMBER: US/09/188,811
CURRENT FILING DATE: 1998-11-09
EARLIER APPLICATION NUMBER: 09/163,116
EARLIER FILING DATE: 1998-09-29
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Pred. No. 0.89;
0; Mismatches 1;
                                                                                       US-08-961-527-34
US-09-397-787-185
US-08-313-075A-49
US-09-326-203A-1
US-08-836-134-1
            US-09-457-046B-4
US-08-336-40BB-1
PCT-US91-00399-1
US-08-336-40BB-3
PCT-US91-00399-3
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US-08-940-424-13
US-08-852-936C-2
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CURRENT APPLICATION NUMBER: US/09/189,760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1998-11-10
EARLIER APPLICATION UNDBER: 09/163,116
EARLIER FILING DATE: 1998-09-29
EARLIER APPLICATION NUMBER: 60/089,467
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: (PENDING)
EARLIER FILING DATE: 1998-11-09
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Patent No. 6031078
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US-09-188-811-5/c
; Sequence 5, Application US/09188811
; Patent No. 6037148
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Best Local Similarity 95.0
Matches 19; Conservative
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US-09-189-760-5
            GENERAL INFORMATION:
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ORGANISM: HOMO
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433374331098
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PRIOR APPLICATION NUMBER: 60/089,467 PRIOR FILING DATE: 1998-06-16
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                  NAME/KEY: CDS
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LENGTH: 2494
                SEQ ID NO 1
LENGTH: 1704
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                                                          TYPE: DNA
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ENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
ENTION: THEREFOR
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Best Local Similarity 95.0%; Pred. No. 0.89
Matches 19; Conservative 0; Mismatches
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CURRENT FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US/09/189,760
PRIOR FILING DATE: 1998-11-10
PRIOR PAPLICATION NUMBER: 09/163,116
PRIOR PRILING DATE: 1998-09-29
PRIOR PRILING DATE: 1998-06-16
PRIOR PELLING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: (PENDING)
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Pred. No. 0
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CURRENT FILING DATE: 1998-11-09
EARLIER APPLICATION NUMBER: 09/163,116
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 8
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1998-11-09
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; Sequence 5, Application US/09514422
; Patent No. 6291193
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Patent No. 603718
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
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Best Local Similarity 95.0%;
Matches 19; Conservative
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                    PatentIn Ver. 2.0
                                                                                             ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
NUMBER OF SEQ ID NOS: 8
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NUMBER OF SEQ ID NOS:
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; LOCATION: (3)..(749)
US-09-188-811-5
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US-09-514-422-5
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APPLICANT: Khodad
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SEQ ID NO 5
                                                                               TYPE: DNA
                SOFTWARE:
SEQ ID NO 5
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APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MNI-046CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
APILICANT: Khodadoust, Mehran
ATITLE OF INVENTION: NOVEL MIBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
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Pred. No. 0.99;
0; Mismatches 1; Indels 0.
                                                                                                                                 92.0%; Score 18.4; DB 3; Length 1704; 95.0%; Pred. No. 0.91; 1. Indels 0
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CURRENT APPLICATION NUMBER: US/09/189,760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION WOMBER: US/09/514,422 CURRENT FILING DATE: 2000-02-28 PRIOR APPLICATION NUMBER: US/09/189,760
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PRIOR FILING DATE: 1998-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1998-11-10
SARLIER APPLICATION NUMBER: 09/163,116
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EARLIER APPLICATION NUMBER: 60/089,467
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EARLIER FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 10
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Patent No. 6031078
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Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                                    Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (164)..(1714)
US-09-189-760-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
                                                                  LOCATION: (1)..(1701)
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APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6006B.AJ172A
CURRENT APPLICATION NUMBER: US/09/175,928A
CURRENT APPLICATION NUMBER: 0998-10-20
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
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SCHERAL INCORMATION:
APPLICANT: Reed, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Modomath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475C1
CURRENT PELICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER PILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
8-09-370-838-217
Sequence 217, Application US/09370838
Patent No. 6444425
                                                                                                                                                     Sequence 29, Application US/09175928A Patent No. 6312921
GENERAL INFORMATION:
                                                388 GCAGGAAAGGCTTGGGCTG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 GCAGGAAAGGCTTGGCTG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GCAGGAAAGGTTTGGTCTG 20
                                                                                                                                                                                                                     APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOY, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 89.55
Best Local 17, Conservative
                                                                                                                                                                                                                                                                                                                               : Merberg, David
: Treacy, Maurice
                                                                                                                                                                                                                                                                                                           APPLICANT: Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unsure
                                                                                                                                      IS-09-175-928-29/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 29
LENGTH: 525
TYPE: DNA
                                                g
                                                                                                                                                                                                                                                                                     Length 2494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
                                                                                                                                                                                                                                                                                Score 18.4; DB 4;
Pred. No. 0.99;
0; Mismatches 1;
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Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Genetics Institute, Inc.
87 CambridgePark Drive
1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                      1369 TGCAGGAAAGGTTGGGTCTG 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/08686878A Patent No. 5708157
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  1 TGCAGGAAAGGTTTGGTCTG 20
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TELEPHONE: (617) 498-824
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCoy, John
LaVallie, Edward
Racie, Lisa
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.0%;
Matches 19; Conservative
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illarity 89.5%;
Conservative
                                                                    Patentin Ver. 2.0
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ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-1;
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2;
SEQ ID NO 1
LENGTH: 2494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
                                                                                                                                                                                           ) NAME/KEY: CDS
; LOCATION: (164)..(1714)
US-09-514-422-1
                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Best Local Similarity
Matches 17; Conserv
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Gaps

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Indels

Length 2052;

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APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.2; I
Pred. No. 32;
                                                                                                                                                                                                                                                                          Mismatches
                 CURRENT APPLICATION NUMBER: US/09/657,481A CURRENT FILING DATE: 2000-09-07 NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-08-545-809A-32/c
; Sequence 32, Application US/08545809A
; Patent No. 6096878
                                                                                                                                                                                                                                                                                                                                 1764 AGGAAAGCTTTGGTCTG 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
human lymphoblast
CGM1
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TELEFAX: 617-542-8906
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85.0%;
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Best Local Similarity 94:1%;
Matches 16; Conservative
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REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                              4 AGGAAAGGTTTGGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 341 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                               CCATION: (1)...(2052) US-09-657-481A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE:
CELL LINE:
                                                                                                                                                                  NAME/KEY: CDS
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                                                                                        LENGTH: 2052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                             TYPE: DNA
                                                                                                                                                 FEATURE
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                                                                                                                                                                                                                                                                                                                            APPLICANT: Kay, Brian K.
APPLICANT: FOWLKES, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYBEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAMENUMBER OF SEQUENCES: 124
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                        Length 466;
                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
                                                        DB 4;
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Pred. No. 38;
0; Mismatches
                                                                                        Mismatches
                                                    Score 15.4;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/630,916A
03-APR-1996
                                                                                                                                                                                                                                                    Sequence 45, Application US/08630916A Patent No. 6011137 GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09657481A
Patent No. 6258601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1764 AGGAAAGCITIGGTCIG 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MISROCK, S. LESILE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION:
TELEPHONE: (212) 790-9090
                                                                                                                                               343 TGCAGGGAAGGTTTGGT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pennie & Edmonds
                                                                                                                           1 TGCAGGAAAGGTTTGGT 17
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APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISE
TITLE OF INVENTION: EXPRESSION
                                                    77.0%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
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                                             Query Match
Best Local Similarity 94.15
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: United States 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2052 bases
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
; ORGANISM: Homo sapien
US-09-370-838-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Bre
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                                                                                                                                                                                                                                    US-08-630-916A-45/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-657-481A-3/C
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SEQUENCE CHARACTERISTICS
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Maryland
                                                                                                                                                              CLASSIFICATION:
                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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        0
        Gaps
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                                                                                                                                                                                                                                  APPLICANT: Glucksmann, M. Alexandra
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS AND
TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR DISEASES INVOLVING TRBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09360220
Patent No. 6046308
GENERAL INFORMATION:
APPLICANT: Glucksmann, M. Alexandra
APPLICANT: Glucksmann, M. Alexandra
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS AND
TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR DISEASES INVOLVING TRBP
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 554;
        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.0%; Score 15.2; Dest Local Similarity 85.0%; Pred. No. 36; Matches 17; Conservative 0; Mismatches
    0; Mismatches
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: FOLEY, HOAG & ELIOT LLP
One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,146
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                          Sequence 16, Application US/08840146
Patent No. 6037173
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490 TGCAGGACTGGTTGGGTCTG 509
                                                                            233 TGCAGGAAATGTTGTGTCTG 214
                                        1 TGCAGGAAAGGTTTGGTCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TGCAGGAAAGGTTTGGTCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Arnold, Beth E. REGISTRATION NUMBER: 35,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MI
FELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic) US-08-840-146-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 554 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
  Conservative
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109-2170 5
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STREET: ULL
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US-09-360-220-16
17;
                                                                                                                                                        US-08-840-146-16
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  Matches
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Sequence 325, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICATE Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1:4Mb storage
COMPUTER: HP Vectra 486/33 .
                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/360,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.2;
                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/840,146
FILING DATE: 11-APP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGCAGGAAAGGTTTGGTCTG 20
E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 554 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : (301) 309-8504
(301) 309-8512
OR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                        TELEPHONE: 61/-00-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
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LENGTH: 1237 base pairs
TYPE: nucleic acid
TYPE: STRANDEDNESS: double
TOPOLOGY: linear
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	Gaps
37;	ô
Length 1237;	; Indels
DB 4;	ω,
76.0%; Score 15.2; D 85.0%; Pred. No. 43;	0; Mismatches
76.0%; 85.0%;	ative
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ch 1 Sim	17;
Query Match Best Local Similarity	Matches 17; Conservative

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Search completed: July 8, 2003, 09:32:01 Job time: 29.6598 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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July 8, 2003, 19:09:54 ; Search time 115.512 Seconds	(without alignments) 273.390 Million cell updates/sec
Run on:	

US-09-647-780A-14 20 1 tgcaggaaaggtttggtctg 20

Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1105431 seqs, 789497651 residues Searched:

2210862 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Description			Sequence 657, App	Sequence 22909, A	Sequence 217, App	Sequence 217, App	Sequence 3, Appli	Sequence 1041, Ap	Sequence 3, Appli	Sequence 24121, A	Sequence 2991, Ap	Sequence 2991, Ap	Sequence 29, Appl	•	Sequence 27372, A	Sequence 7458, Ap	Sequence 157, App	Sequence 32, Appl	Sequence 3428. Ap
ID	US-10-025-380-657	US-09-922-217-657	US-09-833-263-657	US-09-918-995-22909	US-10-079-854-217	US-09-764-878-217	US-09-770-689A-3	US-09-917-800A-1041	US-10-023-335-3	US-09-864-761-24121	US-09-796-692-2991	US-10-040-862-2991	US-10-016-249-29	US-10-040-916-29	US-09-918-995-27372	US-09-864-761-7458	US-10-114-893-157	US-09-974-300-32	US-09-938-842A-3428
DB	6	10	10	6	σ	10	10	10	12	10	6	σ	σ	12	0	10	σ	10	σ
Length	402	402	402	509	16854	16854	98865	929	961	200	323	323	525	525	550	551	1212	1464	2000
Query Match	84.0	84.0	84.0	84.0	84.0	84.0	84.0	80.0	80.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0
Score	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16	16	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8
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	Query Score Match Length DB ID	Query         Score Match Length DB ID         Description           16.8         84.0         402.9         US-10-025-380-657         Sequence 657.	Query       Score Match Length DB ID       DB         16.8       84.0       402       90.5-10-025-380-657       57         16.8       84.0       402       10.9-09-922-217-657	Query         Query         Description           16.8         84.0         402         9 US-10-025-380-657         Sequence 657, 16.8           16.8         84.0         402         10 US-09-922-217-657         Sequence 657, 16.8           16.8         84.0         402         10 US-09-833-263-657         Sequence 657	Score March Length DB ID Description 16.8 84.0 402 9 US-10-025-380-657 Sequence 657, 16.8 84.0 402 10 US-09-922-217-657 Sequence 657, 16.8 84.0 402 10 US-09-933-263-657 Sequence 657, 16.8 84.0 509 9 US-09-918-955-22909 Sequence 2290	Score Match Length DB ID  16.8 84.0 402 9 US-10-025-380-657 Sequence 657, 16.8 84.0 402 10 US-09-922-217-657 Sequence 657, 16.8 84.0 402 10 US-09-918-995-22909 Sequence 557 (16.8 84.0 509 9 US-09-918-995-22909 Sequence 2290 16.8 84.0 16854 9 US-10-079-844-217 Sequence 2190	Score Match Length DB ID  16.8 84.0 402 9 US-10-025-380-657 16.8 84.0 402 10 US-09-922-217-657 16.8 84.0 402 10 US-09-918-935-2299 16.8 84.0 16854 9 US-09-918-938-2299 16.8 84.0 16854 10 US-09-844-217 16.8 84.0 16854 10 US-09-964-217 16.8 84.0 16854 10 US-09-964-217  16.8 84.0 16854 10 US-09-964-217  Sequence 217,	Score Match Length DB ID Description 16.8 84.0 402 9 US-10-025-380-657 Sequence 657, 16.8 84.0 402 10 US-09-922-217-657 Sequence 657, 16.8 84.0 509 9 US-09-918-995-2299 Sequence 527, 16.8 84.0 16854 9 US-10-079-854-217 Sequence 229, 16.8 84.0 16854 10 US-09-918-995-2299 Sequence 221, 16.8 84.0 16854 10 US-09-774-878-217 Sequence 217, 16.8 84.0 16854 10 US-09-774-878-217 Sequence 217, 16.8 84.0 98865 10 US-09-770-6894-3 Sequence 3.7	Score Match Length DB ID  16.8 84.0 402 9 US-10-025-380-657 Sequence 657, 16.8 84.0 402 10 US-09-922-217-657 Sequence 657, 16.8 84.0 16854 9 US-10-099-833-263-657 Sequence 237, 16.8 84.0 16854 9 US-10-079-854-217 Sequence 217, 16.8 84.0 16854 10 US-09-764-878-217 Sequence 217, 16.8 84.0 16854 10 US-09-764-878-217 Sequence 217, 16.8 84.0 98865 10 US-09-764-878-31 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 10.4 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 Sequence 3, 16.8 84.0 656 10 US-09-770-6894-3 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US-10-079-884-217 16.8 84.0 16854 9 US-10-079-884-217 16.8 84.0 18855 10 US-09-764-878-217 16.8 84.0 98855 10 US-09-770-6898-3 16.8 84.0 656 10 US-09-770-6898-3 16 80.0 656 10 US-09-717-800A-1041 16 80.0 656 10 US-03-335-3 16.8 Match Sequence 37, Sequence 207 16.8 84.0 98855 10 US-09-770-6898-3 16 80.0 656 10 US-09-717-800A-1041 16 80.0 656 10 US-09-3135-3	Score Match Length DB ID Description  16.8 84.0 402 9 US-10-025-380-657 Sequence 657, 16.8 84.0 402 10 US-09-922-217-657 Sequence 657, 16.8 84.0 509 9 US-09-918-995-22909 Sequence 227, 16.8 84.0 16854 9 US-10-079-84-217 Sequence 227, 16.8 84.0 16854 10 US-09-917-804-817 Sequence 217, 16.8 84.0 98865 10 US-09-76-898-3 Sequence 217, 16.8 84.0 98865 10 US-09-917-8008-104 Sequence 217, 16.8 84.0 98865 10 US-09-917-8008-104 Sequence 3, 16.8 0.0 951 12 US-10-023-335 Sequence 3, 15.8 79.0 200 10 US-09-917-8018-104 Sequence 3, 15.8 79.0 200 10 US-09-84761-2412 Sequence 24.1	Score Match Length DB ID Description  16.8 84.0 402 9 US-10-025-380-657 Sequence 657, 16.8 84.0 402 10 US-09-922-217-657 Sequence 657, 16.8 84.0 16854 9 US-09-918-955-2290 Sequence 217, 16.8 84.0 16854 9 US-09-918-955-2290 Sequence 217, 16.8 84.0 16854 10 US-09-918-951-217 Sequence 217, 16.8 84.0 16854 10 US-09-918-917 Sequence 217, 16.8 84.0 98865 10 US-09-917-8004-1041 Sequence 3, 16.8 0.0 656 10 US-09-917-8004-1041 Sequence 3, 16.8 0.0 961 12 US-10-023-335-3 Sequence 3, 16.8 0.0 961 12 US-10-023-335-3 Sequence 241 15.8 79.0 200 10 US-09-96-622-2991 Sequence 2911 Sequence 2911	Score Match Length DB ID  16.8 84.0 402 9 US-10-025-380-657 Sequence 657, 16.8 84.0 402 10 US-09-922-217-657 Sequence 657, 16.8 84.0 16854 9 US-10-079-854-217 Sequence 217, 16.8 84.0 16854 9 US-10-079-854-217 Sequence 217, 16.8 84.0 16854 10 US-09-918-955-22099 Sequence 217, 16.8 84.0 16854 10 US-09-764-878-217 Sequence 217, 16.8 84.0 16854 10 US-09-764-878-217 Sequence 217, 16.8 84.0 16854 10 US-09-764-878-217 Sequence 3, 16.8 84.0 656 10 US-09-764-878-217 Sequence 3, 16.8 80.0 656 11 US-09-764-878-31 Sequence 3, 15.8 79.0 200 10 US-09-864-761-24121 Sequence 2991 15.8 79.0 323 9 US-10-040-862-2991 Sequence 2991	Score Match Length DB ID Description  16.8 84.0 402 9 US-10-025-380-657 Sequence 657, 16.8 84.0 402 10 US-09-927-217-657 Sequence 657, 16.8 84.0 16854 9 US-10-928-3290 Sequence 2290 16.8 84.0 16854 9 US-09-918-995-22909 Sequence 217, 16.8 84.0 16854 10 US-09-917 Sequence 217, 16.8 84.0 16854 10 US-09-917 Sequence 217, 16.8 84.0 16854 10 US-09-917 Sequence 217, 16.8 84.0 9865 10 US-09-917 Sequence 217, 16.8 84.0 9865 10 US-09-917 Sequence 217, 16.8 87.0 961 12 US-10-921 Sequence 34, 16.8 87.0 961 12 US-09-917 Sequence 34, 16.8 87.0 323 9 US-10-023335-31 Sequence 24, 15.8 79.0 323 9 US-10-040862-2991 Sequence 2991  Score Match Length DB ID Description  16.8 84.0 402 9 US-10-025-380-657 Sequence 657, 16.8 84.0 402 10 US-09-9272-217-657 Sequence 657, 16.8 84.0 16854 10 US-09-9218-957-2590 Sequence 517, 16.8 84.0 16854 10 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US-10-040-916-29 Sequence 297372 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 Sequence 27378 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US-10-046-29 Sequence 2991 15.8 79.0 525 12 US-10-046-29 Sequence 2991 15.8 79.0 550 9 US-09-918-928-27372 Sequence 2737 Sequence 2737 15.8 79.0 551 10 US-09-918-928-27372 Sequence 2737 15.8 79.0 551 10 US-09-918-928-27372 Sequence 2737 15.8 79.0 1212 9 US-10-114-891-157 Sequence 2737 15.8 79.0 1212 9 US-10-114-891-157 Sequence 2737 15.8 79.0 1212 9 US-10-114-891-157 Sequence 2737	Score Match Length DB ID  16.8 84.0 402 9 US-10-025-380-657 16.8 84.0 402 10 US-09-922-217-657 16.8 84.0 16854 9 US-09-928-217-657 16.8 84.0 16854 9 US-09-938-217 16.8 84.0 16854 10 US-09-918-217 16.8 84.0 16854 10 US-09-918-217 16.8 84.0 16854 10 US-09-917-8044 16.8 84.0 16854 10 US-09-917-8043 16.8 84.0 16854 10 US-09-917-8043 16.8 84.0 16854 10 US-09-917-8004-317 16.8 10 05-60-917-8004-317 16.8 10 05-60-917-8004-317 15.8 79.0 200 10 US-09-796-692-2991 15.8 79.0 323 9 US-10-104-862-2991 15.8 79.0 525 9 US-10-104-862-2991 15.8 79.0 525 9 US-10-040-916-29 15.8 79.0 550 9 US-09-918-995-27372 15.8 79.0 550 9 US-09-918-995-27372 15.8 79.0 551 10 US-09-918-995-27372 15.8 79.0 1212 9 US-10-116-29 15.8 79.0 1212 9 US-10-116-29 15.8 79.0 1212 9 US-10-116-29 15.8 79.0 1212 9 US-10-116-29 15.8 79.0 1212 9 US-10-114-893-157 15.8 79.0 1212 9 US-10-114-893-157 15.8 79.0 1212 9 US-10-114-893-157 15.8 79.0 1464 10 US-09-934-300-32	

DB 9; Length 402;

Score 16.8; DI Pred. No. 53; 0; Mismatches

Similarity

Query Match Best Local S Matches 18

Sequence 8605, Ap	Sequence 8604, Ap	Sequence 3, Appli	7	Sequence 3, Appli	Sequence 8439, Ap	Sequence 32502, A	Sequence 217, App	Sequence 217, App	217,	Sequence 31836, A	Sequence 1180, Ap	54, Ap	Seguence 154, App	Sequence 154, App	Sequence 30327, A	Sequence 9425, Ap	Sequence 40, Appl	Sequence 13, Appl	Sequence 41, Appl	Sequence 22, Appl	Sequence 361, App	Sequence 291, App	Sequence 14038, A	Sequence 37, Appl	Sequence 465, App	
US-09-764-891-8605	US-09-764-891-8604	US-09-900-449A-3	US-09-754-853A-2	US-09-754-853A-3	US-09-918-995-8439	US-09-918-995-32502	US-09-854-133-217	US-10-144-649A-217	US-09-738-973-217	US-09-918-995-31836 .	US-09-917-800A-1180	US-10-025-380-154	US-09-922-217-154	US-09-833-263-154	US-09-918-995-30327.	US-10-198-846-9425	US-10-144-929-40	US-10-036-542-13	US-10-205-823-41	US-10-177-293-22	US-09-764-864-361	US-09-770-445-291	US-10-198-846-14038	.US-10-036-542-37	US-09-925-301-465	
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15.8	15.8	15.8	15.8	15.8	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	
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## ALIGNMENTS

	RESULT 1 US-10-025-380-657	
	; Sequence 657, Application US/10025380	
	GENERAL INFORMATION:	•
	; APPLICANT: Xu, Jiangchun	
	: Secrist,	
	: Benson, I	
	: Meagher	
	: Stolk,	
•	': Wang, T	
•	; APPLICANT: Jiang, Yuqiu	
	; APPLICANT: Smith, Carole L.	
	; APPLICANT: King, Gordon E.	
	; APPLICANT: Wang, Aijun	
	w	
	; APPLICANT: Skelky, Yasir A. W.	
	; APPLICANT: Fanger, Gary R.	
	-	
	; APPLICANT: Carter, Darrick	
	; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DI	7 AND DIAGNOSIS
	CANCER AND METHODS FOR	
	; FILE REFERENCE: 210121.471C14	
	; CURRENT APPLICATION NUMBER: US/10/025,380	•
	; CURRENT FILING DATE: 2001-12-19	
	; NUMBER OF SEQ ID NOS: 1129	
	; SOFTWARE: FastSEQ for Windows Version 4.0	•
	; SEQ ID NO 657	
	; LENGTH: 402	
	; TYPE: DNA	
	; ORGANISM: Homo sapiens	•
	FEATURE:	
	; NAME/KEY: misc_feature	
	, 154	•
	CTHER INFORMATION: D = A,T,C or G	
	10-020-10-01-20 02-11-020-12-12-12-12-12-12-12-12-12-12-12-12-12-	

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Gaps

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Length 16854;
            Length 402;
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TITLE OF INTENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENC:: PA121C1
CURRENT APPLICATION NUMBER: US/10/079,854
CURRENT FILING DATE: 2002-02-22
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 428
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 217
LENGTH: 16854
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                                                     Indels
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APPLICATE: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT APPLICATION NUMBER: US/09/235,076

PRIOR PRILING DATE: 1999-01-20
              DB 10;
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; Pred. No. 63;
.0; Mismatches 2;
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                                                         0; Mismatches
              84.0%; Score 16.8; 90.0%; Pred. No. 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 38054
SOFTWARE: EastSEQ for Windows Version 3.0
SEQ ID NO 22909
LENGTH: 509
                                                                                                                                                                                                                      -09-918-995-22909/c
Sequence 22909, Application US/09918995
Publication No. US20030073623A1
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lo. US20030054368A1
                                                                                                                       366 TGCAGGGAAGGTTTGGTTTG 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (I) ..(509)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22909
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Best Local Similarity 90.0%;
Matches 18; Conservative .
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Best Local Similarity 90.0%;
Matches 18; Conservative
                                    Best Local Similarity 90.0
Matches 18; Conservative
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                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                           Matches
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APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 21012.1.4710.12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                   apper, Jonathan D. THENDOTHERAPY AND DIAGNOSIS TION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TION: OF COLON CANCER AND METHODS FOR THEIR US: 210121.471C13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
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Pred. No. 53;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Application US/09833263
$20020110547A1
                                                                                                                                          7, Application US/09922217
US20020076414A1
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                 366 TGCAGGGAAGGTTTGGTTTG 385
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US-09-833-263-657
                                                                                                                                                                                                                                                                                        eagher, Madeleine Joy
colk, John A.
ng, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                    ang, Yuqiu
nith, Carole Lynn
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ilarity 90.08;
Conservative
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                                                                                                                                                                                                       Jiangchun
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OTHER INFORMATION: n =
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapien
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Patent No. US200.
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LENGTH: 402
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US 60/222,880

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LING DATE: 2000-11-02
PLICATION NUMBER: US 60/290,029
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APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLOO1079
                                                                                                                                                                                                                                                                                                                                                                              Length 16854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 98865;
                                    GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 428
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 84.0%; Score 16.8; E
Best Local Similarity 90.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/770,689A CURRENT FILING DATE: 2001-01-29 NUMBER OF SEQ ID NOS: SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/917,800A CURRENT FILING DATE: 2001-07-31
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PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
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Sequence 217, Application US/09764878 Patent No. US20020090615A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5587 TGCAGGACAGGTTTGGTTTG 5568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGCAGGAAAGGTTTGGTCTG 20
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Best Local Similarity 90.0%;
Matches 18; Conservative
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Castle, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porter, Mark
                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-09-764-878-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3
LENGTH: 98865.
TYPE: DNA
COGANISM: HUMAN
US-09-770-689A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-917-800A-1041
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                                                                                                                                                                                                                                          SEQ ID NO 217
LENGTH: 16854
                                                                                                                                                                                                                                                                                     TYPE: DNA
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TITLE OF INVENTION: COMPOSITIONS AND METHODS USEFUL FOR TREATMENT OF DEPRESSIVE D
TITLE OF INVENTION: BASED ON AN ANIMAL MODEL
FILE REFERENCE: 05366-5002-01
CURRENT APPLICATION NUMBER: US/10/023,335
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION WUMBER: US 09/590,837
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION WUMBER: PCT/US99/17513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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US-09-917-800A-1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 656;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.0%; Score 16; DB 10; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 16; Conservative 0; Mismatches 0;
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1.4e+0;
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PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
                                                                                    PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: US 60/105,459
                                                                                                                                                                      FILING DATE: 2001-06-06
APPLICATION NUMBER: US 60/297,457
                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                          FILING DATE: 2001-06-13
APPLICATION NUMBER: US 60/298,884
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Rattus norvegicus
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: 05/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
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Pred. No. 1.6e+02;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2991
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                                                                                                                                                      Sequence 2991, Application US/09796692
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION UNBABR: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
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PLICATION NUMBER: 60/200,303
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                         129 TGCAGAAAGGTTTGGCCT
                                                                                                                                                                           US20020198362A1
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APPLICANT: Gaiger, Alexander
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US-09-796-692-2991
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SWISSPROT HIT: 043920, EVALUE 3.00e-18
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TN ADULT LIVER, SIGNAL = 1.3
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URRENT FILING DATE: 2001-05-23
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ING DATE: 2001-01-30
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LING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLICATION NUMBER: US 60/236,359
LING DATE: 2000-09-27
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                  US20020048763A1
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PPLICATION NUMBER: GB 24263.6
LING DATE: 2000-10-04
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ORGANISM: Homo sapiens
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US-09-864-761-24121
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RIOR

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TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                              Length 525;
                                                                                                                                                                                                                                                                      Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US,10/040,916
FILING DATE: 07-Jan-2002
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,878
APPLICATION NUMBER: 08/686,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
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tent No. US20020146769A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                        388 GCAGGAAAGGCTTGGGCTG 370
                                                                                                                                                                                                                                                                                                                2 GCAGGAAAGGTTTGGTCTG 20
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Evans, Cheryl
Spaulding, Vikki
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LaVallie, Edward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jacobs, Kenneth
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STATE: Massachusetts
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ilarity 89.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                             ; LOCATION: (59)
US-10-016-249-29
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                                 CATION
                                                                                                                                            NAME/KEY
                                                                         NAME/KE)
                                                                                                                   FEATURE
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TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM FILE REFERENCE: 6006B.AJ172A
CURRENT APPLICATION NUMBER: 105.10/016,249
CURRENT FILING DATE: 2001-10-30
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Pred. No. 1.
                                                                                  APPLICATION NUMBER: US 60/200,545
RILING DATE: 2000-04-27
APPLICATION NUMBER: US 60/200,303
RILING DATE: 2000-04-28
APPLICATION NUMBER: US 60/200,779
RILING DATE: 2000-04-28
APPLICATION NUMBER: US 60/200,999
RILING DATE: 2000-06-01
APPLICATION NUMBER: US 60/200,999
                                                                                                                                                                                                                                                                             R FILING DATE: 2000-05-04

R APPLICATION NUMBER: US 60/206,201

R FILING DATE: 2000-05-22

R FILING DATE: 2000-07-14

R FILING DATE: 2000-07-18,950

R APPLICATION NUMBER: US 60/218,950
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SOFTWARE: FastSEQ for Windows Version 3.(
NUMBER: US 60/186,126
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PPLICATION NUMBER: US 60/223,378
ILING DATE: 2000-08-07
                                              CATION NUMBER: US 60/190,479
3 DATE: 2000-03-17
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PLICATION NUMBER: US 60/223,416
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PRIOR FILING DATE: 1998-10-20
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Publication No. US20030100053A1
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LaVallie, Edward R.
Collins-Racie, Lisa
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Treacy, Maurice
Mi, Sha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-040-862-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                      ILING DATE: :
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SOFTWARE: Fas

IOR IOR

IOR

SOFTWARE: Pate SEQ ID NO 29 LENGTH: 525

TYPE: DNA

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0; Gaps
  Score 15.8; DB 12; Length 525;
Pred. No. 1.7e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 550;
                                                                                                                                                                                                                                          Sequence 27372, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICAMT: Hyseq. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT FILIGH DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/918,995
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27372.
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.0%; Score 15.8; DB 9; Best Local Similarity 89.5%; Pred. No. 1.7e+02; Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(550)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27372
                                                                                       Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                      RESULT 15
US-09-918-995-27372/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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Gaps

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Search completed: July 9, 2003, 02:22:19 Job time : 115.562 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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OM nucleic - nu	nucleic	c search, using sw model	•	,
Run on:	July	8, 2003, 00:45:53 ; Search time (without al 2644.537 Mi	220.098 Seconds .ugnments) .llion cell updates/sec	
Title: Perfect score: Sequence:	US- 20 1 t	US-09-647-780A-14 20 1 tgcaggaaaggtttggtctg 20		• ; •
Scoring table:	IDE	IDENTITY_NUC Gapop 10.0 , Gapext 1.0		
Searched:	205	2054640 seqs, 14551402878 residues		• •
Total number of	hits	s satisfying chosen parameters:	4109280	-
Minimum DB seq Maximum DB seq	length: length:	th: 0 th: 2000000000		
Post-processing:		Minimum Match 0% Maximum Match 100% Listing first 45 summaries		
Database :	ee ,	GenEmb1:*		
		90_ba:* 90_htg:* ab -tr:*		•
		4 db		
		95_0** 95_0** 95.p**		•
		90_pii: 90_pii:*		
•	10:	92-70: 95-70: 95-81:		
	12:	gb_sy:*		
,	4.5	gb_vi:* em_ba:*		
	16:	em fun:*	٠	
	18:	em_in:* em_mu:*		·
	20:	em_om:* em_or:*		
	22:	em_ov:* em_pat:*		
	24:	em_ph:* em_pl:*		
	26:	en_ro:* en_sts:*		
	28:	em_un:*		
	30:	em_htg_hum:*		•
	32:	em_itg_tiver: em_ttg_other:*		
	34.	em_htg_pln:*		<u> </u>
٠	36:	em_ncg_rod:* em_htg_mam:*		
•.	37:	em_htg_vrt:* em_sv:*		
	39:	emem*		
٠	41:	em_ntgo_mus:* em_htgo_other:*		

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

20 100 0 276 6 AX011714 AX011711 AX011711 20 100 0 1745 6 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701 AX011701	20 100.0 220 6 AX014714 AX014714 AX014714 AX014714 AX014714 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014711 AX014714 AX014711 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AX014714 AY 0.0 10829 2 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337 AC10337	Result No. S	Score	% Query Match	Length	, <u>DB</u>	SUMMARIES		н	Description
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Rattus norvegicus clone CH230-516, *** SEQUENCING IN PROGRESS ***,
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eery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
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Mammalia; Eutherla: Rodentia; Sciurognathi; Muridae; Murinae;
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On Dec 20, 2001 this sequence version replaced gi:15624568
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Aguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S
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Center: Baylor College of Medicine
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
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Patent: W0 9953077-A i 21-OCT-1999;
INST WAYS SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OLIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
JOURNAL PATENT: WO 9953077-A 14 21-OCT-1999;
INST NAT SAWE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOWME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
LOCATION/Qualifiers
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Schwartz,J.C., Gros,C., Ouimet,T., Rose,C., Bonhomme,M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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    .2765
/organism="Rattus rattus"
/db_xref="taxon:10117"

                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20;
Pred. No.
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AX014701
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/note="oligonucleotide"
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/organism="synthetic
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FEATURES

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                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                         Consensus quality: 158448 bases at least 030.
Consensus quality: 164461 bases at least 020
Estimated insert size: 155965; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; agarose-fp estimation
Quality coverage: 2.2x in 020 bases; sum-of-contigs estimation
                            Assembly program: Phrap; version 0.990329First call
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KEYWORDS
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                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 396)
Tilford, C.A., Kuroda-Kawaguchi, T., Skaletsky, H., Rozen, S.,
 SY2509 YAC Subtraction Homo sapiens STS genomic, sequence tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                        Brown, L.G., Rosenberg, M., McPherson, J.D., Wylie, K., Sekhon, M. Kucaba, T.A., Waterston, R.H. and Page, D.C. A physical map of the human Y chromosome Nature 409 (6622), 943-945 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enriched for low-copy number, Y-specific sequences.
                                                                                                                                                                                                                                                      Room 425, 9 Cambridge Center, Cambridge, MA 02142, USA Email: tilfordewinit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18.4; DB 11; Length 396;
Pred. No. 38;
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/note-"Vector: pYAC4; V-type: YAC;
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each 100 uM
0.05 units/ul
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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0 2 ml
200 ul
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7.65 ml.
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Primer B: CACGGTTCTCTCGCCATTAT
STS size: 81
PCR Profile:
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Contact: Charles A. Tilford
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Triton X-100
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PAT 17-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL plate: 42 Row: I Column: 3. Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
MAS Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                 MTbx protein and nucleic acid molecules and uses therefor Patent: US 6291193-A 5 18-SEP-2001;
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
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     DNA
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Pred. No. 42;
0; Mismatches
ARI69782.
Sequence 5 from patent US 6291193
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                                                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 TGCAGGAAAGGTTGGGTCTG 385
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                                                                                          AR169782.1 GI:17907690
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ilarity 95.0%;
Conservative
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Strausberg, R.
                                                                                                                                                                                                   Unclassified.
1 (bases 1 to 1529)
Khodadoust, M.
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PQRWLVTPVQQPGTNKLDISSYESEYTSSTLLPYGIKSLPLQTSHALGYYPDPTFPAM
AGWGGRGSYQRKMAAGLPWTSRTSPTVFSEDQLSKEKVKEEIGSSWIETPPSIKSLDS
                                                                                                                                                                                                                                                                                   RLHIVEVTEDGVEDLNEPSKTQTFTFSETQF1AVTAYQNTD1TQLK1DHNPFAKGFRD
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KLDLGKASKKFSGSLSCEAVSGEPAAASAGAPAAMLSDTDAGDAFASAAAVAKPGPPD
GRKGSPCGEEELPSAAAAAAAAAAAAAAAATRYSMDSLSSVRYYLQSPGPQGSELAAPC
                                                                                                                                                                                                                                        /translation="FPFLSFNINGLNPTAHYNVFVEVVLADPNHWRFQGGKWVTCGKA
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Institute; Kanda-Surugadai 2-3-10, Chiyoda-ku, Tokyo 101-0062,
Japan (E-mail:kimumcb@mri.tmd.ac.jp, Tel:+81-3-5280-8063,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kimura,N., Nakashima,K., Ueno,M., Kiyama,H. and Taga,T.
A novel mammalian T-box-containing gene, Tbr2, expressed in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1870;
             /tissue_type="Brain, astrocytoma, grade IV"
/clone_lib="NIH_MGC_98"
/lab_host="DH108"
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Brain Res. Dev. Brain Res. 115 (2), 183-193 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
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Pred. No. 42;
0; Mismatches
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/db_xref="taxon:9606"
/tissue_lib="fetal brain"
                                                                                                                                                                                          /protein_id="AAH25363.1"
/db xref="G1:19263737"
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/db xref="G1:5738952"
/clone="IMAGE:5013504"
                                                                                 /note-"Vector: porB7"
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Mammalia; Eutheria; Primates;
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95.0%;
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Direct Submission
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Mus musculus neprilysin-like peptidase alpha mRNA, complete cds. AF302075.1 GI:10505359
                                                                       EEVANPPQRMLVTPVQQPGTNKLDISSYESEYTSSTLLPYGIKSLPLÖTSHALGYYDD
PTFPAMAGWGGRGSYQRKMAAGLPWTSRTSPTVFSEDQLSKEKVKEEIGSSWIETPPS
IKSLDSNDSGVYTSACKRRRLSPSNSSNENSPSIKCGDINAEEYSKDTSKGMGGYYAF
                                                            AKGFRDNYDSSHQIVPGGRYGVQSFFPEPFVNTLPQARYYNGERTVPQTNGLLSPQQS
                            VTCGKADNNMQGNKMYVHPESPNTGSHWMRQEISFGKLKLTNNKGANNNNTQMIVLQS
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GGINGGGGGPGTYQYSQGAPLYGPYPGAAAGSCGGLGGLGVPSSGFRAHVYLCNRPI
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 2583)
Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W.,
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Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and
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J. Biol. Chem: 276 (24), 21895-21901 (2001).
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Pred. No. 4
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Patent: US 6291193-A 1 18-SEP-
Location/Qualifiers
e 1. 2494
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illarity 95.0%;
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llarity 95.0%;
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Khodadoust, M.
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Matches 19;
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2 (bases 1 to 2583)
Shirotani, K. and Saido, T.C.

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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus soluble secreted endopeptidase delta mRNA, alternatively spliced product, complete cds.
                                                                                                                                                                                                                                                                           translation-"MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIVTLGVFYSIALRD
                                                                                                                                                                                                                                                                                                                                                                        HLANATVPQEKRHDVTALYHRMDLMELQERFGLKGFNWTLFIQNVLSSVEVELFPDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                     )IGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAQRSLKKLREKVDQNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLN
FGGIGMVIGHEITHGFDDNGRNFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCR
                                                                                                                                                                                                                                                                                                                  DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKMVG
                                                                                                                                                                                                                                                                                                                                                        LGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELET
                                                                                                                                                                                                                                                                                                                                                                                            VVVYGIPYLENLEDI IDSYSARTMONYLVWRLVLDRIGSLSORFKEARVDYRKALYGT
                                                                                                                                                                                                                                                                                                                                                                                                                !VEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LADNONVNGFSTLGENIADNGGVRQAYKAYLRWILADGGKDQRLPGLNLTYAQLFFINY

    .. 2287
    /note="SEP(delta); metalloprotease; alternatively spliced"

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hydrolyzes a variety of vasoactive peptides
J. Biol. Chem. 274 (45), 32469-32477 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-JUN-1999) International Center for Medical Research, Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe 6500017, Japan
Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2601)
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Yokoyama,M. and Matsuo,M.
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                                                                                                                                                                                                                   product-"neprilysin-like peptidase alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18.4; DB 10;
Pred. No. 43;
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                     /protein_id="AAG18446.1"
/db_xref="G1:10505360"
                                                                                                                  /organism-"Mus musculus"
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Ikeda,K., Emoto,N. and Matsuo,M.
Direct Submission
                                                                                                                                    /db_xref-"taxon:10090"
                                                                                                                                                                               /note="endopeptidase"
                                                                              Location/Qualifiers
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Best Local Similarity 95.0%;
Matches 19; Conservative
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                                          Science Institit
351-0198, Japan
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KEYWORDS
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ORIGIN
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AUTHORS
      TITLE
JOURNAL
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AF157106
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MEDLINE
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AF3U2076 2652 bp mRNA linear ROD 11-JUN-2001
Mus musculus neprilysin-like peptidase beta mRNA, complete cds.
AF3U2076
                                                                                                                        SSLKSDICTTPSCV1AAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNSRYSVF
DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKWVG
                                                                                                                                                                                 GWPVALDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPT
LGMPSREYYEQEDNNHKVRKAYPEFMTSVATWLRKDQNLSKESAMVREEMAEVLELET
HLANATVPQEKRHDVTALYHRWDLMELQERFGLKGFNWTLFIQNVLSSVEVELFPDEE
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NNAQRSLKKLREKVDQNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLN
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IW"
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QYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRS
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IDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHKYRKAYLEFWTSVATMLRK
DQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRWDLMELQERFGLKG
                                                                                                                                                                                                                                                                                                         TVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELN
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                                                                                        /translation="MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIALRD
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Mammalla, Eutherla, Rodentla, Sciurognathi, Muridae, Murinae, Mus
1 (Bases 1 to 2652)
Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W.,
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secreted endopeptidase delta"
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/protein_id="AAG18447.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
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Pred. No. 43;
0; Mismatches
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/db_xref="taxon:10090"
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   /product="soluble &
/protein_id="AAF131
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Shirotani, K. and Saido, T.C.
Direct Submission
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95.0%;
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Best Local Similarity
Matches 19; Conserva
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Mus musculus
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QIVFPAGILQPPFFSKDQPQSLNFGGIGMYICHEITHGFDDNGRNFDKNGNMLDWWSN
FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLA
DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                                   KSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHL
                                                                              DEEYSSLTFYEDLYFENGLONLKNNAQRSLKKLREKVDQNLW1 IGAAVVNAFYSPNRN
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NFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNG
FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMONYLVWRLVLD
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HSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPWKRCRIW"
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Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T., Neutsubo, T. and Saido, T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and
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Mus musculus neprilysin-like peptidase gamma mRNA, complete cds.
AF302077
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/protein_id="AAG18448.1"
/db_xref="GI:10505364"
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J. Biol. Chem. 276 (24), 21895-21901 (2001)
                                                                                                                                                                                                                                                                                        DB 10;
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Shirotani, K. and Saido, T.C.
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AF157105 25-NOV-1999 MRNA linear ROD 25-NOV-1999 Mus musculus soluble secreted endopeptidase mRNA, complete cds. AF157105
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DGGKDQRLFGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular identification and characterization of novel membrane-bound metalloprotease, the soluble secreted form of which hydrolyzes a variety of vasoactive peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-JUN-1999) International Center for Medical Research,
Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
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Sciurognathi; Muridae; Murinae; Mus
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/note="SEP; metalloprotease"
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Pred. No. 4
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/db_xref="taxon:10090"
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da,K., Emoto,N. and Matsuo,M.ect Submission
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 2892)
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Query Match 92.0%;
Best Local Similarity 95.0%;
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FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLA
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PLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus neprilysin-like metallopeptidase 1 (N11) mRNA
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1 (bases 1 to 2925)
Ghaddar,G., Ruchon,A.F., Carpentier,M., Marcinkiewicz,M.,
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Ghaddar,G., Ruchon,A.F., DesGroseillers,L. and Boileau,G.
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                  AX033272 2925 bp
Sequence 12 from Patent W00047750.
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/db_xref="taxon:10090"
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DGGKDQRLFGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                                                                                                                                                                                                                                                                                                                                                                               /translation="MVERAGWCRKKSPGFVEYGLMVLLLLLLLGAIVTLGVFYSIGKQI
Direct Submission
Submitted (09-AUG-1999) Biochemistry, University of Montreal, 2900
Edouard Montpetlit, Montreal, Que H3T 1J4, Canada
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                   product="neprilysin-like metallopeptidase 1'
protein_id="AAF69247.1"
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Pred. No. 44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPGFSEAFHCPRGSPMHPMKRCRIW
                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                              tissue_type="testis"
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milarity 95.0%;
Conservative (
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                                                                                                                                                                                                       /gene="Nll"
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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 00:47:28; Search time 1013.95 Seconds

(without alignments)
319.453 Million cell updates/sec

Title: US-09-647-780A-14

Perfect score: US-09-647-780A-14

Sequence: 1 tgcaggaaaggtttggtctg 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132*

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 1008

Maximum Match 1008

Listing first 45 summaries
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Database : EST:*

1: em_estba:*
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4: em_estli:*
5: em_estpov:*
6: em_estpov:*
7: em_estpov:*
9: 9b_estl:*
10: 9b_estl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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					,	SUMMARIES		
Result No.		Score	% Ouery Match	å Query Match Length DB	BB.	ΠD	Desci	Description
υ	1 16	18.4	92.0	311	ြက	AA323074	AA323	AA323074 EST25804
ပ	2 16	3.4	92.0	364	10	BE679769	. BE67	BE679769 df56h10.v
v	3 16	3.4	92.0	809	7	AW965242	96MA	5242 EST377315
	4 .17	7.4	87.0	355	12	BG413980	BG41	BG413980 de76c11.x
	5 17	7.4	87.0	385	13	BI041429	BIO	BI041429 PM0-NT091
_	9	4.4	87.0	390	10	BE192046	BE19	BE192046 db86f12.x

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BFC	AW6	AOB	AW633	BG01	BGO	BG4	BG2	BMS	AJ44	B03	A03	A09	BB4	BG1	BJ4	BF3	AA88	BO9	BJ4	BG6	AI072298	AI71	AI070598	W45	AQ283	A05	BJ3	AZ8	BIO	BJ5	AAB7	BG0	BG8	BE3	BJ4	BJ4	BE3	
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## ALIGNMENTS

AA323074/c	
	AA323074 311 bp mRNA linear EST 20-APR-1997
DEFINITION	Cerebellum II Homo sapiens cDNA 5
ACCESSION	AA323074
	AA323074.1 GI:1975399
	EST.
	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 311)
AUTHORS	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
	,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
	,0., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
	Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
	,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
	Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M.,
	Kelley, J.C., Liu, LI., Marmaros, S.M., Merrick, J.M.,
	Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,
	Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
	Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., L1, Y.,
	Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
	Dimke, D., Feng, DF., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.
	, Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
	<pre>Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,</pre>
	Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
	.M.R. Rosen.C.A. Haseltine.W.A. Fields.C. Fraser.C.M. and

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source
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1 (bases 1 to 364)
clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
', Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
',B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE679769 364 bp mRNA linear EST 31-MAY-2002 df56h10.yl Xenopus laevis unfertilized egg cDNA library Xenopus laevis cDNA clone XENOPUS_SOURCE_ID:xlnneg002120 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing Center
al assessment of human gene diversity and expression patterns upon 83 million nucleotides of CDNA sequence 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                             Email: arkerlav@tigr.org
Dro clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information Seq primer: -40RP from Glbco. High quality sequence stop: 359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/note="Organ: brain; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 311;
                                                                                                                                        The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
7el: 3018699056
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Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.4; DB 9;
Pred. No. 1.2e+02;
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washU Kenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="ATCC (inhost):123602"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Cerebellum II"
/tissue_type="cerebellum"
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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      Initial assessment of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 TGCAGGAAAGGTTGGGTCTG 124
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                                                                                                                                                                                                                                                                                                                       Seq primer: M13 Reverse
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Other_ESTs: df56h10.x1
                                                                                              Contact: Kerlavage, AR
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Xenopus laevis
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AUTHORS
                                                JOURNAL
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(pBluescript SK-) in X11-Blue using ExAssist phage. The resulting single-stranded phagemids were used to infect Toplof'. Clones were picked into freezing medium (per liter 15 g tryptone, 10g yeast extract, 5g NaCl, 36 mM KZHPO4, 13.7 mM KH2PO4, 1.7 mM Na-Citrate, 0.4 mM MS5O4*7 H2O, 6.8 mM (NH4, 2504, 4% w/v glycerol) and grown for 24 hours. Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194·196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Note: This is a Xenopus Gene Collection (XC) library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW965242 608 bp mRNA linear EST 01-JUN-2000 EST377315 MAGE resequences, MAGI Homo sapiens cDNA, mRNA sequence. AW965242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. (boses 1 to 608) (boses 1 to 608) (boses 1 to 608) (constantly, K., Dharap, S., Gaspard, R., Gay, C., Holt, C., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                      clone_lib="Xenopus laevis unfertilized egg cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr.; Rockville, MD 20850, USA
                                     clone="XENOPUS_SOURCE_ID:xlnneg002120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.4; DB 10;
Pred. No. 1.3e+02;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, h
/note="Vector: pBluescriptSKm"
'organism="Xenopus laevis"
                db_xref-"taxon:8355
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ilarity 95.0%;
Conservative (
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Fax: 301 838 0208
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Xenopus laevis
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BE192046
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IMAGE:3517461 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library constructed by M. Kirschner (Harvard Medical School). DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov High quality sequence stop: 322.

Location/Qualifiers
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Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylle,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Glbbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Washu Kand Wilson,R.
Washu Kanopus EST project, 1999
Unpublished (1999)
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/lab_host="DH10B (phage-resistant)"
/note="vector: pC25+; Site_1: NotI; Site_2: SalI;
Size-selected for average insert size 1.2 kb. Library was constructed and donated by M. Kirschner (Harvard Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIO41429 BY MRNA Linear EST 14-JUN-2001 PM0-NT0911-280201-017-f07 NT0911 Homo sapiens CDNA, MRNA sequence.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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/clone_lib="Kirschner embryo Stl0 14"
                                             DB 10; 1
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                                                  Score 18.4; DB 10
Pred. No. 1.5e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
      141
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/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
      φ
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                                                                                                                                      539 TGCAGGAAAGGTTGGGTCTG 520
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                                                  92.0%;
95.0%;
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Best Local Similarity 94.7
Matches 18; Conservative
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                                               Query Match
Best Local Similarity
Matches 19; Conserv
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Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application
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                                                                                                                                                                                                                    Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-NT0911-280201-017-f07&t3=2001-02-28&t4=1)
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390 bp mRNA linear EST 07-AUG-2000 db86f12.xl Wellcome CRC pSK animal cap Xenopus laevis cDNA clone IMAGE:3379919 3', mRNA sequence.
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Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 385)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.4; DB 13;
Pred. No. 4e+02;
0; Mismatches 1;
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Site_2: Smal; A mini-library
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/db_xref="taxon:9606"
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High quality sequence stop: 385.
Location/Qualiflers
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BI041429.1 GI:14448055
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Library
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BE491715
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                                                                                                                                                                                                                                                                                                Email: estewatson.wustl.edu
Library constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.
Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington
University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.AG.E. Consortium/Link at: info@image.linl.gov
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="embryo, animal cap"
/lab_host="DH10B (phage-resistant)"
/note="Vector: pBluescript SK-: Site_1: NotI; Site_2:
/note="Vector: pBluescript SK-: Site_1: NotI; Site_2:
ECORI; cDNRs were oligo-dT primed and directionally
cloned. Staging according to Nieuwkoop and Faber. Library
was constructed by N. Garrett, P. LeMaire, A.M. Zorn, and
J.B. Gurdon (Wellcome/CRC Institute). Note: This is a
Xenopus Gene Collection (XGC) library."
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Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
Martin, J., Wyller, Underwood, K., Thaising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                     ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R
Waterston,R. and Wilson,R.
                                                                WashU Xenopus EST project, 1999
Unpublished (1999)
On Jun 23, 2000 this sequence version replaced g1:8672410.
Other ESTs: ch86f12.yl
Contact: Sandy Clifton, Ph.D.
                                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 4e+02;
0; Mismatches 1; Indels 0
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  Theising, B.
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Washington University School of Medicine
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/db_xref="taxon:8355"
/clone="IMAGE:3379919"
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Contact: Sandy Clifton, Ph.D.
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ilarity 94.7%;
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, Martin, J., Wylle, T., Blumberg, B., Song, J., Hillier, L., Pape, D., B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Wastrston, R. and Wilson, R., Wash Xenopus EST project, 1999
Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact
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db95a06.xl Wellcome CRC pSK animal cap Xenopus laevis cDNA clone IMAGE:3380722 3', mRNA sequence.
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Clone distribution: Xenopus clones from this library are available
                                                                                                                                              Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Seq primer: -400P from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anote—Worder pT773-Pac, Site_I: ECORI; Site_2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus Place's eggs. The library was constructed in the vector pT773-Pac as described in Bonaldo, M.E., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research (5791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNAs were ligated to ECORI adapters, digested with NotI, and directionally cloned into the NotI and ECORI-digested pT773-Pac vector.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                             (University of Iowa). DNA Sequencing by: Washington University Genome Sequencing Center
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Fax: 314 286 1810
constructed by Bento Soares and M. Fatima Bonaldo
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Clifton, S., Johnson, S.L., Blumberg, B.,
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/dev_stage="unfertilized egg"
/lab_host="DH10B"
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/db_xref="taxon:8355"
/clone="IMAGE:3302173"
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WashU Xenopus EST project, 1999
Washington University School of
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AUTHORS
TITLE
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                                                                                                                                     /db_xref="taxon:8155"
/clone="IMAGE:3380722"
/clone="IMAGE:3380722"
/clone="IMAGE:3380722"
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/clone="IMAGE:3380722"
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/close="taxon:8155"
/close="taxon:8155"
/cloned:"yearcor: pBluescript SK-; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dr primed and directionally cloned. Staging according to Nieuwkoop and Faber: Library was constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute). Note: This is a Kenopus Gene Collection (RGC) library."
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Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709
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Email: black009@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
Phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
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Amphibia; Batrachla; Anura; Mesobatrachla; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Seq primer: -40UP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
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                                                                                                                        /organism="Xenopus laevis"
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BACKWARD: CAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GCAGGAAAGGTTTGGTCTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African clawed frog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cdna@resgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 18; Conserva
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ORIGIN
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AW633486/c
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AUTHORS
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COMMENT
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KEYWORDS
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                                                                       FEATURES
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ò 요 /organism="Xenopus laevis" /db_xref="taxon:8355"

source

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/note="Vector: pT773-Pac; Site_1: ECORI; Site_2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pT773-Pac as described in Bonaldo, M.F. Lennon, G. and Soares, M.B. Yormalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT773-Pac vector. The library contained approximately 7.2 x 10^5 recombinants, with average insert sizes of 1-1.5 kb."
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the world population, especially those inhabiting highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnollophyta; Liliopsida, Poales, Poaceae; Enrhartoideae, Oryzeae; Oryza.

1 (Dases 1 to 434)
Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note-"Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ860919 434 bp DNA linear GSS 03-NOV-1 nbeb0016A15r CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone nbeb0016A15r, DNA sequence.
                          'clone_lib="Blackshear/Soares normalized Xenopus egg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.4; DB 10;
Pred. No. 4.1e+02;
0; Mismatches 1;
                                                                                                              /tissue_type="unfertilized egg'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                            /cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'tissue_type="Leaf"
'lab_host="E: coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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High quality sequence stop: 337
Location/Qualifiers
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db_xref="taxon:4530"
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/clone="PBX0008D02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 GCTGGAAAGGTTTGGTCTG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GCAGGAAAGGTTTGGTCTG 20
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                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ860919.1 GI:6211376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.08;
94.78;
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18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wing RA
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on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRi as the cloning enzyme. The library contains 55.296 clones with an average insert size of 121 kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AM033397 453 bp mRNA linear EST 26-APR-2001 b107c02.wl Blackshear/Soares normalized Xenopus egg library Xenopus laevis cDNA clone PBX0007C02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G. Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman, J.W., Bonaldo, M.F. and Soares, M.B.
The NIEHS Xenopus maternal EST project: interim analysis of the first 13,879 ESTs from unfertilized eggs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NC 27709,
populated areas of the humid tropics and subtropics, rely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone is available through Research Genetics, Inc., 2130 Memorial Parkway, Huntsville, AL 35901 phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing and analyses performed by National Institutes of lealth Intramural Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17.4; DB 17;
Pred. No. 4.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: TGTAAAACGACGCCAGT
BACKWARD: CAGGAAACAGCTATGACC
Plate: 0007 row: C column:
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Best Local Similarity 94.7%;
Matches 18; Conservative (
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919 541-4571
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LOCUS .
DEFINITION
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COMMENT
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KEYWORDS
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BG016217 455 bp mRNA linear EST 24-JAN-2001 de58a09.yl Kirschner embryo Stl0 14 Xenopus laevis cDNA clone IMAGE:3515801 5', mRNA sequence.
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Library constructed by M. Kirschner (Harvard Medical School). DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/Link at: info@image.llnl.gov
Seq primar: -40RP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D. (11fton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylle, T., Underwood, R., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                         /note="Vector: pT/T3-Pac; Site_1: EcoRI; Site_2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                             approaches to facilitate gene discovery', Genome Researc 6.791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNAs were ligated to ECORI adapters, digested with NotI, and directionally cloned into the NotI and ECORI-digested pT7T3-Pac vector The library contained approximately 7.2 x 10.5 recombinants, with average insert sizes of 1-1.5 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                lacis eggs. The library was constructed in the vector pT/T13-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two
clone_lib="Blackshear/Soares normalized Xenopus egg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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WashU Xenopus.EST project, 1999
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 453;
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/tissue_type="pooled embryos (stage 10-14)"
/lab_host="DH10B (phage-resistant)"
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Pred. No. 4.2e+02;
0; Mismatches 1;
                                                                                  /tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
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Unpublished (1999)
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                                                                                                                                                                /lab_host-"DH10B"
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                                                            /sex="female"
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94.7%;
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Matches 18; Conserv
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BG016217/c
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BG264326/c
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1 (bases 1 to 463)
Clifton.S. Johnson.S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
Martin,J., Wylle,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Glbbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                               BG018230 463 bp mRNA linear EST 24-JAN-2001 de66a08.yl Kirschner embryo Stl0 14 Xenopus laevis cDNA clone IMAGE:3516567 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
Library constructed by M. Kirschner (Harvard Medical School). DNA
Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco.
Location/Qualifiers
/note="Vector: pCS2+; Site_1: Not1; Site_2: Sal1; Size selected for average insert size 1.2 kb. Library was constructed and donated by M. Kirschner (Harvard Medical School). # 55 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:3516567"
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/clone_lib="Kirschner embryos (stage 10-14)"
/lab_host="Phost="By (page-resistant)"
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Size:selected for average insert size 1.2 kb. Library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructed and donated by M. Kirschner (Harvard Medical
                                                                                                                                                                    Gaps
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Contact: Sandy Clifton, Ph.D.
WashU Xenopus EFT project, 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Far: 314 286 1800
Fax: 314 286 1810
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                                                                                                                          Score 17.4; DB 12;
Pred. No. 4.2e+02;
; Mismatches 1;
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Pred. No. 4.2e+02;
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/db_xref="taxon:8355"
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94.7%;
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1 Similarity 94.7%;
18; Conservative
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RESULT 14

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Email: estewatson.wustl.edu
Library constructed by M. Kirschner (Harvard Medical School). DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: infoetmage.llnl.gov
Seq primer: -40UP from Glaco
High quality sequence stop: 460.
Location/Qualifiers
BG414006 475 bp mRNA linear EST 13-MAR-2001 de76g12.x1 Kirschner embryo St10 14 Xenopus laevis cDNA clone IMAGE:3517655 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                              l (bases 1 to 475)
Clifton,S. Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
Amttin,J., Wylle,T., Underwood,K., Theising,B., Bowers,Y., Person
,B., Glbbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
Washd'Xenopus EST project, 1999
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Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
, Martin,J., Wyla,T., Underwood,K., Theising,B., Bowers,Y., Person
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Rischner embryo St10 14"
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/close_type="pooled embryos (stage 10-14)"
/lab_host="PH10B (phage-resistant)"
/note="Vector: pCS2+; Site_1: Not1; Site_2: Sall;
Size-selected for average insert size 1.2 kb. Library was constructed and donated by M. Kirschner (Harvard Medical
                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Pred. No. 4.2e+02;
); Mismatches 1;
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/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTs: de76g12.yl
Contact: Sandy Clifton, Ph.D.
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94.7%;
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IMAGE:3517655 5', mRN
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Email: est@watson.wustl.edu
Library constructed by M. Kirschner (Harvard Medical School). DNA
Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLML at: info@image.llnl.gov
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pooled embryos (stage 10-14)"
/lab_host="PH10B (phage-resistant)"
/note="vector: pCS2+; Site_1: Not!; Site_2: Sall;
Size-selected for average insert size 1.2 kb. Library was constructed and donated by M. Kirschner (Harvard Medical
                                                                                                     Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashIngton University School of Medicine
Math Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R. Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.4; DB 12; Length 488;
Pred. No. 4.3e+02;
0; Mismatches 1; Indels 0;
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tant)"
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/clone_lib="Kirschner embryo St10 14"
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/organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                      WashU Xenopus EST project, 1999
Unpublished (1999)
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Search completed: July 8, 2003, 09:21:51 Job time: 1018.1 secs

424 GCTGGAAAGGTTTGGTCTG 406

ద

2 GCAGGAAAGGTTTGGTCTG 20

0; Gaps

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OM nucleic - nuc	OM nucleic - nucleic search, using sw model
Run on:	July 8, 2003, 00:45:53; Search time 220.098 Seconds (without alignments) 2644.537 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-647-780A-15 20 1 gaacgcctcagagaagcctg 20
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 seqs, 14551402878 residues
Total number of	Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: GenEmbl:*

dense : Gensmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_nt:*
4: gb_on:*
5: gb_on:*
6: gb_pt:*
7: gb_pt:*
11: gb_pt:*
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13: gb_on:*
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15: em_ba:*
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18: em_nu:*
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23: em_or:*
24: em_pt:*
25: em_pt:*
26: em_or:*
27: em_pt:*

37: em_htg_wrt:* 38: em_sy:* 39: em_htgo_hum:* 40: em_htgo_hum:* 41: em_htgo_other:* Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

| ID  AX01470  AX01471  AX01471  AX101470  AF13020  AF1020  DB ID  AX014715  AX014715  AX014715  AX014715  AX03227  AF15710  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF30207  AF0070891  AF01499  AF0120592  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120594  AC120596  AC120596  AC120596  AC120598                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | b AK1014701 b AF302075 10 AF1302076 10 AF1302076 10 AF1302077 10 AF1302077 10 AF1302077 10 AF1302077 2 AC109980 2 AC1059814 2 AC1059814 2 AC1059814 2 AC1059814 2 AC1059814 2 AC1059814 2 AC1059814 2 AC1059814 2 AC1059814 3 AC0920851 3 AC0920851 3 AC0920851 1 AC000885 2 AC102692 2 AC102692 2 AC102694 3 AC002694 3 AC002694 3 AC002694 3 AC002694 3 AC002698 4 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002698 5 AC002608                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 18.4   92.0   2601   10   AF30207   18.4   92.0   2604   10   AF30207   18.4   92.0   2694   10   AF30207   18.4   92.0   2694   10   AF30207   18.4   92.0   2892   10   AF30207   18.4   92.0   2925   10   AF30207   18.4   92.0   2925   10   AF30207   18.4   92.0   2925   10   AF30207   18.4   92.0   114789   2   AC128969   18.4   92.0   114789   2   AC128969   18.4   92.0   15937   2   AC128969   18.4   92.0   15937   2   AC128969   18.4   92.0   169232   2   AC128969   18.4   92.0   169232   2   AC128969   18.4   92.0   169232   2   AC129981   18.4   92.0   108879   2   AC129981   18.4   92.0   108873   2   AC129981   19.4   87.0   146115   10   AL6071331   17.4   87.0   146115   10   AL6071331   17.4   87.0   178871   10   AL6071331   16.8   84.0   178871   10   AC12869   16.8   84.0   18409   2   AC12869   16.8   84.0   18409   2   AC12869   16.8   84.0   18919   2   AC12869   16.8   84.0   18919   2   AC12869   16.8   84.0   18919   3   AC12869   AC12869   3   AC12869   AC12869   AC12869   AC12869   AC12869    | 10 AF157207<br>10 AF157207<br>10 AF37207<br>10 AF37207<br>10 AF37207<br>10 AF37207<br>10 AF176569<br>10 AF176569<br>10 AF176569<br>2 AC109980<br>2 AC109980<br>2 AC109980<br>2 AC109980<br>2 AC105933<br>3 AC105934<br>4 AC0920814<br>5 AC107311<br>6 AC67131<br>7 AC67131<br>8 AC092082<br>10 AE671877<br>10 AE671877<br>10 AE671877<br>10 AE67187<br>10 AC67131<br>11 AC106592<br>2 AC102659<br>3 AC102654<br>4 AC006583<br>5 AC102654<br>6 AC005053<br>10 AE611950<br>11 AC10205<br>12 AC10205<br>13 AC10205<br>14 AC10205<br>15 AC10205<br>16 AC10205<br>17 AC10205<br>18 AC10205<br>18 AC10205<br>19 AC10205<br>10 AC10205<br>10 AC10205<br>10 AC10205<br>11 AC10205<br>12 AC10205<br>13 AC10205<br>14 AC10205<br>15 AC10205<br>16 AC10205<br>17 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC10205<br>18 AC1020                                                                                                                                                                                                                         |
| 5   18.4   92.0   2652   10   AF30207     6   18.4   92.0   2892   10   AF30207     8   18.4   92.0   2892   10   AF30207     9   18.4   92.0   2925   0   AF33232     10   18.4   92.0   3742   10   AF33237     11   18.4   92.0   3742   10   AF33237     12   18.4   92.0   151374   2   AC109980     13   18.4   92.0   169232   2   AC128614     14   18.4   92.0   169232   2   AC128614     18   4   92.0   169232   2   AC128614     18   4   92.0   169232   2   AC128614     18   4   92.0   169232   2   AC128614     18   90.0   208449   2   AC117158     10   87.0   17965   2   AC177331     17   87.0   17965   2   AC177331     17   87.0   17965   2   AC177331     18   87.0   17965   2   AC177331     16.8   84.0   17968   2   AC176694     16.8   84.0   17968   3   AC176694     16.8   84.0   17969   3   AC176694     16.8   84.0   17960   3   AC176694     16.8   84.0   16944   3   AC176696     17.4   16.8   84.0   16944   3   AC176696     17.4   16.8   84.0   16944   3   AC176696     17.4   16.8   84.0   16944   3   AC176696     | 10 AF302076 10 AF302077 10 AF302077 10 AF1502076 2 AC0128969 2 AC128969 2 AC128969 2 AC128969 2 AC15933 2 AC15933 2 AC15933 10 AE671877 2 AC102692 2 AC102692 2 AC102692 2 AC102692 3 AC102693 3 AC008694 4 AE671877 5 AC102692 5 AC102693 6 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008694 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008684 7 AC008                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 6 18.4 92.0 2664 10 AF157100<br>8 18.4 92.0 2925 6 DAC33272<br>18.4 92.0 2925 6 DAC33272<br>18.4 92.0 2925 10 AF157100<br>18.4 92.0 3742 10 AF137101<br>18.4 92.0 114789 2 AC128969<br>18.4 92.0 114789 2 AC128969<br>18.4 92.0 16923 2 AC129646<br>18.4 92.0 16923 2 AC15933<br>18.4 92.0 16923 2 AC15933<br>18.4 92.0 16873 2 AC15933<br>18.4 92.0 108873 2 AC15933<br>18.4 92.0 108873 2 AC15933<br>17.4 87.0 146015 10 AL67187<br>22 17.4 87.0 146015 10 AL67187<br>24 17.4 87.0 17887 1 AC0928814<br>25 17.4 87.0 17887 2 AC126041<br>26 17.4 87.0 17887 1 AC092881<br>27 17.4 87.0 17887 2 AC126037<br>28 17.4 87.0 17887 2 AC126037<br>29 17.4 87.0 198459 2 AC122693<br>16.8 84.0 17388 2 AC122693<br>16.8 84.0 18367 2 AC122693<br>16.8 84.0 18367 2 AC122053<br>16.8 84.0 18367 2 AC122053<br>16.8 84.0 18367 2 AC122053<br>16.8 84.0 18367 2 AC122053<br>16.8 84.0 18367 2 AC122129<br>16.8 84.0 18367 2 AC122053<br>16.8 84.0 18367 2 AC122129<br>16.8 84.0 18367 2 AC122129<br>16.8 84.0 168153 2 AC122129<br>16.8 84.0 168153 2 AC122129<br>16.8 84.0 168153 2 AC122129<br>16.8 84.0 168153 2 AC122129<br>16.8 84.0 168153 2 AC122129                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 10 AF302077 10 AF372105 6 AX033272 10 AF157105 10 AF157105 2 AC128969 2 AC128969 2 AC128214 2 AC128214 2 AC128214 2 AC129646 2 AC129646 2 AC129646 2 AC129646 2 AC129641 2 AC129641 2 AC12074 10 AE607131 2 AC126071 2 AC126081 3 AC126081 3 AC0208135 2 AC120654 3 AC122129 3 AC122129 3 AC122129 4 AC025135 5 AC122129 5 AC1222139 5 AC122129 6 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC122129 7 AC12229 7 AC122129 7 AC122120 7 AC122120 7 AC122120 7 AC122120 7 AC122120 7 AC122120 7 AC122120 7 AC122120 7 AC122120 7 AC122120 7 AC122120 7 AC12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 18:4 92.0 2892   O AFIT710     18:4 92.0 2925   O ANG332724     18:4 92.0 2925   O ANG332724     18:4 92.0 2925   O ANG332724     18:4 92.0 1342   O ANG32272     18:4 92.0 114789   2 ACI29989     18:4 92.0 114789   2 ACI29980     18:4 92.0 18959   2 ACI29949     18:4 92.0 18859   2 ACI29949     18:4 92.0 18859   2 ACI25944     19:4 92.0 18859   2 ACI25981     10:4 87.0 14555   0 ACI2581     17:4 87.0 14555   0 ACI27837     17:4 87.0 172871   O AL60713     18:5 0 191918   2 ACI227337     18:5 0 191918   2 ACI22694     18:5 0 19499   2 ACI22694     18:5 0 18:5 0 19499   2 ACI22629     18:5 0 18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 18:5 0 18:5 0     18:5 0 1   | 10 AF157105  10 AF157105  10 AF157105  10 AF15722  2 AC128980  2 AC1289246  2 AC129646  2 AC129646  2 AC129644  2 AC115554  2 AC115554  2 AC117158  3 AC002851  1 AE000131  2 AC126041  2 AC126041  3 AC126054  4 AC002851  5 AC126054  5 AC126054  5 AC126054  6 AC002891  6 AC002891  7 AC126054  8 AC126054  8 AC126054  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803  8 AC002803                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 18.4 92.0 2925 6 AX033272     18.4 92.0 22925 6 AX033272     18.4 92.0 2324     18.4 92.0 114789     18.4 92.0 114789     18.4 92.0 114789     18.4 92.0 114789     18.4 92.0 114789     18.4 92.0 118189     18.4 92.0 118189     18.4 92.0 118189     18.4 92.0 118189     18.4 92.0 118189     18.4 92.0 118189     18.4 92.0 208249     18.4 92.0 208249     18.4 92.0 208249     18.4 92.0 208249     18.4 92.0 208249     18.4 92.0 208249     18.4 92.0 218249     18.4 92.0 218249     18.4 92.0 218249     18.4 92.0 218249     18.4 92.0 218249     18.4 92.0 218249     18.4 87.0 25738     18.8 84.0 11818     18.8 84.0 11818     18.8 84.0 11818     18.8 84.0 11818     18.8 84.0 11818     18.8 84.0 11818     18.8 84.0 11818     18.8 84.0 11818     18.8 84.0 11818     18.8 84.0 11818     18.8 84.0 11818     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     18.8 84.0 11819     1   | 6 AK033272 A 10 AF332142 2 AC128980 2 AC128946 2 AC15946 2 AC15946 2 AC15554 2 AC15554 2 AC15554 2 AC15554 10 AL607031 2 AC09042 2 AC09042 2 AC12592 2 AC12592 3 AC12592 3 AC12592 4 AC005032 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12505 5 AC12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| 22 17.4 87.0 146015 10 AL651201<br>23 17.4 87.0 171905 2 AC102074<br>24 17.4 87.0 171905 2 AC102074<br>25 17.4 87.0 19871 10 AL67131<br>26 17.4 87.0 233234 2 AL772311<br>27 17 85.0 231234 2 AL772311<br>28 17.4 87.0 233234 2 AL772312<br>29 17.4 87.0 233234 2 AL772313<br>20 17.4 87.0 233234 2 AL772313<br>20 16.8 84.0 19918 2 AC102695<br>31 16.8 84.0 16419 1 AE000885<br>33 16.8 84.0 163149 9 AC046494<br>34 16.8 84.0 123302 2 AC120554<br>35 16.8 84.0 123302 2 AC120554<br>36 16.8 84.0 159101 2 AC122125<br>37 16.8 84.0 159101 2 AC126505<br>38 16.8 84.0 159101 2 AC126505<br>39 16.8 84.0 159101 2 AC126505<br>41 16.8 84.0 161331 0 AL51195<br>42 16.8 84.0 161331 0 AL51195<br>43 16.8 84.0 161331 2 AL772289                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 10 AL671811<br>2 AC102074<br>2 AC102074<br>2 AC102074<br>2 AC102031<br>2 AC172337<br>2 AC126041<br>10 AC102692<br>2 AC126041<br>3 AC1020594<br>4 AC004694<br>5 AC120654<br>5 AC120654<br>6 AC120654<br>7 Y<br>7 Y<br>8 AC120654<br>8 AC120654<br>8 AC120654<br>8 AC120654<br>9 AC005033<br>9 AC005033<br>9 AC005033<br>9 AC005033<br>9 AC005033<br>9 AC005033<br>9 AC005033<br>9 AC005033<br>9 AC005033                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| 22 17.4 87.0 171905 2 ACIO2074<br>23 17.4 87.0 171905 2 ACIO2074<br>25 17.4 87.0 198459 2 ACC72042<br>26 17.4 87.0 233234 2 ACC72042<br>27 17 85.0 257886 2 ACIO20592<br>29 16.8 84.0 191918 2 ACIO20592<br>30 16.8 84.0 101918 2 ACIO20691<br>31 16.8 84.0 10140 1 ACC001851<br>32 16.8 84.0 68914 2 ACIO20594<br>34 16.8 84.0 139227 2 ACIO20594<br>35 16.8 84.0 139227 2 ACIO20594<br>36 16.8 84.0 159101 2 ACIO20594<br>37 16.8 84.0 159101 2 ACIO20594<br>38 16.8 84.0 159101 2 ACIO20594<br>39 16.8 84.0 159101 2 ACIO20594<br>30 16.8 84.0 160344 2 ACIO20594<br>31 16.8 84.0 160344 2 ACIO20594<br>32 16.8 84.0 160344 2 ACIO20594<br>33 16.8 84.0 160344 2 ACIO20594<br>34 16.8 84.0 160344 2 ACIO20594<br>35 16.8 84.0 160344 2 ACIO20594<br>36 16.8 84.0 160344 2 ACIO20594<br>37 16.8 84.0 160344 2 ACIO20594                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 2 AC102074 10 AL607131 2 AC102074 2 AL772311 2 AC127337 2 AC126041 10 AF6104956 11 AE000885 2 AC024970 2 AC024970 2 AC02654 2 AC12654 2 AC12655 2 AC12655 2 AC12655 2 AC12655 2 AC12655 2 AC12655 3 AC12655 3 AC12655 3 AC126505 3 AC126205 3 AC1022129 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC005023 4 AC0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 23 17.4 87.0 172871 10 AL60713 24 17.4 87.0 198459 2 AC079942 25 17.4 87.0 233284 2 AC0773317 26 17.4 87.0 235384 2 AC1773317 27 17 85.0 191918 2 AC1275317 29 16.8 84.0 191918 2 AC126694 31 16.8 84.0 16840 1 AC01495 33 16.8 84.0 16840 1 AC074694 34 16.8 84.0 123302 2 AC126654 35 16.8 84.0 123302 2 AC05917 36 16.8 84.0 133927 2 AC126205 37 16.8 84.0 159101 2 AC126205 38 16.8 84.0 159101 2 AC126205 39 16.8 84.0 159101 2 AC126205 39 16.8 84.0 159101 2 AC126205 31 16.8 84.0 159101 2 AC126205 32 16.8 84.0 159101 2 AC126205 33 16.8 84.0 169344 2 HS2259507 34 16.8 84.0 169342 2 AC126205 35 16.8 84.0 169343 2 AC1726205 36 16.8 84.0 169343 2 AC1726205 37 16.8 84.0 169343 2 AC1726205 38 16.8 84.0 169343 2 AC1726205 39 16.8 84.0 169343 2 AC1726205                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 10 AL607131<br>2 AC079042<br>AL7079042<br>AL7079042<br>AL7079042<br>AL702042<br>AC072737<br>AC126592<br>AC126691<br>AC106694<br>AC004694<br>AC004694<br>AC004694<br>AC004694<br>AC004694<br>AC004694<br>AC005013<br>AC126654<br>AC005013<br>AC126205<br>AC126205<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023<br>AC005023                                                                                                                                                     |
| 24 17.4 87.0 198459 2 AC079042 25 17.4 87.0 233234 2 AL772311 26 17.4 87.0 253234 2 AL772311 27 85.0 6433 10 AY05572 28 17 85.0 191918 2 AC102692 29 17 85.0 191918 2 AC102692 30 16.8 84.0 16842 10 AF01495 33 16.8 84.0 16840 1 AC078694 34 16.8 84.0 139227 2 AC12205940 35 16.8 84.0 139227 2 AC122129 36 16.8 84.0 159101 2 AC122129 37 16.8 84.0 159101 2 AC122129 38 16.8 84.0 159101 2 AC122129 39 16.8 84.0 159101 2 AC122129 39 16.8 84.0 159101 2 AC122129 39 16.8 84.0 159101 2 AC122129 39 16.8 84.0 159101 2 AC122129 39 16.8 84.0 159101 2 AC122129 30 16.8 84.0 159101 2 AC122129 31 16.8 84.0 160344 2 AC122129 32 16.8 84.0 160344 2 AC122129 33 16.8 84.0 161331 10 AL61195 34 16.8 84.0 161331 10 AL61195                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 2 AC079042 A A A C079042 A A A C079042 A A C07273311 A A C027331 A A C072692 A A C072691 A A C072694 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A A C072219 A C072219 A C072219 A A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C072219 A C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 25 17.4 87.0 233234 2 AL772311<br>27 17.8 87.0 257886 2 AC127337<br>28 17 85.0 191918 2 AC102692<br>29 17 85.0 191918 2 AC1026041<br>30 16.8 84.0 6842 10 AC107691<br>31 16.8 84.0 10840 1 XC177691<br>33 16.8 84.0 10840 2 AC106694<br>34 16.8 84.0 13302 2 AC004694<br>35 16.8 84.0 13302 2 AC026135<br>36 16.8 84.0 13302 2 AC026135<br>37 16.8 84.0 139227 2 AC025135<br>38 16.8 84.0 158079 2 AC126126<br>40 16.8 84.0 158079 2 AC126126<br>41 16.8 84.0 158079 2 AC126126<br>41 16.8 84.0 158079 2 AC126126<br>42 16.8 84.0 16914 2 AC126126<br>43 16.8 84.0 158079 2 AC126126<br>44 16.8 84.0 169181 2 AC126126<br>45 16.8 84.0 169181 2 AC126126<br>46 16 16 84.0 16915 3 AC126126<br>47 16.8 84.0 16915 3 AC126126                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 2 AL772311 2 AL772311 2 AC127337 2 AC102692 2 AC102691 10 AF014956 1 XCT17691 1 AE000885 2 AC095135 2 AC095135 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC122129 2 AC095023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 26 17.4 87.0 257586 2 AC127337 27 28 17.9 85.0 64333 10 AC05572 29 17 85.0 191918 2 AC10259572 29 17 85.0 191918 2 AC10259572 29 16.8 84.0 10840 1 AE010495 33 16.8 84.0 10840 1 AE006885 35 16.8 84.0 108302 2 AC0595135 35 16.8 84.0 13927 2 AC055135 39 16.8 84.0 159101 2 AC122129 39 16.8 84.0 159101 2 AC122129 39 16.8 84.0 159101 2 AC122129 41 16.8 84.0 1618153 2 AL772289 41 16.8 84.0 1618153 2 AL772289 41 16.8 84.0 1618153 2 AL772289 41 16.8 84.0 1618153 2 AL772289 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161957 9 AC055023 41 16.8 84.0 161857 9 AC05502 41 16.8 84.0 161857 9 AC05502 41 16.8 84.0 161857 9 AC05502 41 16.8 84.0 161857 9 AC05502 41 16.8 84.0 16.8 41 16.8 84.0  | 2 AC127337<br>2 AC127337<br>2 AC1026041<br>2 AC126041<br>1 XCT17691<br>1 AC00885<br>2 AC120654<br>2 AC120654<br>2 AC12129<br>2 AC122129<br>2 AC122129<br>2 AC122129<br>2 AC126205<br>2 AC126205                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 27 17 85.0 191918 10 AR1025/2<br>29 17 85.0 191918 2 AC126691<br>30 16.8 84.0 16842 10 AFC01495<br>31 16.8 84.0 10490 1 AEC00885<br>33 16.8 84.0 14190 1 AEC00885<br>34 16.8 84.0 68914 2 ACC04694<br>35 16.8 84.0 13302 2 ACC04694<br>37 16.8 84.0 13302 2 ACC0554<br>38 16.8 84.0 159101 2 AC126505<br>40 16.8 84.0 159101 2 AC126505<br>41 16.8 84.0 16044 2 HSZ525P07<br>42 16.8 84.0 161331 10 AL51195/42 16.8 84.0 161331 2 ACC0552                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 10 AC1055/26 2 AC1055/26 2 AC126041 10 ACC117691 1 AE000885 2 AC024970 2 AC025340 2 AC12654 2 AC126505 2 AC126505 2 AC126205 2 AC106205023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 29 17 85.0 210398 2 AC126041<br>30 16.8 84.0 16842 10 AF01495<br>33 16.8 84.0 14190 1 AC018694<br>34 16.8 84.0 14190 1 AC00885<br>35 16.8 84.0 63749 9 AC04694<br>36 16.8 84.0 163922 2 AC02654<br>37 16.8 84.0 139227 2 AC122129<br>38 16.8 84.0 159101 2 AC122129<br>39 16.8 84.0 159101 2 AC122129<br>40 16.8 84.0 16344 2 HS2252940<br>41 16.8 84.0 161331 10 ALG11957<br>42 16.8 84.0 161331 10 ALG11957<br>43 16.8 84.0 161331 10 ALG11957                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 2 AC1262494<br>10 AF014956<br>1 AC014956<br>1 AC004694<br>2 AC004694<br>2 AC12654<br>2 AC12654<br>2 AC12655<br>2 AC12656<br>2 AC12656<br>2 AC12656<br>2 AC12656<br>2 AC12656<br>2 AC12626<br>2 AC12626<br>2 AC12626<br>2 AC12626<br>2 AC12626<br>3 AC12626<br>3 AC006023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
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| 31 16.8 84.0 10840 1 XCT17691<br>32 16.8 84.0 63749 9 AE000885<br>34 16.8 84.0 63749 2 AC024970<br>35 16.8 84.0 68914 2 AC024970<br>36 16.8 84.0 133227 2 AC055135<br>37 16.8 84.0 133227 2 AC05505<br>38 16.8 84.0 158079 2 AC122129<br>39 16.8 84.0 158079 2 AC122129<br>40 16.8 84.0 158079 2 AC122129<br>41 16.8 84.0 16134 1 AL572289<br>42 16.8 84.0 16134 2 AL772289<br>43 16.8 84.0 16135 2 AL772289<br>44 16.8 84.0 16135 2 AL772289                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1 XC117691<br>AE000885<br>9 AC00684<br>2 AC024970<br>2 AC025135<br>AC120654<br>2 AC122129<br>2 AC126205<br>2 AC126205<br>2 AC126205<br>2 AC17289<br>2 AC77289<br>AC005023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 32 16.8 84.0 14190 1<br>34 16.8 84.0 63749 9<br>35 16.8 84.0 63749 9<br>36 16.8 84.0 123302 2<br>37 16.8 84.0 123302 2<br>38 16.8 84.0 158079 2<br>39 16.8 84.0 158079 2<br>40 16.8 84.0 160544 2<br>41 16.8 84.0 160544 2<br>42 16.8 84.0 16054 2<br>43 16.8 84.0 16054 2<br>44 16.8 84.0 16054 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 1 AE000885<br>9 AC004694<br>2 AC024970<br>2 AC025135<br>2 AC120654<br>2 AC122129<br>2 AC126205<br>2 AC126205<br>2 AC126205<br>2 AC126205<br>2 AC126205<br>2 AC12605<br>2 AC72289<br>2 AC005023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| 35 16.8 84.0 133302 2<br>37 16.8 84.0 138227 2<br>39 16.8 84.0 149602 2<br>39 16.8 84.0 159101 2<br>40 16.8 84.0 160544 2<br>42 16.8 84.0 16134 1<br>42 16.8 84.0 161331 2<br>43 16.8 84.0 168153 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 2 AC09135<br>2 AC095135<br>2 AC120554<br>2 AC126205<br>2 HS25807<br>10 AL611950<br>2 AL772289<br>2 AC005023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 37 16.8 84.0 149502 2<br>38 16.8 84.0 149502 2<br>39 16.8 84.0 158101 2<br>40 16.8 84.0 160544 2<br>41 16.8 84.0 16131 10<br>42 16.8 84.0 168153 2<br>43 16.8 84.0 168153 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 2 AC12054<br>2 AC122129<br>2 AC122129<br>2 AC126205<br>10 AL61907<br>10 AL611950<br>2 AL772289<br>2 AC005023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
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| 20 10.0 04.0 1590/7 2 ACLIZALES<br>40 16.8 84.0 159101 2 ACLIZE205<br>41 16.8 84.0 160544 2 HS253P0/7<br>42 16.8 84.0 161331 10 AL61195<br>43 16.8 84.0 168153 2 AL772289<br>43 16.8 84.0 170967 9 ACCOSO23                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ACLIZALZ9 2 ACLIZE205 2 HSZSSP07 10 ALG11950 2 ACL72289 9 AC005023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 40 16.8 84.0 160544 2 AL772289<br>41 16.8 84.0 160543 2 AL772289<br>42 16.8 84.0 168153 2 AL772289<br>43 16.8 84.0 170967 9 AC005023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 2 HS22803<br>10 AL611950<br>2 AL77289<br>9 AC005023<br>2 AP005286                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| 41 16.8 84.0 161331 10 AL61195<br>42 16.8 84.0 168153 2 AL772289<br>43 16.8 84.0 170967 9 AC005023<br>44 16.8 84.0 170967 9 AC005023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 10 AL611950<br>2 AL772289<br>9 AC005023<br>2 AP005286                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 42 16.8 84.0 168153 2 AL72289<br>43 16.8 84.0 170967 9 AC005023                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 2 AL772289<br>9 AC005023<br>2 AP005286                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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          INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
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Schwartz,J.C., Gros,C., Ouimet,T., Rose,C., Bonhomme,M.C. and Facchinetti,P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 2765;
                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                           Indels
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                                                                                        construct
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Pred. No. 8.6;
                                                                                                                                                              100.0%; Scor.
100.0%; Pred: No. 10.
                                                                                                                                                                              DB
13;
Patent: WO 9953077-A 15 21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibitors useful in therapy
Patent: WO 9953077-A 1 21-OCT-1999;
                                                                      1. 20
/organism="synthetic cons
/db_xref="taxon:32630"
/note="oligonucleotide"
a 6 c 6 g 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Rattus rattus"
'db_xref="taxon:10117"
                                                                                                                                                                                                                                                                                                                                          Sequence 1 from Patent W09953077
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
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100.0%;
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Mammalia; Eutheria;
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20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local S
Matches 20
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                                                                                                                               BASE COUNT
ORIGIN
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
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                                                           FEATURES
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Indels

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Mismatches

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AF302075
Mus musculus neprilysin-like peptidase alpha mRNA, complete cds.
AF302075
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AQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLONLPGFSEAFHCPRGSPMHPMKRCR
IW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                               Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                      Shirotani, K., Tsuboki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T., Iwatsubo, T. and Saido, T.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2583;
                                                                                                                                                                                                                                                                                                                                                                        rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases J. Biol. Chem. 276.(24), 21895-21901 (2001)
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Pred. No. 63;
0; Mismatches
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Saido, T.C.
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                                                                                                      GI:10505359
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95.0%;
                                                                                                                                                                                                                                                     1 (bases 1 to 2583)
Shirotani, K., Tsubuk
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                                                                                                                                                        Mus musculus.
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AF157106/c
LOCUS
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ORGANISM

VERSION KEYWORDS

REFERENCE

AUTHORS

TITLE

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QYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSOHRPAVEKAKTLYRS
CMNQSVIEKRDSEPLLSVLKMYGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FINMTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLD
                                                                                                                                          2 (bases 1 to 2652)
Shirotani, K. and Saido, T.C.
Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Institutute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
351-0198, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIGSLSORFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYFENGLQNLKNNAQRSLKKLREKVDQNLWIIGAAVVNAFYSPNRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQERFGLKG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2694)
Shirotani,K., Tsubuki,S., Iwata,N., Takaki,Y., Harigaya,W.,
Maruyama,K., Kiryu-Seo,S., Kiyama,H., Iwata,H., Tomita,T.,
Iwatsubo,T. and Saido,T.C.
Moprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARILENMDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2652;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="neprilysin-like peptidase beta"
rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases J. Blol. Chem. 276 (24), 21895-21901 (2001) 21293028
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Pred. No. 63;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAG18447.
/db_xref="G1:10505362"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="endopeptidase"
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Shirotani, K. and Saido, T.C.
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95.0%;
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Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2601)

Ikeda, K., Emoto, W., Raharjo, S.B., Nurhantari, Y., Salki, K., Yokoyama, M. and Matsuo, M. Molecular: Identification and characterization of novel membrane-bound metalloprotease, the soluble secreted form of which hydrolyzes a variety of vasoactive peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIALRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSLKSDICTTPSCVIAAARILENMDOSRNPCENFYQYACGGWLRHHVIPETNSRYSVF
DILRDELEVILKGVLEDSTSGHRPAVEKAKTLYRSCMNQSVLEKRDSEPLLSVLKMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="SEP(delta); metalloprotease; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWPVALDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPT
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LADNONVNGFSSLGENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINY
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (08-JUN-1999) International Center for Medical Research,
Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2652)
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Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ar302076 2652 bp mRNA linear ROD 11-JUN-
Mus musculus neprilysin-like peptidase beta mRNA, complete cds.
AF302076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="soluble secreted endopeptidase delta"
/protein_id="AAF13153.1"
/db_xref="GI:6467401"
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Pred. No. 63;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
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da, K., Emoto, N. and Matsuo, M.
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     GI:6467400
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Best Local Similarity 95.0%;
Matches 19; Conservative
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                                                     Mus musculus
                                                                             Mus musculus
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AF157106.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6500017,
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DEFINITION ACCESSION

LOCUS

VERSION KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

RESULT'5 AF302076/c

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BASE COUNT ORIGIN

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Gaps

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us-09-647-780a-15.rge

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Query Match 92.0
Best Local Similarity 95.0
Matches 19; Conservative
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AX033272/c
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Mus musculus soluble secreted endopeptidase mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane-bound metalloprotesse, the soluble secreted form of which hydrolyzes a variety of vasoactive peptides
20011457
                                                                                                                                                                                                                                                                                                                                                           GAAVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFDDNGR
                                                                                                                                                                                                                                       GWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPI
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Ikeda,K., Emoto,N., Raharjo,S.B., Nurhantari,Y., Saiki,K.
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                                                                                                                                                                                                    FTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2694;
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Molecular identification and characterization of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                     product="neprilysin-like peptidase gamma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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product="soluble secreted endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-JUN-1999) International Center for Kobe University School of Medicine, 7-5-1 Kusunok
                                                                                                                                                                                                                                                                                                                                                                                                           HSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW
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Pred. No. 63;
); Mismatches 1;
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'note="SEP; metalloprotease"
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/organism="Mus musculus"
/db_xref="taxon:10090"
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/db_xref="G1:6467399"
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Direct Submission
                                                                  'db_xref="taxon:10090'
                                                                                                    'note-"endopeptidase"
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                                                 organism="Mus"
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AF157105.1 GI:6467398
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Best Local Similarity 95.0%;
Matches 19; Conservative
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351-0198,
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AF157105/c
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1 (bases 1 to 2925)
Boileau, G. and Desgroseillers, L.
New metalloproteases of the neprilysin family
Patent: WO 0047750-A 12 17-AUG-2000;
BOILEAU GUY (CA); DESGROSEILLERS LUC (CA); UNIVERSTIE DE MONTREAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAT 21-SEP-2000
CMNQSVIEKRDSEPLLSVLKMVGGWPVALDKWNETMGLKWELERQLAVLNSQFNRRVL
IDLFIWNDDQNSSRHVIÏIDQPTLGMPSREXYFQEDNNHKVRKAYPEFMTSVATMLRK
                                                     DQNLSKESAWVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQERFGLKG
FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLD
RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMĘSAVGSLYIKRAFSKDS
                                                                                                                                                                                   QIVFPAGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNMLDWWSN
                                                                                                                                                                                                               FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSLGENIADNGGVRQAYRAYLRWLA
DGGKDQRLFGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHKVRKAYLEFWTSVATMLRK
DQNLSKESAWVREEMAEVLELETHLANATVPQEKRHDVTALYHKMDLMELQERFGLKG
                                                                                                                                      KSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                              DB 10;
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/note="unnamed protein product"
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95.0%; Pred. No. 62;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              Score 18.4; Pred. No. 62;
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797 c 836 q 582
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Sequence 12 from Patent WO0047750.
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                           92.0%;
illarity 95.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 19; Conserv
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Gaps

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RESULT 9 AF176569/c LOCUS DEFINITION

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

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Molecular cloning and characterization of the Cl(-) pump-associated 55-kDa protein in rat brain Blochem. Blophys. Res. Commun. 289 (2), 363-371 (2001)
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Rattus norvegicus clone CH230-31301, *** SEQUENCING IN PROGRESS
***, 31 unordered pieces,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEKTRTKOTGTPPKMYEVVYKTGSEIHSDFYDIVLVAAPLNRKMSNITFRNFDPPIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNDPYQQLVTTLIKGELNSTLFSSRHKDQFGLSAILVTDDSDMFINSLSIVASVSHKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MGRFAATLVGSLFGLGLLLCGLGRLASAEPRAPPEKIAIVGAGI
                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (26-DEC-2000) Pharmacology, Kansai Medical University,
10-15 Fumizono-cho, Moriguchi, Osaka 570-8506, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="chloride ion pump-associated 55 kDa protein"
/protein id="aak16548 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRLYYLNGIEFAASCMEMSAIAGYNAALLAYHRWIGNEDMIDQDDLYEKLKTEL
            Rattus norvegicus chloride ion pump-associated 55 kDa protein (C1p55) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitagawa, K., Yagyu, K., Hattori, N., Omori, K., Zeng, X.-T. and
                                                                                                                                                                                                                                                            Kitagawa, K., Yagyu, K., Yamamoto, A., Hattori, N., Omori, K., and Inagaki, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.0%; Score 18.4; Dest Local Similarity 95.0%; Pred. No. 61; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Wistar"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'protein_id="AAK16548
                                                                                                                                                  Rattus norvegicus
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="brain"
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HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Clp55"
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                                                                                                                                                                                                                                         (bases 1 to 3742)
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                                                                                                                                                                                                Mammalia; Eutheria;
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                                                                                                                          Rattus norvegicus:
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DGGKDORLPGLNLTYAQLFFINYAQVWCGSYRPFFAVQSIKTDVHSPLKYRVLGSLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 2925)
Ghaddar,G., Ruchon,A.F., DesGroseillers,L. and Boileau,G.
Direct Submission
Submitted (09-AuG-1999) Biochemistry, University of Montreal, 2900
Edouard Montpetit, Montreal, Que H3T 1J4, Canada
Location/Qualifiers
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Ghaddar,G., Ruchon,A.F., Carpentier,M., Marcinkiewicz,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Seidah, N.G., Crine, P., Desgroseillers, L. and Bolleau, G. Molecular cloning and blochemical characterization of a new mouse testis soluble-zinc-metallopeptidase of the neprilysin family Blochem. J. 347 (Pt 2), 419-429 (2000)
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0; Mismatches
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/db_xref="taxon:10090"
/tissue_type="testis"
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Gaps

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Query Match Best Local

Matches

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BASE COUNT ORIGIN

RESULT 10 AF332142/c LOCUS

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
          NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .65591
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
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RS. Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F. R., Allen, C., Atabrachange, H. C., Aret, J. R., Ayele, M., Banks, T., Barberia, J., Benton, J., Binage, H. C., Aret, J. R., Ayele, M., Bonnin, D., Burberia, J., Benton, J., Binage, R., Blankenburg, K., Bonnin, D., Bundy, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, N. C., Carron, T. F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Clen, R., Chen, Z., Chowdhry, I., Dadhorne, S. R., Dayld, R., Dayla, M. L., Dayla, C., Coyle, M.D., Dathorne, S. R., Dayld, R., Dayla, H. H., Douthwaite, K. J., Dayy-Carroll, L., Didy, Y. Durbin, K. J., David, K. J., Daylado, O., Dann-Rocha, S., Durbin, K. J., Douthwaite, K. J., Garz, H. Dugan-Rocha, S., Durbin, K. J., Barnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M. Falls, T., Ferraquico, D., Flagg, N., Forta, J., Foster, P., Frantz, P., Gablsin, H., Guevara, W., Gunaratne, P., Hawes, A., Henrandez, Gorrell, H., Guevara, W., Gunaratne, P., Hawes, A., Henrandez, J., Howards, C., Harris, K., Harris, K., Harr, M., Havlak, P., Hawes, A., Henrandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Valla, Y., Johnson, R., Johlvet, S., Joudah, S., Karlsson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratoson, B., Valla, Y., Johnson, R., Mally, W., Martin, R., 
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On Jul 12, 2002 this sequence version replaced gi:18860410.

Center: Baylor College of Medicine
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Submitted (09-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 65591)
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Consensus quality: 27923 bases at least Q40
Consensus quality: 30152 bases at least Q30
Consensus quality: 32251 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
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-------- Summary Statistics
Sequencing vector: Plasmid;
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                 AUTHORS .
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC128969 114789 bp DNA linear HTG 24-JUL-2002
Rattus norvegicus clone CH230-283G2, *** SEQUENCING IN PROGRESS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S.
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williams, Or, Willeczyk, R., Wooden, S., Worley, R.
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Rives,M., Rojds,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,
Scherer,S., Scott,S., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
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AC128969
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AUTHORS
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_dafa.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 50 contigs. The true order of the pieces
is not known and their order in this sequence record is
of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                  of reads
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Assembly program: Phrap; version 0.990329
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                                                                                                                       ----- Project Information
                                                                                                                                       Center project name: KBXI
Center clone name: CH230-283G2
                                                                                                       Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                          Sequencing vector: Plasmid;
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14 151374 bp DNA linear HTG 19-JUL-2002 norvegicus clone CH230-474C23, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Weinstock,G. and Gibbs,R.
Direct Submission
                                                               unordered pieces.
                                                                                                               AC128214.1 GI:21908823
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Rattus norvegicus
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KEYWORDS
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Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Genome Center
Center: Baylor College of Medicine Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 111011 bases at least Q40 clone name: CH230-474C23 Project Information Contact: hgsc-help@bcm.tmc.edu Center project name: GZMG

50624 GAACACCTCAGAGAAGCCTG 50643

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RESULT 13 AC128214

1 GAACGCCTCAGAGAAGCCTG 20

gap of unknown length contig of 9022 bp in length app of whown length contig of 11244 bp in length

contig of 8319 bp in length

gap of unknown length contig of 10734 bp in length gap of unknown length of 11708 bp in length

110498:

in length

gap of unknown length contig of 18134 bp in

contig

/organism="Rattus norvegicus" /db_xref="taxon:10116"

Location/Qualifiers

151374:

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L (Joses I. C. 1972.2.)

MURDY, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Burbaria, J., Benton, J., Binges, K., Blankenburg, K., Bontin, D., Burbaria, J., Benton, J., Burkett, C., Burnell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavacos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chor, Z., Chowdhry, I., Christopoulos, C., Chen, R., Cren, Z., Chowdhry, I., Dathorne, S.R., David, R., Delaney, K.R., Delaney, K.R., Delaney, Carroll, L., Dedarich, D.A., Delaney, K.R., Delaney, Carroll, L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwardo, O., Esoter, P., Frantz, P., Farls, T., Ferraquto, D., Edwards, C.C., Elhaj, C., Esoter, P., Frantz, P., Gabis, A., Garner, T., Garza, N., Gill, R., Gaoj, J., Garcia, W., Garner, T., Garza, N., Gill, R., Gaoj, J., Garcia, W., Holloway, C., Henrandez, J., Harris, K., Huber, J., Havlak, P., Hawes, A., Hernandez, J., Hoogson, A., Hogues, M., Holloway, C., Hollins, B., Jackson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Liu, J., Li, Z., Lichtarge, O. Lieu, C., Liu, J., Liu, M., Loulseged, H., Mahen, P., Martind, R., Mayer, Martind, R., Mattindale, A., Martind, R., Mattind, P., Martind, R., Mattind, P., Martin, R., Martind, P., Martin, R., Mattind, P., Martin, R., Mattind, P., Martin, R., Mattind, P., Martin, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R., Mattind, R
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Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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KEYWORDS
SOURCE
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                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as Truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Consensus quality: 115816 bases at least 030 Consensus quality: 119457 bases at least 020
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NOTE: This is a "vorking draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
      Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Usnasey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Weinstock, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Weinstock, G. and Gibbs, R.
                                                                                                                                                                       Submitted (31-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics; Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 Shooshtari, N., Sisson, I.,
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                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                            Center: Baylor College of Medicine
Center code: BCM
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 Scherer, S., Scott, G., Shen, H.,
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 188509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., a,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Goyette,M., Graham,L., Grand-Pierre,N., L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 188509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC115933 188509 bp DNA linear HTG 20-JUN-2
Mus musculus clone RP24-53918, WORKING DRAFT SEQUENCE, 6 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goyette, M., Graham, L.

    Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigillo, J., Vassillev, H.,
    Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R. Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., Dewar, K., Diaz, J.S., Dodge, S.
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkly, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J. Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
., Macdonald,P., Major,J., Marquis,N., Matthews,C.
M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
                                                                                                                                                                                                                         Length 169232;
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Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                  ength.
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
                                          ength
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                                                                                                                                                                                                                         Score 18.4;
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                                                                                                                                                                                                                                                                                                                                      86116 GAACGTCTCAGAGAAAGCCTG 86135
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gap of
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Submitted (20-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON JUN 17, 2002 this sequence version replaced g1:19683612. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
Levine, R., Lindblad-Toh, K.
                                 Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., Mebwan,P., McKernan,K., Meldfim,J.,
Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Nell,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.
Strjano,Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 188009; sum-of-contigs
Quality coverage: 8.7 in Q20 bases; agarose-fp
Quality coverage: 8.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: 539_I_8
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
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7154 38916; contig of 21763 bp in length
18917 39016; gap of 100 bp
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17053: contig of 14995 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 187217 bases at least Q40 Consensus quality: 187724 bases at least Q30 Consensus quality: 187784 bases at least Q30 Consensus quality: 187886 bases at least Q20
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/notes 36706 c 36824 g 55842 t 501 others
ORIGIN

Query Match
92.0%; Score 18.4; DB 2; Length 188509;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps

Search completed: July 8, 2003, 03:34:57 Job time: 224.098 secs

Run on:

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(without alignments)
358.431 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for male erectile dysfunction (MED) or female sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction sexual east or sexual disconsistance of east of the sexual disconsistance of east of the sexual disconsistance is such as premature ejacuntation, anorgasmia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disconder: The present sequence is SEP consensus DNA sequence found in human, mouse and rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds.
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to screen for inhibitors,
cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 24; Length 2286;
Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
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Fig 6; 167pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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nes 20; Conserv
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    Disclosure;
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\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf{M}}{\times}\overset{\mathsf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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAZ28811-z28827 represent probes for detecting the rat membrane metalloprotease designated neprilysine II'NEPII) gene (AAZ28810). NEPII is involved in (injactivation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as female sexual arousal disorder -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phillips SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted endopeptidase; SEP; endocrine; vasotropic; analgesic; enzyme; gynaecological; antisense-therapy; male erectile dysfunction; MED; female sexual dysfunction; FSD; female sexual arousal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds
                                        of
                                New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soluble secreted endopeptidase (SEP) consensus DNA.
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1664..2286
/*tag= a
/note= "Encodes catalytic domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 20;
Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD28130 standard; DNA; 2286 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         · .
                                                                                                                                                                                               Claim 3; Page 22; 29pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stacey P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-155042/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
tes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PFIZ ) PFIZER LTD. (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200206492-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD28130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
AAD28130/c
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Matches
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/product= "neutral endopeptidase metallopeptidase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEP-like enzyme; protein production; protein secretion;
neurological disease; Alzheimer's disease; pain; psychiatric disorder;
fertility; bone disease; abnormal phosphate metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a murine neutral endopeptidase metallopeptidase-like enzyme, designated NL-1. The specification also describes NL-2 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimeric constructs containing the foreign protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of neurological diseases such as Alzhelmer's disease, pain, and psychiatric disorders. Nr enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases,
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neprilysin; neutral endopeptidase metallopeptidase-like enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  downstream from and in phase with the N-terminal region. The NI are have been localised to the brain, and may be useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate metabolisms related to improper peptide
                                                                Length 2765;
                                                                                                             Indels
                    BP; 684 A; 735 C; 787 G; 559 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2925 BP; 710 A; 797 C; 836 G; 582 T; 0 other;
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                                                              DB 20;
                                                                                                           Mismatches
                                                              Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                       2377 GAACGCCTCAGAGAAGCCTG 2358
                                                                                                                                                 1 GAACGCCTCAGAGAAGCCTG 20
                                                                                                                                                                                                                                                                                                  AAA63763 standard; cDNA; 2925 BP.
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                                                            Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAB08130
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                    Sequence 2765
                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-2000
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                                                                                                                                                                                                                                                                                                                                            AAA63763;
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                                                                                                                                                                                                                                                       RESULT 4
AAA637637c
ID AAA63
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Brevibacterium flavum MJ-233 dihydroxy acid dehydratase coding region
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     determined (i.e. the present sequence) and was found to encode a protein of 612 amino acids. The enzyme is involved in biosynthesis of the amino acids isoleucine and valine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA fragment contg. a gene coding for di:hydroxy-acid dehydratase derived from Brevibacterium flavum MJ 233, useful for prodn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brevibacterium flavum MJ-233. The sequence of the 1836 bp ORF was
                                                                                                                                                                                                                                                                                                                                          Dihydroxy-acid dehydratase; EC 4.2.1.9; amino acid biosynthesis; isoleucine; Ile; valine; Val; Coryneform bacterium; ds.
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   Length 2925;
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(ORF) coding for dihydroxy-acid dehydratase was isolated from
                                    Indels
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Pred. No. 1.4e+02;
); Mismatches 1;
   21;
                                    ij
     DB
 Score 18.4; Di
Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1836
/*tag= a
/EC_number= 4.2.1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                        1 GAACGCCTCAGAGAGCCTG 20
                                                                                                                                                                                                AAT29734 standard; DNA; 1836 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MITU ) MITSUBISHI CHEM CORP
                                                                                                                                                                                                                                                                                                                                                                                              Brevibacterium flavum MJ-233
92.0%;
llarity 95.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 82.0%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-0234612
                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-isoleucine and L-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-233342/24.
P-PSDB; AAR91947.
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH66364 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP08089249-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-1994;
 Query Match
Best Local Simi
Matches 19;
                                                                                                                                                                                                                                                                    27-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                 AAT29734;
                                                                                                       2575
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                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                 AAT29734
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L-valine (I) which uses a microorganism in which either the dihydroxyacid dehydratase (ilvD) activity and/or gene expression or the acetohydroxy acid synthase (ilvBN) and isomeroreductase (ilvC) activity and/or gene expression has been increased. (I) is useful in animal and human nutrition and as a medicine. Increasing expression of the dihydroxyacid dehydratase, BN and/or C genes results in increased yields of (I), particularly when used in conjunction with inactivation of genes involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel method for the microbial production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence encodes the Corynebacterium glutamicum ilvD protein which is
                                                                                                                                                                                                                                                                                                                                                                                                                                               growing bacteria that have increased activity of selected j. dihydroxyacid dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in synthesis of D-pantothenate e.g. threonine dehydratase (ilvA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-pantothenic acid; panB; panC; ilvD; pantotheanate synthatase;
ketopantoathydroxymethyltransferase; dihydroxyaciddehydratase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microbial production of L-valine useful as medicine and comprises growing bacteria that have increased activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2952 BP; 710 A; 933 C; 743 G; 566 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.4; DB 21;
Pred. No. 1.5e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to illustrate the method of the invention.
                                                                                                                                                                                                                                             (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 10-12; 24pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA40283 standard; DNA; 2952 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAACGCCTCAGAGAGCC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. glutamicum ilvD genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.0%;
                                                                                                                           99DE-1007567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-566215/53.
P-PSDB; AAB10681.
                                                                                                                                                                                                                                                                                                        Sahm H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-pantothenic acid;
      DE19907567-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1006189-A2
                                                                                                                        22-FEB-1999;
                                                                                                                                                                                      22-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jenes, e.g.
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                                                                24-AUG-2000.
                                                                                                                                                                                                                                                                                                        Eggeling L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-2000
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AAA40283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention provides a number of nucleotide and protein
                                                          Coryneform bacterium; amino acid synthesis; vitamin; saccharide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.4; DB 22; Length 1839;
Pred. No. 1.4e+02;
); Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO: 1399; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S, Hayashi M, Ochiai K,
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1839 BP; 423 A; 610 C; 478 G; 328 T; 0 other;
C glutamicum coding sequence fragment SEQ ID NO: 1399
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Senoh A, Ikeda M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK
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1 Similarity 94.4%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     99JP-0377484
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                                                                                                                                                                                                                                                                                                                                                                                                                    2000JP-0159162
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                                                                                      organic acid synthesis; ds
                                                                                                                                                 Corynebacterium glutamicum
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P-PSDB; AAG91145.
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07-APR-2000;
03-AUG-2000;
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AAA71996;

Query Match

Matches

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Nakagawa Tateishi

Claim 8;

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Gaps

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Length 2952; Indels The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium are useful for producing amino acids, nucleic acids, vitamino, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

8 x 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 8 8 8

pantothenic

Disclosure; SEQ ID NO: 7063; 246pp + Sequence Listing; English.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the

European Patent Office

Sequence 349980 BP; 80727 A; 91049 C; 97618 G; 80586 T; 0 other;

0; Gaps

Indels

Length 349980;

Score 16.4; DB 22; Pred. No. 2.4e+02; 0; Mismatches

Query Match 82.0%; Best Local Similarity 94.4%; Matches 17; Conservative

133559 GAACGCCTCCGAGAAGCC 133542

qq

1 GAACGCCTCAGAGAGCC 18

AAH99656 standard; cDNA; 2480 BP.

AAH99656/c RESULT 10

Gaps

; 0

Indels

DB 21; Length 2952;

.5e+02;

Score 16.4; DE Pred. No. 1.5e+ 0; Mismatches

82.0%; 94.4%;

1 GAACGCCTCAGAGAGCC 18

(first entry)

(first entry)

16-OCT-2001

AAH99656;

DEGUSSA-HUELS AG. FORSCHUNGSZENTRUM JUELICH GMBH.

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This invention describes novel recombinant Corynebacterium DNA (1), present in microorganisms of the Corynebacterium genus and comprising at least one of the panB (Ketopantohydroxymethyltransferase), panC (pantothenicacidsynthetase), especially the panBC operon, and/or livp (dihydroxyaciddehydratase) genes. (1) is useful for the preparation of medicine and human and animal nutrition. The new preparation method using fermentation techniques produces the required stereo-isoform D form of pantothenic acid. This sequence encodes the Corynebacterium glutamicum ilvD protein which is described in the method of the invention.
                                                                                                                          Recombinant Corynebacterium DNA useful for production of pantother acid vitamin, comprises panB, panC or ilvD genes encoding enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                Sequence 2952 BP; 710 A; 933 C; 743 G; 566 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C glutamicum coding sequence fragment SEQ ID NO: 7063
                                                                                                                   Recombinant Corynebacterium DNA useful for
                                                                                                                                                          Claim 1c; Page 18-20; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH68528 standard; DNA; 349980 BP
                                                                                                                                                                                                                                                                                                                                                                                                                               2008 GAACGCCTCCGAGAAGCC 2025
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                                                    Eggeling L, Thierbach G,
                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 94.4
Matches 17; Conservative
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                                                                             2000-378263/33
                                                                                        P-PSDB; AAB10035
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(KERJ
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antibacterial, endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia, antiaggregant; haemostatic; vulnerary; antiuloer; osteopathic; eczema; dermatological; antialergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
                                                                                                                                                                                                                                                                                                         cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                          Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human polynucleotides encoding polypeptides, useful for the
                                                                                                                                                                                                                                                                                  antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
                                                                                   antiinflammatory; antirheumatic; antiarthritic; immunosuppressive
                                                      cancer; ulcer; HIV infection; human immunodeficiency
Human protein encoding cDNA sequence SEQ ID NO:491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lang YT, Liu C, Drmanac RT;
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-2000; 2000WO-US35017
                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurological disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene

Yokoi

Ochiai K,

Mizoguchi H, Ando S, Hayashi M, Senoh A, Ikeda M, Ozaki A;

Nakagawa S, Tateishi N,

WPI; 2001-376931/40.

(KYOW ) KYOWA HAKKO KOGYO KK.

2000JP-0159162. 2000JP-0280988.

03-AUG-2000;

6.-DEC-1999; J7-APR-2000;

18-DEC-2000; 2000EP-0127688

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central nervous system; virugide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antialabetic; ottostatic; antiaggregant; haemostatic; vulnerary; antidlabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis; septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                              antirheumatic
                                                                                                                                                                                                                                                                                                                                                                      thrombocytopaenia, wounds, burns, ulcers, immunodeficiency, eczema, allergic
                                                                    AAM199166 to AAM199904 encode the human proteins given in AAM25255 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                          osteoporosis, severe combined immunodeficiency, eczema, allergic
rhinitis, asthma, diabètes, cancer, multiple sclerosis, depression,
 treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                              disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 16; DB 22; Length 2480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2480 BP; 373 A; 777 C; 864 G; 466 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein 5' EST, SEQ ID NO: 24885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID 24885; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC20810 standard; cDNA; 155 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2255 GCCTCAGAGAAGCCTG 2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GCCTCAGAGAAGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                      anaemia, platelet disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC20810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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The present sequence is one of a large number of 5' ESTs derived from

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The invention relates to an isolated polypeptide encoded by a protective sequence, which is a polynucleotide comprising sequences which, when introduced into a cell either predisposed to undergo cell death or in the process of undergoing cell death, prevent, delay, or rescue the cell from death, relative to a corresponding cell into which exogenous nucleic acids have been introduced. The sequences of the invention are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ischaemia; open reading frame; ORF; cerebral herniation; septic embolism; cerebral oedema; meningitis; protozoal infection; malaria; CNI-00733; ss; metazoal infection; vascular disease; eye; macular degeneration; trauma; diabetic retinopathy; epidural haematoma; tumour; degenerative disease; nutritional condition; environmental condition; metabolic condition; CNI-00736; CNI-00738; CNI-00742; CNI-00748; cancer; gene therapy.
              identified within the present sequence. The 5'ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptides and polynucleotides comprising protective sequences useful for preventing, delaying or rescuing a cell from death in disease, condition or disorders such as Alzheimer's disease, stroke, tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protective sequence; cell death; central nervous system; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Juman protective DNA sequence CNI-00748 open reading frame DNA #21.
secreted proteins. No ORF has yet been conclusively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas MB
                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                            Length 155;
                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 21;
Pred. No. 2.3e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                    Sequence 155 BP; 52 A; 14 C; 50 G; 39 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Katz LC,
                                                                                                                                                                                                                                               expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COGE-) COGENT NEUROSCIENCE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 2; Fig 8U; 228pp; English
                                                                                                                                                                                                                                                                                                                                                                                                              2 AACGCCTCAGAGAGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                   92 ATCTCCTCAGAGAAGCCTG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS98541 standard; cDNA; 267
                                                                                                                                                                                                                                                                                                                              79.0%;
                                                                                                                                                                                                                                                                                                                                                  89.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )9-APR-2001; 2001WO-US11501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11:APR-2000; 2000US-0547938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-066433/09.
                                                                                                                                                                                                                                                                                                                                                  Similarity
17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAU73375.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Portbury SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS98541;
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trauma
                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS98541,
  8888888888888888888
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diagnosing a protective sequence-mediated condition, disorder or disease in an individual. The treatable disorders are preferably of the central nervous system of humans including isohaemia-related conditions such as stroke, cerebral herniation, septic embolism, cerebral oedema, infections such as meningitis, protozoal infections such as malaria, metazoal infections such as echinococcosis, vascular diseases such as ischaemic encephalopathy, conditions involving the eye such as macular degeneration, diabetic retinopathy, trauma such as epidural haematoma, tumnours such as primary intracranial tumours, degenerative diseases such as Alzheimer's disease and nutritional, environmental and metabolic conditions. Sequences AASSB409-AASSB544 represent human protective sequence DNA and open reading frames of the polynucleotides.
      88888888888888888
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85 G; 53 T; 0 other; Sequence 267 BP; 49 A; 80 C;

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Gaps
Score 15.8; DB 24; Length 267;
Pred. No. 2.4e+02;
0; Mismatches 2; Indels 0
                        0
                                                             102 GAACGCCTGAGAGCAGCCT 84
                                               1 GAACGCCTCAGAGAAGCCT 19
79.0%;
          Local Similarity 89.5%; es 17; Conservative
Query Match
                       Matches
                                                                    g
                                              õ
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RESULT 13 AAF11088/c

AAF11088 standard; cDNA; 274 BP AAF11088; 

Fusarium venenatum EST SEQ ID NO:3611.

(first entry)

13-MAR-2001

expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss. Multiple gene expression; filamentous fungal cell; EST;

Fusarium venenatum

WO200056762-A2

28-SEP-2000.

22-MAR-2000; 2000WO-US07781

99US-0273623 22-MAR-1999;

(NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.

Clausen IG, Shuster JR, Kauppinen S, WPI; 2000-594572/56. Rey MW, Berka RM,

genes in filamentous fungal cells

Olsen PB;

Monitoring differential expression of genes in filamentous fungal cell uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -Claim 86; Page 1643; 3161pp; English.

expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be The present invention describes a method for monitoring differential

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Identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venematum; AAF11248 to AAF11853 represents ESTs from Aspergillus
                                                                                                                                                                                                                                                                                                                                            niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesel, which are
                                                                                                                                                                                                                                                                                                                                                                             AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
   possible functions of unknown open reading frames can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 G; 67 T; 15 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 274 BP; 67 A; 64 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
888888888888888888888888
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; Score 15.8; DB 21; Length 274; Pred. No. 2.4e+02; Mismatches 3; Indels 0 ó 79.0%; 85.0%; Conservative Best Local Similarity Matches 17; Conserv

Gaps

144 GAAAGCNTCATAGAAGCCTG 125 1 GAACGCCTCAGAGAAGCCTG 20 g ò

AAS98540 standard; cDNA; 321 BP. RESULT 14 AAS98540/c

AAS98540;

12-MAR-2002 (first entry)

Human; protective sequence; cell death; central nervous system; stroke; ischaemia; open reading frame; ORF; cerebral herniation; septic embolism; cerebral ocdema; meningitis; protozoal infection; malaria; CNI-00733; ss; metazoal infection; vascular disease; eye, macular degeneration; trauma; diabetic retinopathy; epidural hematoma; tumour; degenerative disease; nutritional condition; environmental condition; metabolic condition; cNI-00738; CNI-00748; cancer; gene therapy. Human protective DNA sequence CNI-00748 open reading frame DNA #20. 

Homo sapiens.

WO200181361-A1

09-APR-2001; 2001WO-US11501.

11-APR-2000; 2000US-0547938

(COGE-) COGENT NEUROSCIENCE INC.

Thomas MB; Barney S, 5 5 7 Katz LC, Portbury SD, Puranam WPI; 2002-066433/09. P-PSDB; AAU73374. 

Polypeptides and polynucleotides comprising protective sequences useful for preventing, delaying or rescuing a cell from death in disease, condition or disorders such as Alzheimer's disease, stroke, tumours,

Claim 2; Fig 8T; 228pp; English.

The invention relates to an isolated polypeptide encoded by a protective sequence, which is a polynucleotide comprising sequences which, when introduced into a cell either predisposed to undergo cell death or in the process of undergoing cell death, prevent, delay, or rescue the cell from death, relative to a corresponding cell into which exogenous nucleic

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Search completed: July 8, 2003, 02:19:04 Job time: 127.659 secs
                                                   nervous system of humans including ischaemia-related conditions such as stroke, cerebral herniation, septic embolism, cerebral oedema, infections such as maningitis, protozoal infections such as malaria, metazoal such as meningitis, protozoal infections such as malaria, metazoal infections such as echinococcosis, vascular diseases such as ischaemic encephalopathy, conditions involving the eye such as macular degeneration, diabetic retinopathy, trauma such as epidural haematoma, tumnours such as primary intracranial tumnours, degenerative diseases such as Alzheimer's disease and nutritional, environmental and metabolic conditions. Sequences AAS98409-AAS98544 represent human protective sequence DNA and open reading frames of the polynucleotides.
have been introduced. The sequences of the invention are useful for
                   in an individual. The treatable disorders are preferably of the central pervous system of humans including ischaemia-rolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in ART19001-T206837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constructed so as to reflect accurately the relative abundance or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene signature; messenger RNA; mRNA; relative abundance; frequency,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dentifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                  Length 321;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                           Sequence 321 BP; 65 A; 92 C; 101 G; 63 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    DB 24;
                                                                                                                                                                                                                                                                                                                               Score 15.8; DB 24;
Pred. No. 2.4e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT19761 standard; cDNA to mRNA; 373 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; cloning; mapping; non-biased libr
cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 466; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                         156 GAACGCCTGAGAGCAGCCT 138
                                                                                                                                                                                                                                                                                                                                                                           ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luman gene signature HUMGS00836.
                                                                                                                                                                                                                                                                                                                                  79.0%;
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                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2-NOV-1993;
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AAT19761
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Gaps
different mRNAs in the particular tissue from which it was derived
                  The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                .
0
                                                                                                                                                       Length 373;
                                                                                                                                                                                                Indels
                                                                                                                   Sequence 373 BP; 89 A; 71 C; 98 G; 102 T; 13 other;
                                                                                                                                                       Score 15.8; DB 16;
Pred. No. 2.5e+02;
                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                              2 AACGCCTCAGAGAAGCCTG 20
                                                                                                                                                         Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
  88888888
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Appl Appl Appl

Sednence Sednence Sednence Sednence Sednence Sednence Sednence

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Sequence Sequence Sequence

48

Sequence Sequence

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Perfect score:

Sequence:

OM nucleic

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Scoring table:

Searched:

Database

Result Š.

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Sequence 4, Application US/09318794A
Patent No. 6177264
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
TITLE OF INVENTION: ACID USING CORYNEFORM BACTERIA
FILE REFERENCE: eggeling
CURRENT APPLICATION NUMBER: US/09/318,794A
CURRENT FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: DE 198 55 312.9
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 2952;
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                                                     US-08-609-583A-11
US-08-937-399-11
US-09-310-367-11
                          -08-480-070C-11
-08-829-525-11
                                                                                               US-09-032-337-11
US-09-398-395A-41
                                                                                                                                         US-08-817-436A-1
                                                                                                                                                                     US-08-976-259-64
                                                                                                                                                        -09-202-893B-
                                                                                                                            US-09-391-104-1
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Pred. No. 19;
0; Mismatches
                                                                                                                                                                                                                                            US-09-426-436-1
                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 505, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steinmann, Kathleen E.
Astle, Jon H.
Burgess, Christopher C.
Bushnell, Steven E.
Carroll III, Eddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2008 GAACGCCTCCGAGAGCC 2025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.0%;
ilarity 94.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: CDS
; LOCATION: (290)..(2125)
US-09-318-794A-4
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Best Local Similarity
Matches 17; Conserv
US-09-328-111-505/c
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APPLICANT:
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6, Appli
INFORMAT
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                                                                                                       (without alignments)
222.151 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                        ; Search time 27.6098 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence (
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        5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-927-219-133
US-09-161-241-76
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US-08-850-910A-40
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                                                                                                                                                                                                                                                   441362 segs, 153338381 residues
        GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                           nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                           1 gaacgcctcagagaagcctg 20
                                                                                        8, 2003, 01:24:03
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Gapop 10.0 , Gapext 1.0
                                                                                                                                           US-09-647-780A-15
20
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Maximum DB seq length: 200000000
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Match Length
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14044
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14086
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Gaps

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Lewis, Marcia E. Monahan, John E. Schlegel, Robert Ford, Donna M.

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DB 3; Length 4503;
                                                Length 4503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/175,581
                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                US-09-175-581-2
US-09-175-581-2
US-09-175-581-2
US-03-175-581
Patent No. 6034232
GENERAL.INFORMATION:
APPLICANT: KANEDA, JUN
APPLICANT: YANGOI, HIDEKI
APPLICANT: YANGOI, HIDEKI
MAPLICANT: YANGOI, HIDEKI
TITLE OF INVENTION: NOVEL STRESS PROTEINS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.4; DB
Pred. No. 65;
0; Mismatches
                                                                                            Mismatches
                                                  77.0%; Score 15.4; 94.1%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,301
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 6, Application US/08706391B
                                                                                                                                                            2739 CGCCACAGAGAAGCCTG 2755
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                                                                                                                                    4 CGCCTCAGAGAGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MORPHY JR. GERALD M
REGISTRATION NUMBER: 28,97
REFERENCE/DOCKET NUMBER: 1
IELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CGCCTCAGAGAGCCTG 20
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Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (703)-202-800(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703)-205-8050
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                  Query Match
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; IDENTIFICATION METHOD:
US-09-175-581-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid. STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FALLS CHURCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-08-706-391B-6/c
        US-08-770-301A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US) CURRENT APPLICATION NUMBER: US/09/328,111 CURRENT FILING DATE: 1999-06-08 EARLIER APPLICATION NUMBER: US 60/088,801 EARLIER FILING DATE: 1998-06-10 NUMBER OF SEQ ID NOS: 850 SOFFWARE: EastSEQ for Windows Version 3.0 SEGU ID NO 505 LENGTH: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,301A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH <sup>C</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.8; DE Pred. No. 32; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: IKEDA, JUN
APPLICANT: KANEDA, SUMIKO
APPLICANT: YANAGI, HIDEKI
APPLICANT: YANAGI, HIDEKI
APPLICANT: YURA, TAKASHI
TITLE OP INVENTION: NOVEL STRESS PROTEINS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08770301A Patent No. 5948637 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(652)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 AACGCCACAGAGCAGCTG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATORNEY AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTATION NUMBER: 28,977
REFERENCE/DOCKET UNDRER: 1422
TELEPONE: (703)-205-8000
TELEPAX: (703)-205-8000
TELEFAX: (703)-205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AACGCCTCAGAGAAGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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Patent No. 6174725

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E: Floppy disk
IBM PC compatible
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ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 9
FELECOMMUNICATION INFORMATION
TELEPHONE: 608-251-5000
                                                                                                                                                                                                (608) 831-2100
                                                                         FILING DATE: 17-OCT-1996
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 85.0%
Matches 17; Conservative
                                                                                                                   NAME: Sara, Charles S. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1425 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          608-251-916
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25..1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 53701-2113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION:
US-08-883-515-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE
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                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: USDA, AGRICULTURAL RESEARCH SERVICE, PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic Plants as an Alternative
Source of Lignocellulosic-Degrading Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 477;
                                         TITLE OF INVENTION: ALTERING DOUGH VISCOELASTICITY WITH MODIFIED GLUTENINS
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,043
REFERENCE/DOCKET NUMBER: 0235.95/USDA96-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.3
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/706,391B
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Pred. No. 62;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Ste. 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                   BUCHANAN STREET
                                                                                                                                                                             CITY: ALBANY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94710
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Austin-Phillips, Sandra APPLICANT: Burgess, Richard R. APPLICANT: German, Thomas L. APPLICANT: Ziegelhoffer, Thomas L. TITLE OF INVENTION: Transgenic Plan TITLE OF INVENTION: Source of Ligno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,495
                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (510) 559-6067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CONNOR, MARGARET A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 GAACGCTGCGGAGAAGCCTG 322
                       APPLICANT: ANDERSON, OLIN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAACGCCTCAGAGAAGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PELEFAX: (510) 559-577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 477 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                 NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                               STREET: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53717-1914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-08-706-391B-6
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DB 2; Length 1425;
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                                                                                                                                                                                                            APPLICANT: Osteryoung, Katherine W
TITLE OF INVENTION: PLANT CHLOROPLAST DIVISION GENES
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Christensen, Tove
TITLE OF INVENTION: A Transcription Factor
FILE REFERENCE: 4484.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/197,814A
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09820.036
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,515
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street:
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1167 GAATGACTGAGAGGAGCCTG 1148
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; Sequence 1, Application US/09197814A
; Patent No. 6316220
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                                                                                                                                     Sequence 1, Application US/08883515
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Score 14.8; DB 4; Length 777;
Pred. No. 1e+02;
0; Mismatches 2; Indels (
                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 187.08_1.09_1.00 PILING DATE: US/08/27.219 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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Pred. No. 98;
0; Mismatches
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Patent No. 6344541
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TILLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 76
LEAST CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CO
                                                                                                                                                                                                                                                             FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 435
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT-1996
PRIOR APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-OCT-1996
PRIOR APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: ARCD:272
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 ATGTCTCAGAGAAGCCTG 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 74.0%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 467 base pairs
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Wilson, Mark B. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
JS-08-927-219-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Human
US-09-161-241-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us-09-161-241-76/c
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                                                                                                                                                                                                                                                                                                                                                                Length 3980;
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                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A Transcription Factor
FILE REFERENCE: 4484.204 US
CURRENT APPLICATION WUMBER: US/09/197,814A
CURRENT FILING DATE: 1996-11-23
EARLIER APPLICATION NUMBER: 0740/96
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1997-07-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 3980
                                                                                                                                                                                                                                                                                                                                                                Query Match 76.0%; Score 15.2; D
Best Local Similarity 85.0%; Pred. No. 81;
Matches 17; Conservative 0; Mismatches
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EARLIER FILING DATE: 1996-07-05
EARLIER APPLICATION NUMEER: PCT/DK97/00305
EARLIER FILING DATE: 1997-07-07
NUMBER OF SEO ID NOS: 14
SOFTWARE: FASTSEO for Windows Version 3.0.
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Pred. No. 8
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P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND HNF-4ALPHA
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||||| ||| ||| |||| |||
2062 GAACGACTCCGAGAAGTCTG 2043
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Patent No. 6187533
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2062 GAACGACTCCGAGAAGTCTG 2043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09197814A Patent No. 6316220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAACGCCTCAGAGAGCCTG 20
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: Oda, Naohisha
: Kaisaki, Pamela J.
: Furuta, Hiroto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                               LENGTH: 3980
TYPE: DNA
ORGANISM: Aspergillus oryzae
US-09-197-814-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA; ORGANISM: Aspergillus oryzae
US-09-197-814-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horikawa, Yukio
Menzel, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Christensen, Tove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION:
FITLE OF INVENTION:
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-09-197-814-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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Length 467; Indels ö

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Gaps

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Indels

Length 3191;

Score 14.8; DB 4; Pred. No. 1.2e+02; 0; Mismatches 2;

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; SEQUENCE DESCRIPTION: SEQ ID NO: 70: US-09-453-7028-70
                                                                                                                                                                            ||||| ||||| 275 GAACTCCTCAAAGAAGCC 258
                                                                                                                                                     1 GAACGCCTCAGAGAAGCC 18
                                                                      Ouery Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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US-08-850-910A-40
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                                                                        GENERAL INFORMATION:
APPLICANT: Musso, Richard
APPLICANT: Musso, Richard
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES DIAGNOSTIC FOR PATHOGENIC E.
TITLE OF INVENTION: CULL 0157, METHODS OF IDENTIFICATION AND KIT THEREFOR CURRENT APPLICATION NUMBER: US/09/179,221D
CURRENT FILING DATE: 1998-10-27
NUMBER OF SEQ ID NOS: 16
SOFTHARE: No. 6291168epad
SED ID NO 3
LENGTH: 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coll 0157
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö
                                                                                                                                                                                                                                                                                                                                                                                          Length 1331;
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ZIP: 53701-2113
COMPUTER: US
ZIP: 53701-2113
COMPUTER: DISKETLE, 3.50 inch. 1:44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                        ; Db
1.1e+02;
2;
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 70, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
                                       Sequence 3, Application US/09179221D
Patent No. 6291168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 70:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 GAACTCCTCAAAGAAGCC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAACGCCTCAGAGAGCC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                        74.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                urland,
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 16; Conserva
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                                                                                                                                                                                                                                                                                                                      ; ORGANISM: E. coli
US-09-179-221D-3
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RESULT 11
US-09-179-221D-3
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Gaps
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Sequence 40, Application US/08850910A
Patent No. 5948761
GENERAL INFORMATION:
APPLICANT: SELLHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUGTIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.0%; Score 14.4; DB 2; Length 707; Best Local Similarity 93.8%; Pred, No. 1.6e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                     ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                     NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAME/KEY: CDS
COCATION: 100...4
COTHER INFORMATION:
US-08-850-910A-40
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Length 1504;
                                                                                                                                      PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
                                                                                                                                                                                           E: MORRISON & FOERSTER, LLP
2000 Pennsylvania Avenue, NW, Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.0%; Score 14.4; DB 2; Best Local Similarity 93.8%; Pred. No. 1.8e+02; Matches 15; Conservative 0; Mismatches 1;
                                                                                                                    TECHNIQUES FOR
                                                                                                                                                                                                                                                                                                                                                          COMPUTER: .... - ... Hindows CORFULING SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/850,910A FILING DATE: 05-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8, 2003, 09:32:02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
Sequence 17, Application US/08850910A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE DOCKET NUMBER: 21
FELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               550 GCCTCACAGAAGCCTG 565
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LOCATION: 100...630
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1504 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Murashige, Kate
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE CHARACTERISTICS
                                                       APPLICANT: SEILHAMER, J
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH,
TITLE OF INVENTION: REC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    Washington
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Job time: 28.6598 secs
                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                       APPLICANT: Gayle, Margit
APPLICANT: Slack, Jennifer
APPLICANT: Slack, Jennifer
APPLICANT: Sluss, John E.
APPLICANT: Sluss, John E.
APPLICANT: Dower, Steven K.
TITLE OF INVENTION: No. 5576191e1 Cytokine That Binds ST2
CORRESPONDENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.0%; Score 14.4; DB 1; ilarity 93.8%; Pred. No. 1.8e+02; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/265,086 FILING DATE: June 17, 1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                             SEE: Immunex Corporation
: 51 University Street
Seattle
                                                                                                                Sequence 3, Application US/08265086 Patent No. 5576191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATORNEY AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2825
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
305 GCCTCACAGAAGCCTG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GCCTCAGAGAGCCTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1251 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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1..63
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64..672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                         Washington
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1..675
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Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           muST2-lig
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                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                   98101
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LOCATION:
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-265-086-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 OUNTRY:
                                                                           RESULT 14
US-08-265-086-3
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RESULT 15 US-08-850-910A-17

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sequence 93, Appl
Sequence 6543, App
Sequence 6543, App
Sequence 1876, App
Sequence 124, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1282, App
Sequence 1922, App
Sequence 1922, App
Sequence 1922, App
Sequence 1922, App
Sequence 20258, I
Sequence 505, An
Sequence 526, An
Sequence 364, Ap
Sequence 179, App
Sequence 300, App
Sequence 601, App
Sequence 601, App
Sequence 601, App
                                                                                                                                                                                                                                               Sequence 15509
                                                                                                                                                                                         Sequence 1
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                           -761-15509
                                                                 US-10-106-698-364
US-09-919-039-179
US-10-205-823-300
US-10-152-661-601
US-09-866-050A-601
US-09-954-531-1351
                                                                                                                                                                                                                                                                                                                                                                                                        US-09-764-868-1282
US-10-091-504-1922
US-09-764-869-1922
US-09-764-891-9556
                                                                                                                                                                                   US-09-946-807
                                                                                                                July 8, 2003, 19:09:54 ; Search time 115.512 Seconds (without alignments) 273.390 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                . 2210862
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      1105431 seqs, 789497651 residues
                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                 1 gaacgcctcagagaagcctg 20
                                                                                                                                                                                                                                                                  IDENTITY_NUC Gapon 10.0 , Gapext 1.0
                                                                                                                                                                                           US-09-647-780A-15
                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Title: Perfect score: Sequence:

Run on:

Scoring table:

## ALIGNMENTS

Published_Applications_NA:

Database

Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_6/pp / Cgn2_		RESULT 1	US-09-738-626-1399 ; Sequence 1399, Application US/09738626	GENERAL INFORMATION:	z 	; APPLICANT: ANDO, SEIKO APPLICANT: HAVASHI MITTED		; APPLICANT: YOKOI, HARUHIKO ; APPLICANT: TATEISHI, NAOKO	; APPLICANT: SENOH, AKIHIRO	APPLICANT: OZAKI, AKIO	; TITLE OF INVENTION: NOVEL POLYNUCLEOTII ; FILE REFERENCE: 249-125	CURRENT APPLICATION NUMBER: US/09/738,6	_	PRIOR FILING DATE: 1999-12-16 PRIOR ADDITION NIMBER: 15 00 71 60162	; PRIOR FILING DATE: 2000-04-07	; PRIOR APPLICATION NUMBER: JP 00/280988	; NUMBER OF SEQ ID NOS: 7059	; SOFTWARE: PatentIn ver. 3.0	LENGTH: 1839	TYPE: DNA	; ORGANISM: Corynebacterium glutamicum		82.08;	Best Local Similarity 94.4%; Pred. No Matches 17; Conservative 0: Misma			Db 1722 GAACGCCTCCGAGAAGCC 1739	
CGGG_CFPCGGGGATAZ/PUDDAGA_USDY_NEW_PUB.seq:*   CGGG_CFPCGGGATAZ/PUDDAGA_USDY_NEW_PUB.seq:*   CGGG_CFPCGGGATAZ/PUDDAGA_USDG_NEW_PUB.seq:*   CGGG_CFPCGGGATAZ/PUDDAGA_USOC_NEW_PUB.seq:*   CGGG_CFPCGGGATAZ/PUDDAGA_USOC_NEW_PUB.seq:*   CGGG_CFPCGGGTAZ/PUDDAGA_USOC_NEW_PUB.seq:*   CGGG_CFPCGGGTAZ/PUDDAGA_USOC_NEW_PUB.seq:*   CGGG_CFPCGGGTAZ/PUDDAGA_USOS_NEW_PUB.seq:*   CGGG_CFPCGGTAZ/PUDDAGA_USOS_NEW_PUB.seq:*   CGGG_CFPCGGGAGA_USOS_NEW_PUB.seq:*   CGGG_CFPCGGGAGA_USOS_NEW_PUB.seq:*   CGGG_CFPCGGGAGA_USOS_NEW_PUB.seq:*   CGGG_CFPCGGGAGA_USOS_NEW_PUB.seq:*   CGGG_CFPCGGGAGA_USOS_NEW_PUB.seq:*   CGGG_CFPCGGGGAGA_US			:									*				_												
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	2													Resu	:													

NVENTION: NOVEL POLYNUCLEOTIDES (ENCE: 249-125 PLICATION NUMBER: US/09/738,626 ICATION NUMBER: JP 99/377484 NG DATE: 1999-12-16 ICATION NUMBER: JP 00/159162 Length 1839; Indels

DB 9;

Score 16.4; Di Pred. No. 42; 0; Mismatches

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Gaps
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILL REPERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/215,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SEQ ID NO 7732

SEQ ID NO 7732

LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020192678A1 1398377.1
US-10-071-766-97
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                                                                                                                                                                                                         TITLE OF INVENTION: GENES EXPRESSED IN SENESCENCE FILE REFERENCE: PA-0043 US CURRENT APPLICATION NUMBER: US/10/071,766 CURRENT FILING DATE: 2002-02-07 NUMBER OF SEQ ID NOS: 144.
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Pred. No. 92;
0; Mismatches
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Pred. No. 92;
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Publication No. US20030073623A1
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Patent No. US20020165144A1
GENERAL INFORMATION:
                                                                                                                                   Sequence 97, Application US/10071766 Publication No. US20020192678A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 GAACGCCTGAGAGCAGCCT 220
                  160 AACGCCACAGAGCAGCTG 178
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milarity 89.5%;
Conservative 0
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Huei-Mei Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-7732
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 17; Conserv
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GENERAL INFORMATION
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                                                                                              RESULT 4
US-10-071-766-97
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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ITLE OF INVENTION: ODC Allelic Analysis Method For Assessing Carcinogenic Susceptibi
ILE REFERENCE: 9855-32U2
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Pred. No. 29;
0; Mismatches
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Pred. No. 94
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CURRENT FILING DATE: 2001-07-24
                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
                                                                                                                                                                                                                                                                                               OF INVENTION: NOVEL POLYNUCLEOFIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/122,301 PRIOR FILING DATE: 1999-03-01 PRIOR APPLICATION NUMBER: US 09/516,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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APPLICANT: O'Brien, Thomas
                                    Application US/09738626
No. US20020197605A1
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NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 31
LENGTH: 234
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1 Similarity 89.5%;
17; Conservative (
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Best Local Similarity 94.4%;
Matches 17; Conservative
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; OTHER INFORMATION: n = c or
US-09-911-935A-31
                                                                                                APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                          AYASHI, MIKIRO
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ENOH, AKIHIRO
                                                                                                                                                                                                   KOI, HARUHIKO
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Best Local Similarity
Matches 17; Conserv
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us-09-647-780a-15.rnpb

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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F.
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                     Length 401;
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PAPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTERO FOR MINDOWS VETSION 3.0
                                                                                                                       DB 10;
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                                                                                                                     Score 15.8;
Pred. No. 92;
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Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR APPLICATION NUMBER: US 60/180,312
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PRIOR FILING DATE: 2000-08-03
PRIOR PELING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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Publication No. US20030073623A1
GENERAL INFORMATION:
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                   199 AACGCCACAGAGCAGCCTG 217
                                                                                                                                                                                                            1 GAACGCCTCAGAGAGCCT 19
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Best Local Similarity 89.5%;
Matches 17; Conservative
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illarity 89.5%;
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                             .; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-686-837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        JS-09-918-995-17753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: HOMO
US-09-918-995-17753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 17753
LENGTH: 411
         LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                        DB .9;
                                                                                                                                                                                                                                                                                                                                                      Score 15.8; DE
Pred. No. 92;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.8; Di
Pred. No. 92;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Guicher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
E OF INVENTION: HUMAN SCHIZOPHRENIA GENE REFERENCE: 2345.2004-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TILE APPLICANTION: HUMAN SCHIZOPHRENIA GENE
FLIE REPERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 837
                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 837
                                         CURRENT APPLICATION NUMBER: US/09/946,807 CURRENT FILING DATE: 2001-09-05
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 837
                                                                                     PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
                                                                                                                                PRIOR APPLICATION NUMBER: US 09/515,716 PRIOR FILING DATE: 2000-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 837, Application US/09795686. Patent No. US20020094954Al. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09795668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 GAAAGCTTCAGAGAAGCCT 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAACGCCTCAGAGAGGCT 19
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Best Local Similarity 89.5%;
Matches 17; Conservative
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ilarity 89.5%;
Conservative
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                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-946-807-837
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Best Local Similarity
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; ORGANISM: HOM
US-09-795-668-837
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Gaps
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                                                                                                       Length 453;
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Pred. No. 91;
0; Mismatches 2;
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ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR 1
ITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                       DB 9;
                                                                                                                                                Mismatches
                                                                                                       Score 15.8;
Pred. No. 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/902,941 CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/849,626 CURRENT FILING DATE: 2001-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 828, Application US/09849626 Publication No. US20020197669A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Sequence 828, Application US/09902941
Patent No. US20020172952A1
                                                                                                                                                                                                              374 AACGCCACAGAGCAGCCIG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AACGCCTCAGAGAGCCTG 20
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Watanabe, Yoshihiro
Johnson, Jeffrey C.
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                                                                                                    Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5%;
Matches 17; Conservative
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McNeill, Patricia
Clapper, Jonathan
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Wang, Aijun
Wang, Tongtong
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; ORGANISM: Homo sapiens
US-09-902-941-828
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 442;
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                                                                                                                                                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-06-30
                                                        PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
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Pred. No. 91
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 828
                                   LING DATE: 2001-01-30
PLICATION NUMBER: PCT/USO1/00665
TING DATE: 2001-01-30
                   CATION NUMBER: PCT/US01/00669
3 DATE: 2001-01-30
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Patent No. US20020168637A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.5-
....hes 17; Conservative
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arter, Darrick
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US-09-864-761-4088
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Gaps

Length 454; Indels

DB 9;

Score 15.8; DE Pred. No. 91; 0; Mismatches

9, 2003, 02:22:26

436 GAACGCCTGAGAGCAGCCT 418 1 GAACGCCTCAGAGAAGCCT · 19

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; OTHER INFORMATION: n = A,T,C or US-09-918-995-2506
                                                                          Ouery Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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me : 122.562 secs
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Job time
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 2011-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1909-01-20
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: Fastseq for Windows Version 3.0
SEQ ID NO 2506
LENGTH: 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VedVick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C18
                                                                                                                                    Indels
                                                                                       Score 15.8; DB 9;
Pred. No. 91;
0; Mismatches 2;
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Pred. No. 91;
0; Mismatches
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CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SEQ ID NO 828
LENGTH: 453
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Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             Sequence 828, Application US/10017754
Publication No. US20030054363A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
                                                                                                                                                                                                374 AACGCCACAGAGCAGCCTG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 AACGCCACAGAGCAGCCTG 392
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Carter, Darrick
Fanger, Gary R.
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Watanabe, Yoshihiro
Johnson, Jeffrey C.
Retter, Marc W.
                                                                                     Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative (
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Best Local Similarity 89.5%;
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-10-017-754-828
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-626-828
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ORGANISM: Homo sapiens
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LOCATION: (1)...(454)
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US-09-918-995-2506/c
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Scoring table:

Total number

Searched:

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Sequence: Title: Perfect :

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AW445429 B1587 MAR
BG992210 RC4 +HT125
BO375929 IL5-TN000
AQ100155 HS_3049_B
BG382418 298310 MA
AL775847 AL775847
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 507)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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AL652033 AL652033
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UI-R-BO1-ask-h-09-0-UI.S1 UI-R-BO1 Rattus UI-R-BO1-ask-h-09-0-UI 3', mRNA sequence.
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AQ169284
AA226901
BE233903
AQ183015
AI150181
AQ125886
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AL644837
BC52696
AQ252696
BC725146
BC715312
AC15325
AL639255
AL639255
AL639255
BC4875
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AC162875
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Rodentia;
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                                                                                                                                                                  8, 2003, 00:47:28; Search time 1013.95 Seconds
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16154066 seqs, 8097743376 residues
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Listing first 45 summaries
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                                                                                                                                                                       July
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AGENCOURT 602388838 602139970 875 mgxb0016B 753 RST43393

Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A

BE106100 UI-R-B01-AA146423 mr66e08.r AI641353 mr66e08.y BG153322 mag12d11.AQ209617 HS_3236_A AZ223089 RPCI-23-9

BE106100 AA146423 AI647353 BG153322 AQ209617 AZ223089

177

507 378 388 704 516

100.0 92.0 92.0 92.0 87.0 87.0

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Description

DB

Query Match Length

Score

Š. Result

IA 52242, USA

451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565

Contact: Soares, MB Program for Rat Gene Discovery and Mapping

University of Iowa

Wed

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Putative full length read
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                                                                                                                                                                                                                                                                                                                     /lab_nost="pHIOB (Life Technologies)"
/lab_nost="Nector: pT713D-Pac (Pharmacia) with a modified
/note="Nector: Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B01) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived, please visit our web site at ratest eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research
                                          normalized medulla library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Gags,M., Martin,J., Morris,M., Gassel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., 'Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sstis (#937308) Mus musculus cDNA
to WP:F26G1.6 CE02698 NEPRILYSIN ;,
tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the
                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum and hippocampus. For a detailed description of the library from which this clone was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:367870
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Contact: Marra MyMouse EST Project
Washb-HHMI Mouse EST Project
Washb-HHMI University School of Medicinep
4444 Porset Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 507;
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Pred. No. 49;
0; Mismatches 0;
                                                                                                                                                                                                                                     /db_xref="taxon:10116"
/clone="UI-R-BO1-ask-h-09-0-UI"
/clone_lib="UI-R-BO1"
                                                                                                                                                                                          /organism="Rattus norvegicus"/strain="Sprague-Dawley"
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clone IMAGE:602438 5' similar to WP
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TAG_LIB=UI-R-BO1
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                                                                                     Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_SEQ=GAACCG"
                                                                                                       Seg primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lln!gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone this read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                             mr66e08.yl Stratagene mouse testis (#937308) Mus musculus CDNA clone IMAGE:602438 5' similar to WP:F26G1.6 CE02698 NEPRILYSIN ;,
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                          /clone="IMAGE:602438"
/clone_lib="Stratagene mouse testis (#937308)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                             /dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.4; DB 9;
Pred. No. 2.4e+02;
0; Mismatches 1;
vector to vector length is 390
Seg primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 157.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
                                                                                                                                        /organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388. pb
                                                                                                                                                                                        'db_xref-"taxon:10090"
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vector to vector length is 389
MGI:367870
                                                                                                                                                                                                                                                                                          /tissue_type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                             strain="CD-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.0%;
illarity 95.0%;
Conservative 0
                                                                                                                                                                                                                                                                  /sex="males"
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
AI647353
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us-09-647-780a-15.rst

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1 (bases 1 to 574)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B. Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rodentia;
1 GAACGCCTCAGAGAAGCCTG
                                                                                                                                                                                        AQ209617.1 GI:3622352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 87.0%;
1 Similarity 90.0%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                 (bases 1 to 516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 3236 rov
Class: BAC ends
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                     DEFINITION
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ORIGIN
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AUTHORS
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VERSION
KEYWORDS
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AUTHORS
                                                                                  RESULT 5
AQ209617
LOCUS
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AZ223089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                   XR Vector;
adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 05-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    BG15332.

104 bp mRNA linear EST 05-FEB-2001
mag12d11.x1 NCI_CGAP_Emb2 Rattus norvegicus CDNA clone
IMAGE:4176045 3' similar to TR:0902V6 G902V6 SOLUBLE SECRETED
ENDOPEPTIDASE DELTA. [1] ;contains PTR5.D2 PTR5 repetitive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="embryo"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: embryo, pluripotent cell line; Vector:
pCMY-SPORT6: Site_1: Not1; Site_2: Sal1; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                    Site_1:
                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library
Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                         /clone_lib="Stratagene mouse testis (#937308)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 704;
                                                                                                                                                                                                                                          Length 388;
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197 c 217 g 155 t
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                                          /tissue_type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.4; DB 12;
Pred. No. 3.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                      Score 18.4; DB 9;
Pred. No. 2.4e+02;
; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="IMAGE:4176045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib-"NCI_CGAP_Emb2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               info@image.llnl.gov
Seg primer: -400P from Gibco
High quallity sequence stop: 422.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              1 GAACGCCTCAGAGAAGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG153322.1 GI:12665352
                         /sex="males"
                                                                                                                                                                                                                                    th 92.0%;
Similarity 95.0%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.0%;
ilarity 95.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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Unpublished (1997
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                    Query Match
Best Local 3
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ORIGIN
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ORIGIN
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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BG153322
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Library D Homo
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RPCI-23-94H20.TJ RPCI-23 Mus musculus genomic clone RPCI-23-94H20,
                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="Plate=3236 Col=14 Row=I"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                               Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                            ANZUNDI/
HS_3236_A2_E07_T7 CIT Approved Human Genomic Sperm Library E sapiens genomic clone Plate=3236 Col=14 Row=1, DNA sequence. AQ209617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 Queen Anne Avenue North, Seattle, WA 98109, Tel: (206) 616-5618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.4; DB 17;
Pred. No. 8.3e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 516.
Location/Qualifiers
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Mammalla; Eutheria; Primates;
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355 GAATGCCTCAGAGAAGCCTG 374
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High quality sequence stop: 6
Location/Qualifiers
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Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:14229049
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                                                                                                                                                                                                                                                                                                                                      87.0%;
ilarity 94.7%;
Conservative
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                                                                                                                                                                                                                                                                                 242
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ORIGIN
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BG847865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 30-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                   library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 94 row: H. column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kidney and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 944)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602352942F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4450906 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
BcoRI; Site_2: EcoRI; Female C57BL/G4 mouse kidney and,
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
                                                                                                                                                                           Email: szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Lissue Procurement: ATCC
CDNA Library Preparation: Life Technologies. Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 574;
                                                                                                                        USA
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                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-94H20.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.4; DB 17;
Pred. No. 8.8e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'clone="RPCI-23-94H20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                            strain="C57BL/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 AACTCCTCAGAGAGGCTG 334
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94.7%;
                                                              Contact: Shaying Zhao
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BG121418
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TITLE
JOURNAL
COMMENT
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COMMENT
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Matches
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BG121418
LOCUS
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KEYWORDS
SOURCE
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/note-"Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAPP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
POLYA mRNA was purified from each sample, pooled and cDNA
synthesized The CDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRN (5') and XhoI (3') sites
pBluescript II SY- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage: The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
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Lambda 2ap II
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                                                                                                                                                                                                                    /note-"Organ: liver; Vector: pcMv-SPORT6; Site_1: Not1; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full:length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales, Chlamydomonadaceae, Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Chases 1 to 2091)
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardtil Genome: A Model,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.4; DB 12; Length 944;
Pred. No. 1.1e+03;
0; Mismatches 1; Indels 0
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                               /db_xref="taxon:9606"
/clone="ImAGE:4450906"
/clone=b=NIH_MGC_90"
/tissue_type="adenocarcinoma, cell
/lab_host="DH10B (phage-resistant)
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/organism="Homo sapiens"
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el: +55-11-2704922
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                                                                          Homo sapiens
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Matches 18; Conserv
                      BG992210.1
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BQ375929/c
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COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                   Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            normalized bovine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
43 c 67 g 34 t
                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -min
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                                      Length 2091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                AW445429 182 bp mRNA linear 81587 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
                                                                     Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
                                      DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.8; DB 10;
Pred. No. 9.5e+02;
); Mismatches 2;
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                                  Score 17.4; DB 12
Pred. No. 1.7e+03;
                                                                     Mismatches
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/tissue_type="pooled"
/lab_host="DH10B"
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Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                    342 GAACGCCACAGAGAAGCCT 360
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                                                                                                   1 GAACGCCTCAGAGAGCCT 19
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0
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ilarity 94.7%;
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90.0%;
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Best Local S:
Matches 18;
                                  Query Match
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Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
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mRNA sequence..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC4&t2=RC4-HT1256-
020201-011-f05&t3=2001-02-02&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                    1 (bases 1 to 227)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costar,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 252)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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IL5-TN0008-010800-123-g09 TN0008 Homo sapiens CDNA,
BQ375929
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Pred. No. 1.1e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: 35 High quality sequence stop: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'dev_stage="Adult
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GI:14396280
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Sequence Tagged Connector
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BG382418.1
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Best Local S
                                                                                                               source
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ACCESSION
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ORIGIN
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                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: testis_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; Site_2: SmaI; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ100155 27-AUG-1998 HS_3049_B2_D07_MR CIT Approved Human Genomic Sperm Library D. Homo saplens genomic clone Plate=3049 Col=14 Row=H, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                         This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-TN0008-010800-123-g09&t3=2000-08-01&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (ases 1 to 293)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
  Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                      expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                 Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                             U.S.A. 97 (7), 3491-3496 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen anne Avenue North, Seattle, WA 98109, 1
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.8; DB 14;
Pred. No. 1.1e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 21. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone_lib="TN0008"
                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'dev_stage="Adult
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                                                                                                             Natl. Acad. Sci.
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larity 90.0%;
Conservative
                                                                                        sequence tags
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nes 18; Conserv
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DEFINITION
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ORGANISM
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ORIGIN
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MEDLINE
COMMENT
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MEDLINE
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                                                                 TITLE
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Casas, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                                                                                                                    /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3049 Col=14 Row=H"
/clone_lib="CIT Approved Human Genomic Sperm Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG382418 365 bp mRNA linear 298310 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                 Score 16.8; DB 17;
Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Plate: 3049 row: H column: 14
Class: BAC ends
High quality sequence stop: 293.
Location/Qualifiers
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/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: 4 row: D column: 1
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
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PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                   84.0%;
90.0%;
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Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 402 762 4366.
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Email: smith@email.marc.usda.gov
Sindle pass sequencing. Bases called and trimmed with phred
v0.980904 e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from day 20 and day 40
                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4830
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                 Plate: 37 row: H column: 7
Seq primer: ATTTAGGTGACACTATAG
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9913"
/clone_lib="MARC 4BOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
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                                                                                         Contact: Smith TPL
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18; Conserv
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Job time : 1019.1 secs
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Smith,T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Grosse, White, J. Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.E., Lapteraid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was oligo dr primed from 5ug of poly A+ RNA from neurula. EcoRr.NotI cut cDNA was then ligated into pcS107 with EcoRI at the 5' end and NotI at the 3' end."

1. 108 c 116 g 81 t
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                             Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2002 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu073n20.plcsP6
Sequencing primer: PICSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
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/lab_host="Escherichia coll DH10B"
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Pred. No. 1.4e+03;
0; Mismatches 2;
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/clone="TNeu073n20"
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                                                                                                                                                                                                                                          AL775847.1 GI:21561551
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90.0%;
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Silurana tropicalis
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Matches 18; Conservative
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                                                                                                                                                                                                mRNA sequence.
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Length 384; Indels

Score 16.8; DB 10; Pred. No. 1.4e+03; 0; Mismatches 2;

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	July 8, 2003, 00:45:53; Search time 220.098 Seconds (Without alignments) 2644.537 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-647-780A-16 20 1 atgaccagaactccagrog 20
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 seqs, 14551402878 residues
rotal number of	Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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base : Ge	.i	 %	4:	5:	9	7:	 80	:6	10:	. 11:	12:	13:	. 14:	. 15:	16:	17:	18:	19:	20:	21:	22:	23:	24:	25:	26:	27:	28:	29:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 Similarity 100.0%;
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Boute, J., Burset, C., Burset, C., Burset, C., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burket, C., Burset, C., Brown, M., Bryant, N.P., Buhay, C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chon, Z., Chowdhry, J., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Dann, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.Y., Delgado, O., Denn, A.L., Ding, Y., Dubin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gall, R., Garza, N., Gall, M., Havlak, P., Hamel, C., Harris, C., Harris, K., Mart, M., Havlak, P., Hame, J., Jackson, E., Jackson, E., Jackson, B., Jia, Y., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Leal, B., Lewis, L.C., Katson, E., Katsoni, E., Katsoni, E., Katsoni, E., Garsh, J., Leal, B., Lewis, L.C., Fill, R., Kovar, C., Fill, R., Katsoni, E., Katsoni, E., Leal, B., Lewis, L.C., Fill, R., Kovar, C., Fill, R., Katsoni, E., Leal, B., Lewis, L.C., Fill, R., Fill, R., Kovar, C., Fill, R., Katsoni, E., Leal, B., Lewis, L.C., Fill, R., Katsoni, E., Leal, B., Lewis, L.C., Fill, R., Katsoni, E., Katsoni, E., Katsoni, E., Katsoni, E., Katsoni, E., Leal, B., Lewis, L.C., Fill, R., Katsoni, E., Katsoni, E., Katsoni, E., Katsoni, E., Katsoni, E., Katsoni, E., Leal, B., Lewis, L.C., Fill, R., Katsoni, E., Katsoni, E., Katsoni, E., Katsoni, E., Leal, B., Lewis, L.C., Fill, R., Katsoni, E., 
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DNA linear HTG 20-DEC-2001
*** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Shooshtari, N.,
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liams, G., Williamson, A., Wleczyk, R., Wooden, S.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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uyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scott, G., Shen, H
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Rattus norvegicus clone CH230-516,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sson, I., Sodergren, E., Sonaike, T
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                                          Consensus quality: 152255 bases at least 040
Consensus quality: 158448 bases at least 030
Consensus quality: 1646461 bases at least 020
Estimated insert size: 155965; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; agarose-fp estimation
Quality coverage: 2.2x in 020 bases; sum-of-contigs estimation
                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
             Assembly program: Phrap; version 0.990329First call to
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PAT 08-JUN-2001

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SRHIIYIDQPTLGMPSREYYFNGGSNRKVREAYLQFMVSVATLLREDANLPRDSCLVQ
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LTHEQLFFINYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCAR
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                                                                                                                                                              linear PAT 08-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MGKSEGPVGMVESAGRAGQKRPGFLEGGLLLLLLLLVTAALVALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVKIKLLPDEEVVVYGIPYLQNLENIIDTYSARTIQNYLVWRLVLDRIGSLSQRFKDT
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                                                                                                                                                                                                                                                                       Homo saplens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2262)

Deleersnijder,W., Wiegers,R. and Weske,M.

Human enzymes of the metalloprotease family

Patent: WO 0136610-A 5 25-MAY-2001;

Solvay Pharmaceuticals B.V. (NL)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Deleersnijder, W., Wiegers, R. and Weske, M.
Human enzymes of the metalloprotease family
Patent: WO 0136610-A 3 25-MAY-2001;
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Pred. No. 30;
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 Mismatches
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                                                                                                                                                          Sequence 5 from Patent W00136610.
AX146980
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:9606"
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                                                         1 ATGACCAGAACTCCAGCCGG 20
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Best Local Similarity 95.0%
Matches 19; Conservative
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   19; Conservative
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AX146978
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AX146980
LOCUS
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QLFFINYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVLGSLQNLAAFADTFHCARGTPM
                                                                                                                                                                                                                                                                                                                                                                                                          translation="CTTPGCVIAAARILQNMDPTTEPCDDFYQFACGGWLRRHVIPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSLONLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFFSK
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                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2076)

Deleersnijder,W., Wiegers,R. and Weske,M.

Human enzymes of the metalloprotease family
Patent: WO 0136610-A 1 25-MAY-2001;

Solvay Pharmaceuticals B.V. (NL)

Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 30;
0; Mismatches
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Patent: WO 0183782-A 28 08-NOV-2001;
Sugen, Inc. (US)
Location/Qualifiers
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Pred. No. 30;
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/db_xref="GI:14346248"
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/db_xref="taxon:9606"
Sequence 1 from Patent W00136610.
AX146976
AX146976.1 GI:14346247
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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llarity 95.0%;
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AX319864
LOCUS:
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Gaps

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AF157106 26-NOV-1999 MARNA linear ROD 25-NOV-1999 Mus musculus soluble secreted endopeptidase delta mRNA, alternatively spliced product, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
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                                                                                 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (asses 1 to 2583)
Shirotan1.K., Tsubuki,S., Iwata,N., Takaki,Y., Harigaya,W.,
                                                                                                                                      Advicani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T., Iwatsubo, T. and Saido, T.C.
Iwatsubo, T. and Saido, T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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I. and Matsuo, M.
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protein_id="AAG18446.1"
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/note="endopeptidase"
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Shirotani, K. and Saido, T.C.
Direct Submission
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      GI:10505359
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1 Similarity 95.0%;
19; Conservative
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Ikeda, K., Emoto, N., R
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RTIONYLVWRLVLDRIGSLSORFKDTRVNYRKALFGTMVEEVRWRECVGYVNSNMENA
                                                                                                                                                                                                                                                                                                                                                                                                                      NFDKNGNMMDWWSNFSTQHFREQSECMIYQYGNYSWDLADEQNVNGFNTLGENIADNG
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                                                                                                                                                                                                                                                                                QLALMNSQFNRRVLIDLFIWNDDQNSSRHIIYIDQPTLGMPSREYYFNGGSNRKVRE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                    /translation="MGKSEGPVGMVESAGRAGOKRPGFLE
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Pred. No. 30;
0; Mismatches 1;
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                                                                                                                     /note="unnamed protein product"
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Patent: WO 0226958-A 3 04 APR-2002;
MILENNIUM PHARMACETICALS, INC. (US)
Location/Qualiflers
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Pred. No. 30;
                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                             'protein_id="CAC41160.1"
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/db_xref="taxon:9606"
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AF302076.
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                                                                                                                                                                                                                                                                                                                                                                                         ranslation="MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIVTLGVFYSIALRD
                                                                                                                                                                                                                                                                                                note="SEP(delta); metalloprotease; alternatively spliced"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELN
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VVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGT
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                  the soluble secreted form of which
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                    Submitted (08-JUN-1999) International Center for Medical Resear
Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
                                                                                                                                                                                                                                                                                                                                    product="soluble secreted endopeptidase delta"
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Jagerschmidt, A., Agnel, M. and Culouscou, J.M.
Three neprilysin-like membrane metallopeptidases
Patent: EP 1069188-A 3 17 JAN-2001;
                                  hydrolyzes a variety of vasoactive peptides
J. Biol. Chem. 274 (45), 32469-32477 (1999)
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Pred. No. 31;
0; Mismatches
                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                     protein_id="AAF13153:1"
db_xref="G1:6467401"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/protein_id="CAC39975.1"
                                                                                                   2 (bases 1 to 2601)
Ikeda,K., Emoto,N. and Matsuo,M.
Direct Submission
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Similarity 95.0%;
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BYDVQYLELETOLARATVPORERHDYTALYHRWGEBELGSGPGELGFDWTLEFQTVLS
SVKIKLLPDEEVVYGATPYLONLENIIDTYSARTIONYLWRIVLDRIGSLSOFFKDT
RVNYRRALFGTMVEEYRWRECVGYWSNMENNYGSLYYREAPFGDSKSMYRELIDKVR
TVFVETLDELGWMDDESKKRAQEKAMSIREOIGHPYILETWRRLDEEYSNLNFSED
FFENSLQNIKVGAQRELRKREKVDFWDLMIIGAAVNAFYSPNRNQIVFPAGILOPP
FFENSLQNIKVGAQRELRKREKVDFWDNIIGAAVNAFYSPNRNQIVFPAGILOPP
FYSKEDPQALNFGGIGWIGHBITHGFDDNGRNFDKNGNMMWMSSTGHPREQSEC
MIXQYGNYSWDLADEONVNGFNTLGENIADNGGVROMMWWSBSTGHPREQSEC
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GTPMHPKERCRVW"
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RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
I PETNSRY SIFDVLRDELEVILKAVLENSTAKDRPAVEKARTLYRSCMNQSVIEKRGS
                           QPLLDILEVVGGWPVAMDRWNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNS
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Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Tsubuki, S., Kiyama, H., Iwata, H., Tomita, T.; Iwatsubo, T. and Saido, T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
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protein_id="AAG18447.1"
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Best Local Similarity 95.0%;
Matches 19; Conservative
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Mus musculus
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AX033274 2676 bp
Sequence 14 from Patent WO0047750.
                                             AX033274.1 GI:10280089
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FSARHFQQGSQCMIYQYGNESWELADNONVNGFSTLGENIADNGGVRQAYKAYLRWLA
DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPFFAVQSIKTDVHSPLKYRVLGSLQN
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FADTFHCARGTPMHPKERCRVM"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2663)
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/db_xref="taxon:9606"
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Sequence 5 from Patent EP1069188.
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ilarity 95.0%;
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RESULT 14 AX033274

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LKWMAEGGKDQQLPGLDLTHEQLFFINYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVL
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1 (bases 1 to 2676)

Boileau, G. and Desgroseillers, L.

Boileau, G. and Desgroseillers, L.

Patent: WO 0047750-A 1 17-Au neprillysin family
Patent: WO 0047750-A 1 17-Au 0067750-2000,

BOILEAU GUY (CA); DESGROSEILLERS LUC (CA); UNIVERSTIE DE MONTRE.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Shirotani,K., Tsubuki,S., Iwata,N., Takaki,Y., Harigaya,W.,
Maruyama,K., Kiryu-Seo,S., Kiyama,H., Iwata,H., Tomita,T.,
Iwatsubo,T. and Saido,T.C.
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J. Biol. Chem. 276 (24), 21895-21901 (2001)
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nilarity 95.0%; Pred. No..31; Conservative 0; Mismatches
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/db_xref="G1:10280090"
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Shirotani, K. and Saido, T.C.
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'translation="MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIALRD
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DILRDELEVIILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKMVG
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GVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDV
HSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW"
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SRVLGLKGFNWTLFIQNVLSSVEVELFPDEEVV VYGIPYLENLEDIIDSYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPI
Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Institute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
351-0198, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELET
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/protein_id="AAG18448.1"
/db_xref="GI:10505364"

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    organism="Mus musculus"
    db_xref="taxon:10090"

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Ouery Match 92.0%; Score 18.4; DB 10; Length 2694; Best Local Similarity 95.0%; Pred. No. 31; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps

g

Search completed: July 8, 2003, 03:34:59 Job time : 222.098 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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OM nucleic - nucleic search, using sw model

8, 2003, 00:43:28; Search time 125.659 Seconds July Run on:

(without alignments) 358.431 Million cell updates/sec

US-09-647-780A-16 20 1 atgaccagaactccagccgg 20 Perfect score: Sequence:

Scoring table:

IDENTITY_NUC Gapox 1.0

Searched:

4370478 Total number of hits satisfying chosen parameters: 2185239 seqs, 1125999159 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_101002 Database :

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Rat membrane metal	Rat membrane metal	Nucleotide segment	Human metalloprote	Nioleotide segment	Soluble secreted o	Human protesse DR	Ninchestide segience	Human SEP endopent
ID	AAZ28822	AAZ28810	AAF89737	AAS97186	AAF89739	AAD28130	AAD30580	AAF89738	ABN84280
DB DB	20	20	22	24	22	24	24	22	24
Query Match Length DB ID	20	2765	2076	2232	2262	2286	2318	2340	2580
Query	100.0	100.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0
Score	20	20	18.4	18.4	18.4	18.4	18.4	18.4	18.4
Result No.	Н	7	e	4	'n	•	. 7	8	თ

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n neprilysin-l		a	neprilys			encoding	encoding	SEP CDNA	ori	cell	foet		pone m		foeta	brain e	pone m	#8518	депоше			N. magadaii bacter	Mycobacterium tube	Mycobacterium tube	Human vitronectin	VN derived insulin	n biallelic po	biallelic	bone marro	n genome-deriv		Arabidopsis thalia		n genome-deriv	
Human	Human	CDNA	Human	Human	Human	CDNA	CDNA	Human	H.			Human	Human	Probe	Human	Human	Human	Probe	Human	Human	Prop	N. H	Mycc	Myce	Humaı	VN Q	Human	Human	Human	Human	Human	Arab	Humai	Human	DNA
																					•					5.4									
AAF59660	AAF59661	AAA63764	AAF59659	ABN84279	AAD28544	AAA63763	ABK48251	AAD28547	AAV24738	AAV24986	ABA59487	AAK07758	AAK33626	AAI39348	ABA59960	AAK08231	AAK34109	AAI39832	ABS08878	AAT26034	AAS59660	AAF61282	AA199683	AA199682	AAQ26040	AAQ23650	AAX12937	AAX11733	AAK46527	ABS20893	ABA12943	ABL94011	59	ABS08480	AAS76146
22	22	21	22	24	24	21	24	24	18	18	22	22	22	22	22	22	22	22	24	16	23	22			13	13	13	13	22	24	22	24	22		23
1 2636	2663	2676	2714	2893	2893	2925	2953	2975	339	342	517	517	517	517	509	509	509	509	509	265	4364	10198	4403765	4411529	162	162	251	251	300	300	397	446	456	456	624
92.0	92.0	92.0	٠.	٠.	٠.	٦.		•	84.0	84.0	84.0	84.0	84.0	84.0	82.0	82.0	82.0	82.0	82.0	79.0	79.0	9.	6	٥.	7	•	•	٠	٠	•	٠	77.0	77.0	77.0	77.0
18.4	18.4	18.4				18.4	18.4	18.4	ė	Ğ.		ė.	٠.	16.8	16.4	16.4	16.4	16.4	16.4	15.8	15.8	15.8	15.8	15.8	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4
10	Ξ	12	13	14.	15	16	17	18	19	50	21	22	23	24	52	56	27	58	53	30	31	32	33	34	35	36	37	38	6	40	41	42	43	. 44	45
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## ALIGNMENTS

AAZ28822 standard; DNA; 20 BP RESULT 1 AAZ28822

AAZ28822;

(first entry) 01-FEB-2000

Rat membrane metalloprotease NEPII gene probe #12.

Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; ss; neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; probe; hybridsation. 

Synthetic. Rattus rattus

FR2777291-A1.

15-0CT-1999.

98FR-0004389. 08-APR-1998;

(INRM ) INSERM INST NAT SANTE & RECH MEDICALE. 98FR-0004389. 08-APR-1998;

Bonhomme MC, Facchinetti P; Gros C, Haret C, Ouimet T, G Schwartz JC;

WPI; 1999-593429/51.

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WO200136610-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                            AAF89737;
                                                                                 Query Match
                                                                                                          Matches
                                                                                                                                                                                            RESULT 3
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                                                                                            membrane metalloprotease designated neprilysine II (NEPII) gene (AAZ28810) NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and itssues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic- hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the gene for the rat membrane metalloprotease designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to edect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds.
                                                                                  the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardlovascular disease
           involved in proteolysis of
to screen for inhibitors,
                                                                                                                                                                                                                                                                       ;
0
           New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardiovascular disease
                                                                                                                                                                                                                                            Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonhomme MC, Facchinetti P;
                                                                                  Sequences AAZ28811-Z28827 represent probes for detecting
                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                            Score 20; DB 20;
Pred. No. 2.4;
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                                                                                                                                                                                                                     Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat membrane metalloprotease NEPII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 12-16; 29pp; French.
                                                                                                                                                                                                                                                                                                         1 ATGACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                              1 ATGACCAGAACTCCAGCCGG 20
                                                          Claim 3; Page 23; 29pp; French.
                                                                                                                                                                                                                                                                                                                                                                                 AAZ28810 standard; cDNA; 2765
                                                                                                                                                                                                                                           Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haret C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98FR-0004389.
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-593429/51.
P-PSDB; AAY44177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus rattus
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Schwartz JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-0CT-1999
                                                                                                                                                                                                disorders
                                                                                                                                                                                                                                                                                                                                                                                                          AAZ28810;
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AAZ28810
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Whetalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;
a norexia; bulimia; asthma; parkinson's disease; acute heart failure;
whypotension; urinary retention; osteoporosis;
whypotension; urinary retention; osteoporosis;
whypotension; myocardial infarction; stroke; ulcer; altery;
whencological disorder; autism; multiple sclerosis; Alzheimer's disease;
whencological disorder; sieep disorder; epilepsy; kidney disease;
whencological disease; sleep disorder; epilepsy; kidney disease;
whencological hemorrhage; cerebral isorder; epilepsy; kidney disease;
whencological hemorrhage; cerebral isorder; epilepsy; kidney disease;
whetheral vascular disease; Raynaud's disease; motility disorder;
peripheral vascular disease; Raynaud's disease; motility disorder;
whencological motive production in disorder; astric emptying; gastroparesis; diarrhoea;
whilm manton; chemotherapy induced injury; tumour invasion;
whencological retardation; dyskinesia; Huntington's disease;
where mental retardation; dyskinesia; Huntington's disease;
disorders related to peptidergic signalling in which NEPII in involved e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine disorders.
                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 20; Length 2765; 100.0%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of a human metalloprotease enzyme IGS5.
                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                          Sequence 2765 BP; 684 A; 735 C; 787 G; 559 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weske M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             de la Tourette's syndrome; ss.
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1..2076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      813 ATGACCAGAACTCCAGCCGG 832
                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGACCAGAACTCCAGCCGG 20
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                                                                                                                                                                                                                                                                                                       1 Similarity 100.0%;
20; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF89737 standard; DNA; 2076
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19-NOV-1999; 99NL-1013616.
31-MAY-2000; 2000EP-0201937.
31-MAX-2000; 2000NL-1015356.
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                                                                                                                                                                                                                                                                                                               Local Similarity
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ids5. Ids5 polynucleotides and polypeptides are useful for treating infections; pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoprosis, angina pectoris, myocardial infarction, sstroke, ulcers, allergias, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autilism, multiple sclerosis, alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis, cerebrovasospasm, subarachnoid hemorrhage, cerebral isochemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney diseases, gastrointestinal disorders, motility disorders and conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; protease; PCR primer; cytostatic; immunomodulator; cardiant; vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic; antimiflammatory; aspartyl protease; cysteine protease; metalloprofease; serine protease; cancer; haematopoletic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardlovascular disease; neuronal disease;
                                                                                                                                                                                                                                  of delayed gastric emptying, post-operative or diabetto gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sapsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
      enzyme designated
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cognition disorder; hypotension; hypertension; psychotic d dyskinesia; metabolic disorder; inflammatory disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                          Sequence 2076 BP; 493 A; 578 C; 636 G; 369 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human metalloprotease partial DNA sequence #15.
                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.4; DB
Pred. No. 21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS97186 standard; cDNA; 2232 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                 92.0%;
95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plowman GD, Whyte D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
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                                                                                                      S (which modulates procease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoietic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune related diseases and disorders, cardiovascular disease, brain or neuronal associated diseases. Cet. central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or procease coding sequences and primers of the invention.

    may be used to
ty. Administering

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus;
severe mental retardation; dyskinesia; Huntington's disease;
silles de la Tourette's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subarachnoid hemorrhage; cerebral ischemia; cerebral infarction; peripheral vascular disease; Raynaud's disease; motility disorder; gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metalloprotease; IGSS; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; unimary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple sclerosis; Alzheimer's disease. cardiovascular disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of a human metalloprotease enzyme IGS5
                                                                 polypeptide (I) and polynucleotide (II) encoding (I). (I) screen for substances (S) that may modulate its activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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/product=."metalloprotease enzyme IGS5"
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2232 BP; 512 A; 620 C; 705 G; 395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 92.0%; Score 18.4; DB 24;
Best Local Similarity 95.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 1;
                                            to an isolated, enriched,
Claim 30; Figure 1R-S; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      614 ACGACCAGAACTCCAGCCGG 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF89739 standard; DNA; 2262 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99NL-1013616.
2000EP-0201937.
2000NL-1015356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-0203862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                          The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200136610-A1
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31-MAY-2000;
31-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF89739;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF89739
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    8 X C C C C C C C C C C C C C C X X
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Phillips SC;

Wayman CP,

Walsh RT, Wayman CP,

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The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male arectile dysfunction (MED) or female sexual dysfunction in particular (e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such as premature ejaculation, anorgammia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is SEP consensus DNA sequence found in human, mouse and rat.
                                                                                                                            An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful.for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as female sexual arousal disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
                                                                                                                                                                                                                     Disclosure, Fig 6; 167pp; English
                                                                 Stacey P,
                                                                                                 WPI; 2002-155042/20
              (PFIZ ) PFIZER LTD.
(PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200208396-AŹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                 Harrow ID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD30580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
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 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a human metalloprotease enzyme designated 1GS5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes; obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis, Alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                         infarction, peripheral vascular disease, Raymoud's disease, kidney diseases, gastrointestainal disorders, motility disorders and conditions of delayed gastrio emptying, post-operative or diabetic gastroperations diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                               ischemia, cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme; gynaecological; antisense-therapy; male erectile dysfunction; MED; female sexual dysfunction; FSD; female sexual arousal disorder; FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vasotropic; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                     cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 2262;
                                                                                                                New IGS5 polypeptides useful for treating infections, pain, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2262 BP; 520 A; 628 C; 716 G; 398 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                             cerebrovasospasm, subarachnoid hemorrhage, cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soluble secreted endopeptidase (SEP) consensus DNA.
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/note= "Encodes catalytic domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.4;
bred No. 21;
                                   Weske M;
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1664..2286
                                                                                                                                                                                     Claim 11; Page 8-9; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641 ACGACCAGAACTCCAGCCGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD28130 standard; DNA; 2286 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 92.0%;
Local Similarity 95.0%;
les 19; Conservative
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                                 Wiegers
(SOLV ) SOLVAY PHARM
                                                                 2001-343815/36.
                                 Deleersnijder W,
                                                                                   P-PSDB; AAB83842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                        anaemia; asthma; atherosclerosis; hypertension; myocardial infarction; hepatitis; cancer; psorlasis; cushing's syndrome; hypothyroidism; eczema; epilepsy; Alzheimer's disease; Huntington's disease; Parkinson's disease; pick's disease; infertility; vitiligo; drug screening; gene therapy; ss.
                                       Gaps
                                     ö
   Length 2286;
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mature PRTS-13 protein'
   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
   DB
11arity 92.0%; Score 18.4; in 11arity 95.0%; Pred. No. 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Human PRTS-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
338..1651
                                                                                                  1 ATGACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                               AAD30580 standard; cDNA; 2318
                                                                                                                                                                                                                                                                                                                             Human protease, PRTS-13 cDNA.
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428..1648
/*tag= c
/product= '
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cardiovascular disease; arteriosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated human protease polypeptide (PRTS).

PRTS protein and DNA are useful for diagnosing, treating and preventing gastrointestinal disorders (gastriits, cirrhosis, crohn's disease).

Cautoimmune/Inflammatory disorders (AIDS, allergy, rheumatoid arthritis, anaemia, asthma), cardiovascular disorder (atherosclerosis, hypertension, myocardial infarction), cell proliferative disorders (hepatitis, cancer, psoriasis), developmental disorders (Cushing's syndrome, hypothyroidism), epithelial disorder (vitiligo, Reloid, eczema), neurological disorders (epithelial disorder (vitiligo, Reloid, eczema), neurological disorders (epithelisy, Albehmer's disease, Pick's disease, Huntington's disease, Parkinson's disease, and reproductive disorders (infertility). PRTS protein is useful in a number of drug screening techniques and to an insulate the proteome of a tissue or cell type. PRTS DNA is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy and in microarrays curing a libration of the patients to detect altered PKIN
                                                                                                                                                                                                                                                                                                                              New human protease polypeptide, useful in diagnosis, prevention and treatment of gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction, stroke; ulcer; allergy; benign prostatic hypertrophy; midrachie; psychotic disorder; neurological disorder; autism; multiple sclerosis; Alzheimer's disease; neurodegenerative disease; sleep disorder; epilepsy; kidney disease;
                                                                                                                                                                                                                                           Lee S, Todd
                                                                                                                                                                                     Khan Fa;
T Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                            Borowsky ML;
                                                                                                                                                                 Nguyen DB, Lee EA, Khr
'c'v JL, Ramkum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of a human metalloprotease enzyme IGS5
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                                                                                                                                                                                        Pribouley ...,
Yue H, Au-Young J, Griffin ...,
Thangavelu K, Ding L, Kearney L, Baughn Mk, ...
Sanjanwala MS, Yao MG, Burford N, Walia NK, Lal P, Sanjanwala MS, Yao MG, Burford N, Walia NK, Lal P, ...
Tang YT, Elliott VS, Azimzai Y, Lu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression. The present sequence is human PRTS-13 cDNA
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                                                                                                                                                                             Kallick DA, Nguy...
Kallick TA, Policky JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.4; DE Pred. No. 21; 0; Mismatches
                                                                                                                                                                         Hafalia AJA,
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 174-175; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gandhi AR, Hafali
Das D, Kallick DP
19 J, Griffin JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF89738 standard; DNA; 2340 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.0%;
17-JUL-2001; 2001WO-US22397
                                                2000US-221680P
2000US-223544P
                                                                               0000S-224717P
                                                                                             2000US-225988P
2000US-227568P
                                                                                                                                          (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                                                                                                  P-PSDB; AAE19176.
                                                                                                                                                                         Delegeane AM,
                                                                                                          23-AUG-2000;
                                21-JUL-2000;
                                                              04-AUG-2000;
11-AUG-2000;
                                                                                             6-AUG-2000:
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The present sequence encodes a human metalloprotease enzyme designated 1655. 1655 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, barkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angine pectoris, myocardial infarction, stroke, uleers, allergies, benign prostatic hypertrophy, migraine, sychotic and neurological disorders, autism, multiple sclerosis, laychotic and neurological disorders, autism, multiple sclerosis, alzahaner's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis, cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raymaud's disease, kidney diseases, gastrointestinal disorders, motility disorders and conditions of diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, anthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such
                    pertpheral vascular disease; Raynaud's disease; motility disorder; gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion; mimune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; ss.
                                                                                                                                                          diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 2340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New IGS5 polypeptides useful for treating infections, pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as Huntington's disease or Gilles de la Tourette's syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product- "metalloprotease enzyme IGS5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2340 BP; 539 A; 649 C; 739 G; 413 T; 0 other;
subarachnoid hemorrhage; cerebral ischemia; cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Pred. No. 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weske M;
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 6-7; 115pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN84280 standard; cDNA; 2580 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deleersnijder W, Wiegers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-NOV-1999; 99NL-1013616.
31-MAY-2000; 2000EP-0201937.
31-MAY-2000; 2000NL-1015356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000; 2000WO-EP11532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SOLV ) SOLVAY PHARM BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-343815/36.
P-PSDB; AAB83841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200136610-A1
                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .9-NOV-1999;
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Use of an inhibitor of neuropeptide Y in the preparation of medicament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a nucleotide sequence coding for human SEP, a soluble secreted endopeptidase, with an additional 5' vector partial sequence. The invention relates to the use of an inhibitor of NPY, or an inhibitor of NPY XI receptor, especially an inhibitor selective for an NPY or NPY XI receptor associated with male genitalia, in the preparation of a medicament for the erectile dysfunction (MED). The NPY inhibitor may be used with auxiliary active agent such as an SEP inhibitor. The invention provides a SEP assay that can be used to detect candidate inhibitors of SEP. In addition to treatment of MED, NPY inhibitors can also be used to treat abnormal drink and food intake disorders,
                                                                                              male sexual dysfunction; male erectile dysfunction; obesity;
anorexia; bulimia; vasotropic; anorectic; therapy; inhibitor; gene;
                                                                                                                                                                                                                                                                                             note- "the CDS does not include a stop codon"
                                                                                                                                                                                                                                                                                                                     /*tag= c
/note= "the 3' end of the sequence is missing
from Figure 8 of the specification"
                                                                               enzyme; human; neuropeptide Y1; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for the treatment or prevention of male erectile dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               such as obesity, bulimia, anorexia and metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2580 BP; 587 A; 741 C; 794 G; 458 T; 0 other;
                                                                                                                                                                                                         /*tag= a
/note= "5' partial vector sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wayman CP;
                                                     Human SEP endopeptidase coding sequence.
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 8; 179pp; English.
                                                                                                                                                                                                                                                                 product "SEP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Naylor AM, Van Der Graaf PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001GB-0008730.
2001GB-0009910.
2001GB-0011037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-0905846.
2001GB-0020679.
                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-IB02399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0895367
                          (first entry)
                                                                                                                                                                                                                                    58..2580
                                                                                                                                                                                                                                                                              partial
                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-547828/58.
                                                                                 SEP; endopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PFIZ ) PFIZER LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABB79521.
                                                                                                                                                                                                                                                                                                                                                                           WO200247670-A1
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUL-2001;
24-AUG-2001;
                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2001;
29-JUN-2001;
                                                                                                                                                                                            misc_feature
                          23-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2002
ABN84280;
                                                                                                                                                                                                                                       SOS
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Score 18.4; DB 24; Length 2580; Pred. No. 21; 0; Mismatches 1; Indels 0;

92.0%; 95.0%;

Conservative

Query Match Best Local Similarity Matches 19; Conserva

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The invention relates to the human SNEPa, SNEPb and SNEPC proteins, and the cDNAs encoding them. SNEPa, SNEPb and SNEPC are neprilysin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SNEP nucleotides may be used as hybridisation probes for cDNA and genomic DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa, SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues; as research reagents and material for the discovery of treatments and diagnostics for animal and human diseases; and for chromosome identification. The SNEP proteins may be used as immunogens to produce antibodies immunospensecific for SNEPa or SNEPb or SNEPc. Such antibodies are used to isolate or identify chones expressing the protein, or to purify the proteins by affinity chromatography.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      splice variant; alternative splicing; zinc endopeptidase family;
neuropeptide; peptide hormone; processing; metabolism; vaccine;
drug screening; renal insufficiency; hepatic disease; ischaemia; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuronal disease; pancreatic disease; prostatic disease; respiratory disease; gene therapy; nephrotropic; vasotropic; cerebroprotective; hypotensive; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug screening; renal insufficiency; hepatic disease; ischa
hypertension; cancer; inflammation; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human neprilysin-like membrane metallopeptidase SNEPb cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNEPb; neprilysin-like membrane metallopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Culouscou J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 30-33; 72pp; English.
                                                           968 ACGACCAGAACTCCAGCCGG 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular; hepatotropic; ss.
20
                                                                                                                                                                                                                                   AAF59660 standard; cDNA; 2636 BP.
1 ATGACCAGAACTCCAGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99EP-0401767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and hepatic ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-212582/22
P-PSDB; AAB60562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .5-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001.
                                                                                                                                                                                                                                                                                                          AAF59660;
                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                       AAF59660
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respiratory or hepatic diseases. they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnormal expression of SNEPa, SNEPb or SNEPc. The present sequence represents
                                                                                               cDNA encoding
  88888888
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Sequence 2636 BP; 601 A; 759 C; 813 G; 462 T; 1 other;

ö Length 2636; Indels DB 22; 1; Score 18.4; DB Pred. No. 21; 0; Mismatches ; 92.0%; Best Local Similarity 95.0 Matches 19; Conservative Query Match

1 ATGACCAGAACTCCAGCCGG 20

à ద

648 ACGACCAGAACTCCAGCCGG 667

AAF59661 standard; cDNA; 2663 BP

27-APR-2001 (first entry)

Human neprilysin-like membrane metallopeptidase SNEPc cDNA.

respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic; cerebroprotective; hypotensive; cytostatic; antiinflammatory; splice variant; alternative splicing; zinc endopeptidase family; neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia; pain; hypertension; cancer; inflammation; cardiovascular disease; Human; SNEPc; neprilysin-like membrane metallopeptidase; neuronal disease; pancreatic disease; prostatic disease; cardiovascular; hepatotropic; ss.

Homo sapiens

EP1069188-A1

17-JAN-2001.

99EP-0401767. 15-JUL-1999;

15-JUL-1999;

(SNFI ) SANOFI-SYNTHELABO

Jagerschmidt A, Agnel M,

Culouscou J;

WPI; 2001-212582/22

P-PSDB; AAB60563

New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal and hepatic ischemia

Claim 5; Page 35-38; 72pp; English.

The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SNEP nucleotides may be used as hybridisation probes for cDNA and genomic DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa, SNEPD or SNEPC; to isolate cDNA and genomic clones of SNEP homologues; as research reagents and material for the discovery of treatments and diagnostics for animal and human diseases; and for chromosome identification. The SNEP proteins may be used as immunogens to 

produce antibodies immunospecific for SNEPa, SNEPA or SNEPC. Such antibodies are used to identify clones expressing the protein, or to purify the proteins by affinity chromatography. SNEP proteins may also be used in screening for compounds which modulate SNEP proteins may also be used in screening for compounds which modulate SNEP endopertidase activity, and to assess enzymatic cleavage of small molecule substrates in cells, cell-free preparations, chemical libraries SNEP nucleotides, and SNEP proteins (as vaccine compositions), to treat acute and chronic renal insufficiency, renal and hepatic ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as respiratory or hepatic diseases, they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnormal expression of SNEPa, SNEPb or SNEPc. The present sequence represents CDNA encoding SNEPc. 

Sequence 2663 BP; 609 A; 769 C; 816 G; 468 T; 1 other;

Gaps ö Length 2663; Indels 92.0%; Score 18.4; DB 22; 95.0%; Pred. No. 21; ive 0; Mismatches 1; Conservative Local Similarity nes 19; Conserv Best Loca Matches

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RESULT 12 AAA63764

AAA63764 standard; cDNA; 2676 BP.

AAA63764;

(first entry) 04-DEC-2000

CDNA encoding neutral endopeptidase metallopeptidase-like enzyme

Neprilysin; neutral endopeptidase metallopeptidase-like enzyme; MBP-like enzyme; protein production; protein secretion; neurological disease; Alzheimer's disease; pain: psychiatric disorder; fertility; bone disease; abnormal phosphate metabolism; ss.

Homo sapiens

Location/Qualifiers

/*tag= a /product= "neutral endopeptidase metallopeptidase-like

40200047750-A2.

7-AUG-2000.

11-FEB-2000; 2000WO-CA00147.

11-FEB-1999;

UYMO-) UNIV MONTREAL. 

Desgroseillers L, Boileau G;

WPI; 2000-549148/50.

PSDB; AAB08131.

Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders

Disclosure; Fig 4; 59pp; English

The present sequence encodes a human neutral endopeptidase

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The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although
                                                                                      downstream from and in phase with the N-terminal region. The NL enzymes are have been localised to the brain, and may be useful in the treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders. NL enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; SNEPa; neprilysin-like membrane metallopeptidase; splice variant; alternative splicing; zinc endopeptidase family; neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia; pain; hypertension; cancer; inflammation; cardiovascular disease; neuronal disease; pancreatic disease; prostatic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal
               also describes NL-1 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimeric constructs containing the foreign protein
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                                                                                                                                                                                                                                                                                                      DB 21; Length 2676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    !uman neprilysin-like membrane metallopeptidase SNEPa cDNA
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                Sequence 2676 BP; 608 A; 771 C; 823 G; 474 T; 0 other;
                                                                                                                                                                                                                                                                                                    Score 18,4; Dl
Pred. No. 21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jagerschmidt A, Agnel M, Culouscou J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 25-28; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                               cardiovascular; hepatotropic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF59659 standard; cDNA; 2714 BP.
                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                               processing by the NL-3 enzyme.
                                                                                                                                                                                                                                                                                                    92.0%;
ilarity 95.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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P-PSDB; AAB60561.
                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 19; Conserv
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Matches
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the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SNEP morelectides may be used as hybridisation probes for CDNA and genomic DNA; to isolate full-length CDNAs and genomic clones encoding SNEPs, SNEP or SNEPc; to isolate CDNA and genomic clones of SNEP homologues; as research reagents and material for the discovery of treatments and diagnostics for animal and human diseases; and for chromosome identification. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPs, SNEP or SNEP or SNEP proteins and antibodies are used to identify clones expressing the protein, or to purify the proteins by affinity chromatography.
                                                                                                                                                                                                                                      SNEP endopeptidase activity, and to assess enzymatic cleavage of small molecule substrates in cells, cell-free preparations, chemical libraries and product mixtures. The SNEP proteins (as vaccine compositions), SNEP nucleotides, and SNEP activators or inhibitors may used to treat acute and chronic renal insufficiency, renal and hepatic ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as well as cardiovascular, neuronal, pancreatic, prostatic, renal,
                                                                                                                                                                                                                                                                                                                                                                    respiratory or hepatic diseases, they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       inother organ, or to diagnose or treat any disorder related to abnorm
expression of SNEPa, SNEPb or SNEPc. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         male sexual dysfunction; male erectile dysfunction; obesity;
anorexia; bulimia; vasotropic; anorectic; therapy; inhibitor; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2714;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2714 BP; 621 A; 780 C; 836 G; 476 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.4;
Pred. No. 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human SEP endopeptidase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
185..2524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           726 ACGACCAGAACTCCAGCCGG 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN84279 standard; cDNA; 2893 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.0%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-2001; 2001WO-IB02399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001GB-0008730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-0905846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001GB-0009910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001GB-0020679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.0
Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-2001
13-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04 - MAY - 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN84279
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Wayman CP, Wayman CP, Phillips SC;

Walsh RT,

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An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as female sexual arousal disorder.
                                                                                                                                                                                                                                                                                                               (e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such as premature ejaculation, anorgasmia, sexual pain (e.g. vaginismus) and hypoactive sexual desire disorder. The present sequence is human SEP
                                                                                                                                                                                                            The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD)
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2893 BP; 658 A; 854 C; 876 G; 505 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                903 ACGACCAGAACTCCAGCCGG 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGACCAGAACTCCAGCCGG 20
                                                                                                                                                                               Claim 1; Fig 1; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.0%;
ilarity 95.0%;
Conservative
     Harrow ID, Stacey P,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity
                                     WPI; 2002-155042/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: July
Job time: 129,659 secs
                                                        P-PSDB; AAE17779
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                                                                                                                 Use of an inhibitor of neuropeptide Y in the preparation of medicament for the treatment or prevention of male erectile dysfunction \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ne; gynaecological; antisense-therapy; male erectile dysfunctior
female sexual dysfunction; FSD; female sexual arousal disorder;
                                                                                                                                                                                                      The present sequence is a nucleotide sequence coding for human SEP, a soluble secreted endopeptidase. The invention relates to the use of an inhibitor of NPY, or an inhibitor of NPY il receptor, especially an inhibitor selective for an NPY or NPY Il receptor associated with male genitalia, in the preparation of a medicament for the treatment or prevention of male sexual dysfunction, may be used with an auxiliary active agent such as an SEP
                                                                                                                                                                                                                                                                                                                                                 bitor. The invention provides a SEP assay that can be used to ct candidate inhibitors of SEP. In addition to treatment of NPY inhibitors can also be used to treat abnormal drink and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.4; DB 24; Length 2893;
Pred. No. 21;
0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                      intake disorders, such as obesity, bulimia, anorexia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'SAD; premature ejaculation; anorgasmia; vaginismus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2893 BP; 658 A; 854 C; 876 G; 505 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Encodes catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human soluble secreted endopeptidase (SEP) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEP; endocrine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human SEP protein"
                                     Wayman CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
185..2524
                                                                                                                                                                        Disclosure; Fig 7; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            903 ACGACCAGAACTCCAGCCGG 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD28544 standard; cDNA; 2893 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted endopeptidase;
                                  Van Der Graaf PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.0%;
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1711..2893
/*tag- b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-2002. (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.0
Matches 19; Conservative
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                                                               WPI; 2002-547828/58
                                                                                                                                                                                                                                                                                                                                                                                                                      netabolic disorders.
(PFIZ ) PFIZER INC
                                                                                    P-PSDB; ABB79521
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                                Naylor AM,
                                                                                                                                                                                                                                                                                                                                              inhibitor
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                                                                                                                   Use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enzyme;
                                                                                                                                                                                                                                                                                                                                                                    detect
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14-JUL-2000; 2000GB-0017387

(PFIZ ) PFIZER LTD. (PFIZ ) PFIZER INC.

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Gaps

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DB 24; Length 2893; Indels

Score 18.4; Di Pred. No. 21; 0; Mismatches

8, 2003, 02:19:08

RESUUS-(; Se; Pa; G.

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Antonius
Sana, Theodore R.
Bazan, J. Fernando
Kastelein, Robert A.
VENTION: Human Receptor Proteins; Related Reagents and Methods
                                                                                                                                                                                                             Gaps
                                                                                                                                                                  Length 1862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                  Score 14.8; DB 4;
Pred. No. 2.2e+02;
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Timans, Jacqueline C.
Debets, Johannes Eduard Maria
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/173,151A FILING DATE: 14-OCT-1998 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/062,066 FILING DATE: 15-OCT-1997
TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US 60/078,008
12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MBER: US 60/081,883
15-APR-1998
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10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09173151A
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                                                                                                                                                                                                                                                 3 GACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                  74.0%;
88.9%;
                                                                                                                                                 Ouery Match
Best Local Similarity 88.5.
These 16; Conservative
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                           ; LENGTH: 1862
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-434-427-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 2.2e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                       ; DB 5; Length 540;
2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/999,723A
CURRENT FILING DATE: 1997-10-06
NUMBER OF SEC ID NOS: 2
SOFTWARE: PALENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GH-70262-D1
CURRENT APPLICATION NUMBER: US/09/434,427
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: US 08/999,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: UK 9626022.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08999723A Patent No. 6025180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09434427 Patent No. 6162630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 GACCAGAACTTCAGCCAG 345
                                                                                                  TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 523-3400
TELEFAX: (617) 523-6400
TELEFAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GACCAGAACTCCAGCCGG 20
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APPLICANT: POWELL, DAVID J.
APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: CHAPMAN, CONRAD G.
APPLICANT: EVANS, JOANNE R.
TITLE OF INVENTION: ASP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Powell, David J.
APPLICANT: Southan, Christopher
APPLICANT: Chapman, Conrad G.
                                          NAME: Resnick, David R. REGISTRATION NUMBER: 34235 REFERENCE/DOCKET NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                       Ouery Match 74.0%;
Best Local Similarity 88.9%;
Matches 16; Conservative
  FILING DATE: 10-JUN-1994
                                                                                                                                                                                                                              LENGTH: 540 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chapman, Conrad APPLICANT: Evans, Joanne R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ASP1 FILE REFERENCE: GH70262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRGANISM: Homo sapiens
US-08-999-723-1
                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                             PCT-US95-07541-17
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                Length 3271;
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                                                    Indels
                                                                                                                                                                                                                                                                                                                  Vertebrate Embryonic Pattern-Indue Proteins and Uses Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.8; DB 2;
Pred. No. 2.4e+02;
0; Mismatches 2;
                 Score 14.8; DB 4;
Pred, No. 2.3e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JMBER: US/08/356,060A
14-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US 08/176,427
30-DEC-1993
                                                                                                                                                                                                        Sequence 42, Application US/08356060A Patent No. 5844079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 42, Application US/084609000C Patent No. 6165747
                                                                                                             1761 TGCCCAGAACTCCAGCAG 1778
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                                                                                                                                                                                                                                                                                                                                                                                   E: LAHIVE & COCKFIELD 60 State Street
                                                                                       2 TGACCAGAACTCCAGCCG 19
                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Ingham, Phillip M.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Ciliford J.
TITLE OF INVENTION: Vertebrait
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID 00: 42:
SEQUENCE CHARACTERISTICS:
                     74.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 1 ATGACCAGAACTCCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3900 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
 Query Match
Best Local Similarity 88.5.
Local Similarity 18.5.
Local Similarity 18.5.
Local Similarity 18.5.
Local Similarity 18.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                       Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-08-460-900C-42/c
                                                                                                                                                                            RESULT 14
US-08-356-060A-42/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02109
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US-08-356-060A-42
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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APPLICANT: Robison, Keith E.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nuclease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILICA DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; DB 4; Length 2514;
2.3e+02;
                                                                                                                                                                          Score 14.8; DB 4; Length 2061; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                              Indels
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Pred. No. 2.3e+
0; Mismatches
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/770,170
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: aspartyl proteases US-09-280-116-32
                                                                                                                                                                                                                                                                                                                                                               Sequence 32, Application US/09280116A Patent No. 6331427
                                                                                                                                                                                                                                                                  1765 ATGACCAGTACTTCAGCC 1782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V: PAS Kinase
UTSD:0761
                                                                                                                                                                                                                                                1 ATGACCAGAACTCCAGCC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McKnight, Steven
Gardner, Kevin
Harper, Shannon
Rutter, Jared
Michnoff, Carolyn
                                                                                                                                                                          74.0%;
88.9%;
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GACCAGAACTCCAGCCGG
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9%
Matches 16; Conservative
                                                                                                                                                                     Query Match
Best Local Similarity 88.99
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amezcua, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (121)..(3135)
US-09-770-170-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                  1..2058
                                                                     MOLECULE TYPE: CDNA
                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FITLE OF INVENTION:
                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3271
                                                       TOPOLOGY:
                                                                                                                                          US-09-173-151A-3
                                                                                                                                                                                                                                                                                                                                                   JS-09-280-116-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 32
LENGTH: 2514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                         FEATURE
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Score 14.8; DB 4; Length 3900;
Pred. No. 2.4e+02;
0; Mismatches 2; Indels 0
                                                                                                  TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYZHEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,900C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
PRIOR APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
FILING DATE: 14-DEC-1994
                                                                                                                                         NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                               Bumcrot, David A.
Marti-Gorostiza, Elisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HWV-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
INFORMATION FOR SEO ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 3900 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1..3897
US-08-460-900C-42
                                                                                                                                                                                                                                              MA
USA
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                                                                                                                                                                                                                                                                                              02109
APPLICANT:
APPLICANT:
                                         APPLICANT:
APPLICANT:
                                                                                   APPLICANT:
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Search completed: July 8, 2003, 09:32:16 Job time: 41.6598 secs

1403 ATGAGCAGAACTCCGGCC 1386

1 ATGACCAGAACTCCAGCC 18

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Sequence 94, Sequence 44, Sequence 46, Sequence 2, Sequence 2, Sequence 1, Sequence 20, Sequence 26, Sequence 26, Sequence 26, Sequence 26, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 27, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Sequence 96, Se
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6-60-SD
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273.390 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                          Seconds
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                                                                                                                                                                                                                                                                                                                                               July 8, 2003, 19:09:54 ; Search time 115.512
                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1105431 seqs, 789497651 residues
                                                                                                                                                                                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 atgaccagaactccagccgg 20
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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20
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Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

## ALIGNMENTS

RESULT

/cgn2_6/ptodata/2/pubpna/U
 /cgn2_6/ptodata/2/pubpna/P

Published_Applications_NA

Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Naylor, Alasdair M. Van Der Graaf, Pieter Wayman, Christopher P

PLICATION NUMBER: US/10/017,273A ICATION NUMBER: US 60/265,358 NG DATE: 2001-01-31

ING DATE: 2001-01-31 LICATION NUMBER: GB 0030647.2 TMC DATE: 2000-12-15

ING DATE: 2001-08-24 LICATION NUMBER: US 09/905,846 ING DATE: 2001-07-13 LICATION NUMBER: US 60/291,722

2001-05-17

PatentIn version 3.1

ING DATE: 2001-04-06 LICATION NUMBER: GB 0120679.6

ICATION NUMBER: GB 0108730.3

Sequence 6997, Ap Sequence 1440, Ap Sequence 38, Appl

Seguence 21569, A

US-09-864-761-5193 US-09-918-995-21569

		du '/o** aciienbac	TO 08-08-383-802-4407	4 U.I	2.0/	7.01	י דע
Qy 1 ATGACCAGAACTCC		Sequence 30/1, Ap Sequence 22, Appl Sequence 11, Appl	10 US-09-880-10/-36/1 9 US-10-001-873-22 9 US-09-954-9878-11	5387	77.0	15.4	17
,at		Sequence 10, Appl	10 US-09-840-787-80	7	77.0	15.4	c 15
Query Match 92 Rest Local Similarity 95		Sequence 2681, Ap. Sequence 32818, A	9 US-09-918-995-2681 9 US-09-918-995-32818 9 US-10-169-646-15	461	77.0	15.4	13
CKGANISM: HOMO Sapiens US-10-017-273A-4		Sequence 776, App Sequence 14677, A	10 US-09-770-444-776 10 US-09-864-761-14677	446 456	77.0	15.4	c 10
TYPE: DNA		Sequence 7854, Ap	9 US-09-918-995-7854		77.0	15.4	00
; SEQ ID NO 4 : LENGTH: 2893		Sequence 195, App	9 US-10-171-311-195		80.0	15.4	7 0
; SOFTWARE: PatentIn versio		Sequence 12054, A	10 US-09-864-761-12054	203	82.0	16.4	ი დ ი
PRIOR FILING DATE: 2001-0		Sequence 5, Appli	10 US-09-905-846-5	2975	92.0	18.4	4° u
PRIOR APPLICATION NUMBER:		Sequence 5, Appli	9 US-10-017-273A-5	2975	92.0	18.4	7 6
PRIOR APPLICATION NUMBER:		Sequence 4, Appli	9 US-10-017-273A-4	2893	92.0	18.4	, <del></del> (
PRIOR FILING DATE: 2001-0 PRIOR APPLICATION NUMBER:		Description	B ID	Duery Match Length DB	<b>Ouery</b> Match	Score	Result No.
			SUMMARIES		de		,
FILING DATE: APPLICATION N	• • • •	tribution.	score greater than of equal to the total score distribution	y analys:	rived h	nd is de	Δασ
; PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-0 PRIOR APPLICATION NUMBER:		chance to have a	Pred. No. is the number of results predicted by chance to have a	number	is the	red. No.	<u>α</u> , ι
; CURRENT APPLICATION NUMBE ; CURRENT FILING DATE: 200		PUB.seq:*	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*	/cgn2_6/p1	13:	٠	
; TITLE OF INVENTION: ITEMAC; FILE REFERENCE: PC22013	2	PUB.seq:*	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.sed:	/cgn2_6/pi	11:		
, APPLICANT: Wayman, Chris		ONB.seq:*	:gn2_6/ptodata/2/pubpna/USU9_N≿W_FUB.seq: 'cqn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq	:gn2_6/ptc /cqn2_6/p1	9: 10:		
; APPLICANT: Naylor, Alasd		MB. seq: *	cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:	gn2_6/ptc	:::		
; GENERAL INFORMATION:		MB.seq:*	cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:	gn2_6/ptc	; ; ;		
; Publication No. US20030119		)MB.seq:* :OMB.seq:*	/cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:	gn2_6/ptc	∴		
US-10-017-273A-4		UB. seq: *	cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*	cgn2_6/ptc	3.5		

Gaps

Length 2893; Indels

Score 18.4; DB 9; Pred. No. 7.3;

92.0%;

Similarity 95.0 19; Conservative

)3 ACGACCAGAACTCCAGCCGG 922 1 ATGACCAGAACTCCAGCCGG 20

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PPLICANT: Hanzel, David K.
LOLOANT: Chen, Wenshenger
TILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FC
TILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LE REFERENCE: Aeomica-x-1
RRENT APPLICATION NUMBER: US/09/864,761
RRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/US01/00667
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PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIOR APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11840, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LICATION NUMBER: GB 24263.6
968 ACGACCAGAACTCCAGCCGG 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           968 ACGACCAGAACTCCAGCCGG 987
                                                                                                                                  Sequence 5, Application US/09905846 Patent No. US20020102707A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                           APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LING DATE: 2000-10-04
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                                                                                                                                                                                                     APPLICANT: Ian Dennis Harrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-846-5
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                            Sequence 1, Application US/09905846
Patent No. US20020102707A1,
GENERAL INFORMATION:
APPLICANT: Lan Dennis Harrow
APPLICANT: Peter Stacey
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
FILE REFERENCE: PCS10926APME
CURRENT APPLICATION NUMBER: US/09/905,846
CURRENT APPLICATION NUMBER: US/09/905,846
FILE REFERENCE: PCS10926APME
PRIOR APPLICATION NUMBER: 00/10-13
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 8
SOUTHARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Naylor, Alasdair M.
APPLICANT: Van Der Graaf, Pieter H
APPLICANT: Wayman, Christopher P.
TITLE OF INVENTION: Treatment of Male Sexual Dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.4; DB 10;
Pred. No. 7.3;
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CURRENT PELLING DATE: 2001-12-12
PRIOR PAPLICATION NUMBER: US 60/265,358
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: GB 0108730.3
PRIOR APPLICATION NUMBER: GB 0120679.6
PRIOR PELING DATE: 2001-04-06
PRIOR PELING DATE: 2001-04-06
PRIOR PELING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-06-24
PRIOR FILING DATE: 2001-06-3
PRIOR PELING DATE: 2001-06-3
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-05-17
PRIOR PELING DATE: 2001-05-17
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Pred. No. 7.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10017273A Publication No. US20030119714A1 GENERAL INFORMATION: APPLICANT: Pfizer Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.0%;
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SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-06-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-905-846-1
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Best Local Similarity
Matches 19; Conserv
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US-10-017-273A-5
         -09-905-846-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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0; Mismatches

Conservative

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Gaps
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Pred. No. 7.3;
1 ATGACCAGAACTCCAGCCGG 20
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DATE: 2001-01-30

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APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REPRENDE: MIL-035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 509;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0. OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                              Annomax Sequence Listing Engine vers. 1.1
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                                                                            PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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                /uso1/00668
                                                           APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                  PILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/234,687
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Kamatkar, Shubhangi
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PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2001-11-14
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                             NUMBER SOFTWARE: AnnounCSEQ ID NO 12054
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NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                             Annomax Sequence Listing Engine vers. 1.1
                                                         PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2010-01-30
PRIOR PLING DATE: 2010-01-30
PRIOR PLING DATE: 2010-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/234,687
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
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Pred. No. 5
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LELING DATE: 2000-10-04
LING DATE: 2000-09-27
LING DATE: 2000-09-27
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MION NUMBER: PCT/US01/00667
DATE: 2001-01-30
                       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
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PRIOR APPLICATION NUMBER: PCT/US01/00665
NUMBER: PCT/US01/00668
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PPDLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
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Patent No. US20020048763A1
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Best Local Similarity 90.0%;
Matches 18; Conservative
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Hanzel, David K.
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APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NOS: 49117
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Gaps
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                                                                                          Length 300;
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                                                                                                                                                                                                                                                                                                                                Sequence 7854, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2011-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/08/235,076
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
; OTHER INFORMATION: NT HIT: 9111426686, EVALUE 0.00e+00; OTHER INFORMATION: SWISSPROT HIT: P04004, EVALUE 7.00e-56 US-09-864-761-31210
                                                                                                                                         Indels
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                                                                                        Score 15.4; DB 10;
Pred. No. 2.5e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.4; DB 9;
Pred: No. 2.5e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(417)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-7854
                                                                                                                                                                                                          172 ACCAGAACTCCCGCCGG 188
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Haas, William David
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94.1%;
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Ledford, Brooke L.
                                                                                        Ouery Match
Best Local Similarity 94.1%;
Matches 16; Conservative
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Rameaka, Joshua G.
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Hamilton, Carol M
Price, Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garcia, Carlos A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: Hanzel, David K.
PPLICANT: Hanzel, David K.
PPLICANT: Chen, Wensheng
ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
ILE REFERENCE: Acomica-X-1
                                                                                            Gaps
                                              Length 2972;
                                                                                          Indels
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                                            Ouery Match 80.0%; Score 16; Best Local Similarity 100.0%; Pred. No. Matches 16; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URRENT APPLICATION NUMBER: US/09/864,761
URRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LICATION NUMBER: PCT/US01/00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 60/207,456
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                                                                                                                                                                                                                                                                                             Sequence 31210, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB 24263.6
                                                                                                                                                           1148 ACCAGAACTCCAGCCG 1163
  US-10-171-311-195
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                                                                                                                                                                                                      CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.53
CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.75
CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.46
US-09-864-761-14677
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERBNCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
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IIILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
IIILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                       Score 15.4; DB 10;
Pred. No. 2.4e+02;
0; Mismatches 1;
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Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/09/235,076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32818, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
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Publication No. US20030073623A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         4 ACCAGAACTCCAGCCGG 20
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(461)
; OTHER INFORMATION: n
US-09-918-995-2681
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                                                                                         SEQ ID NO 14677
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                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                Length 446;
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                                                                                                                                                                                                                                                                                                                                              4; DB 10;
2.5e+02;
                                                                                                                                                                                                                                                                                                                                            Score 15.4; DE
Pred. No. 2.5e+
0; Mismatches
                                                      PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATION NUMBER: US/09/864,761
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CON NUMBER: US 60/236,359
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PRIOR FILLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/180,312
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LING DATE: 2000-05-26
PPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14677, Application US/09864761
Patent No. US20020048763A1
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ON NUMBER: GB 24263.6
                                                                                                                                                                                                                                                           , LUCATION: (1)...(446)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-776
2027 (PARA-016PRV)
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                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 94.1%;
Matches 16; Conservative
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                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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                                                                                                                                                                                                                                 Score 15.4; DB 9; Length 465; Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lasek, Amy R.W.
Springary, Sornasse, Thierry
FITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0030-1 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.4; DB 9;
Pred. No. 2.3e+02;
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 32818
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/295,239
PRIOR FILING DATE: 2001-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillman, Jennifer L
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/10158646 Publication No. US20030073105A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 80, Application US/09840787 Patent No. US20020058264A1 GENERAL INFORMATION:
APPLICANT: Lal, Preeti
                                                                                                                         NAME/KEY: misc_feature
| LOCATION: (1)...(465)
| CTHER INFORMATION: n = A,T,C or G
US-09-918-995-32818
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                                                                                                                                                                                                                                                                                                                                                 408 ACCAGAACTCCCGCCGG 424
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                                                                                                                                                                                                                              Query Match 77.0%;
Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 88.9%;
Matches 16; Conservative
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SOFTWARE: PERL Program
                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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CTHER INFORMATION: a,
US-10-158-646-15
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                                       LENGTH
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Length 1330;
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77.0%; Score 15.4; DB 10;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF-0356 US
                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/840,787
FILING DATE: 23-Apr-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/518,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: 1600518
; SEQUENCE DESCRIPTION: SEQ ID NO: 80
US-09-840-787-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: July 9, 2003, 02:22:30 Job time : 119.562 secs
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1330 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1135 ACCAGAACTCCAGGCGG 1119
                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 80:
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CITY: Palo Alto
STATE: CA
                                               COUNTRY: USA
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Run on:

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600 bp mRNA linear EST 20-DEC-2001
4044-75 Mouse E14.5 retina lambda ZAP II Library Mus musculus CDNA,
B1989738
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BG051841 RHIZ2_5_D
AA157567 ZO68912.S
AW746546 WS1_53_A1
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BM327354 PICL_12_E
BG053545 RHI22_10_
BG556222 EM1_67_C0
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601273386
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AI724897 RHIZ1_31_
BM383171 UI-R-DSO-
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                                                                                                                                BQ339913 RC6-NN118
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                                                                                            BG167146 602344666
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BB797023 BB797023
                                  NF004A01S
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                                                                                                                                                                                                    AZ110368
BE384005
BI145086
AZ957296
                                                                                                                                                                   BQ250191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, Tx 77030,
Tel: 713 792 3646
Fax: 713 790 0329.
Location/Qualifiers
1. 600
/organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                            AV319627
B1335608
BF582934
BI519715 -
BG167146
AK019848
                                                                                                                                BQ339913
AA695177
AZ055663
                                                                                                                                                                                                    AZ110368
BE384005
BI145086
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BG053545
BG556222
BM308600
AW755678
BM521528
AW688064
                                                                                                                                                                   BQ250191
AZ881214
                                                                                                                                                                                                                                         AZ957296
CNS04B83
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BG051841
AA157567
                                                                                                                     BB604959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Klein WH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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BI989738
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AJ425022 AJ425022
BB726338 BB796338
BG751501 602730080
BE241645 TCAAPIE06
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                                                                                                 (without alignments)
319.453 Million cell updates/sec
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                                                                                    8, 2003, 00:47:28 ; Search time 1013.95 Seconds
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             5.1.6
Compugen Ltd.
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                version :
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Maximum Match 100%
Listing first 45 summaries
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                                                             nucleic search, using sw model
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                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                GenCore
Copyright (c) 1993
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Maximum DB seq length: 2000000000
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Match Length
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Database :

4. rv o

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Result Š.

Searched:

Sequence:

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1, .596
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Matches 18; Conserv
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AJ425022/c
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BB796338/c
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                         //dev_stage="embryonic day 14.5 post-fertilization"
//dev_stage="embryonic day 14.5 post-fertilization"
//note="vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps
(Manniatis); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCCACTGAATTCTGAGTG-->. Other
information regarding entire library may be found at
http://pga.swmed.edu/Data/Libraries/microarray_cdna_librar
les.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
Glound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 827 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stops: 430.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: parathyroid gland; Vector: pT7T3D (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. Fatima Bonaldo
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A204409.x1 Soares_parathyroid_tumor_NNHPA Homo saplens CDNA clone IMAGE:1647761 3' similar to contains Alu repetitive element contains element PTR7 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 453)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
clone_lib="Mouse E14.5 retina lambda ZAP II Library"
                                                                                                                                                                                                                                                                                                         Gaps
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0
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Pred. No. 3.7e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone" IMAGE:1647761"
clone_lib="Soares_parathyroid_tumor_NbHPA"
'tissue_type="parathyroid tumor"
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D.,
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/db_xref="taxon:9606"
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AI034466.1 GI:3255419
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Unpublished (1997)
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Matches 19;
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BB796338 RIKEN full-length enriched, Leydig cells CRL-2065 MLTC-1 CDNA Mus musculus cDNA clone G4D0007M04 3', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I pases 1 to 462)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishil
adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
                                                                                                                                                                                                                                                                                                                                                            AJ425022 Salmo salar spleen adult Salmo salar EST 31-JUL-21 mRNA sequence.
AJ425022 Salmo salar spleen adult Salmo salar CDNA clone s02A12, AJ425022 Salmo salar CDNA CLONE S02A12, AJ425022 Salmo salar CDNA CLONE S02A12, SST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                Gaps
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Cairney, M. and Taggart, J. Gene sequences in atlantic salmon (Salmo salar)

Umpublished (2002)

Contact: Taggart JB

Institute of Aquaculture
University of Stirling
Airthrey Road, FK9 41A, United Kingdom.
                                                                                                                                                                                ö
                                                                                                                                  Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.4; DB 9; Length 596;
Pred. No. 1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                              Indels
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/tissue_type="spleen"
/dev_stage-"adult"
                                                                                                                                  Score 17.4; DB 9;
Pred. No. 1e+03;
                                                              129 t
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/db_xref="taxon:8030"
/clone="s02A12"
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ilarity 94.7%;
Conservative
                                                                                                                               ch 87.0%;
1 Similarity 94.7%;
18; Conservative
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                                                                 107 c
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820 bp mRNA linear EST 15-MAY-2001 602730808F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4873962 5', BG751501

RESULT 5 BG751501/c

DEFINITION

ACCESSION

VERSION

BG751501.1 GI:14062154

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/cell_line="CRL-105 MLTC-1"
/cell_line="CRL-151 WEHI 164),
/cell_line="CRL-216 JC), (cell_line=CRL-1751 WEHI 164),
(cell_line=RCB-0464 Meth-A), (cell_line=RCB-05545 OHTA),
(cell_line=RCB-0559 K-1 F1), (cell_line=RCB-1283 B16
melanoma), (cell_type=Be cells, cell_line-CRL-1702 WEHI 231),
(cell_type=Leydig cells, cell_line=CRL-2055 MLTC-1),
(cell_type=Leydig cells, cell_line=CRL-205 MLTC-1),
(tissue_type=Dladder, cell_line=RCB-070 NE),
(tissue_type=bone marrow, cell_type=stroma cell,
cell_line=_CRL-2028 SR-4987), (tissue_type=colon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) 10 (11), TSF-1771 (2000) 10 (11), Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-resegsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp/
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C, cell_type=B cells, cell_line=CRL-1669 BCL1 Clone 13.20-3B3
'Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Soqabe,Y., Suzuki,H., Tagawa,A., Takaku,A., Tanaka,T., Tanaka,T., Tanaka,T., Tanaka,T., Tanaka,T., Tanaka,T., Tanaka,T., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 line-RCB-0549 Cle-H3), (tissue_type=xidney,
line-CCL-142 RAG), (tissue_type=submandibular gland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell_type=B cells, cell_line=CRL-1669 BCL1 Clone 13.20
), (strain-C3H, tissue_type=brain, cell_line=CRL-1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, Leydig cells
PRL-2065 MLTC-1 cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell_type="Leydig cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Y. and Hayashizaki, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
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BE241645 110-201 195 bp mRNA linear EST 03-OCT-2001 TCAAPLE0655 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0655, mRNA
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                                                                                                                    S NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammallan Gene Collection (WGC)
National Institutes of Health, Mammallan Gene Collection (WGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArC.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: eye; Vector: poTBB; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="normal pigmented retinal epithelium"
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Pred. No. 1.6e+03;
0; Mismatches 0;
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High quality sequence stop: 807
Location/Qualifiers
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Primates;
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100.0%; Pre
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Mammalia; Eutheria;
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                                                Homo sapiens
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Gaps

Score 17; DB 10; Length 462; Pred. No. 1.5e+03; 0; Mismatches 0; Indels

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17; Conservative

Query Match Best Local Similarity Matches 17; Conserv

TGACCAGAACTCCAGCC 18 69 TGACCAGAACTCCAGCC 53

g ò

85.0%; S 100.0%;

Louis, MO 63108, USA

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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linkers dapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORII vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lil Vookin by Anu Khanna at the University of Illinois at Urbana-Champalgn. e-mail: 1-vookin@uluc.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: psport1; Site_1: Not1; Site_2: Sal1; This cDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months cultured on mSD 20. The library was prepared using the Life Technologies psuperscript CDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not1 restrictions site. Sal1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="somatic embryos cultured on MSD 20"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="taxon:3847"
clone="SOYBEAN CLONE ID: Gm-c1036-6212"
'clone_lib="Gm-c1036"
                           Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.0%; Score 16.8; DB 13; 90.0%; Pred. No. 1.8e+03;
                                                 Public Soybean EST Project
Washington University School of Medicine
                                                                                                   4444 Forest Park Parkway, Box 8501, St. 11 : 134 - 286 1800 Fax: 314 286 1810 Enail: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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-40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Glycine max"
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Location/Qualifiers
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AW755678.1 GI:7685030
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Unpublished (1999)
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COMMENT
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BM308600
                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_lib="Pediatric acute myelogenous leukemia cell (FAB
il) Baylor_HGSC project=TCAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5, AGGAGCTCGGATCCGCGCCGCATAATAATAATAAT(C) 3'].

Touble-stranded cDNA was then digested with BamHl and XhoI and directionally cloned into the BamHl and Sall sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabalés; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     First strand cDNA was primed with an anchored Mont-oligo(dr) primer [5'66A6GACTCGA6CGGCGCGCAGGAGGT(T)VN 3'Y, V*A,C,G; N*A,C,G,T] and then dG tailed. Second strand was primed with a BamHI-dC primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schheider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"
                        Unpublished (2000)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                   Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Seq primer: M13 primer.
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                                                                                                   at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fex: 832-825-4038
  Pediatric Leukemia cDNA Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.8; DB 10;
Pred. No. 1.7e+03;
); Mismatches 2;
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cell_type="myeloid cell"
dev_stage="pediatric 6 years"
                                                                                                                                                                                                                                                                                                                                            1. 195
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCAAP0655"
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                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                               Email: clones@txccc.org
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90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 connection was constructed from 2 months to 9 months) cultured on MSD 20. The library was prepared using the Life Technologies psuperScript conv library construction kit. Complementary DNA was synthesized from mRNA using poly (dT) sequence with a NoII restrictions site. Sall linkers adapters were ligated to the blunt-ended CDNA fragments followed by NoII digestion. The CDNA fragments were directionally cloned into the NoII sall restriction site. Sall site of the pSPORTI vector. The ligated CDNA fragments were transformed into E.coli ElectroMax DHIOB host cells. This library was constructed in the laboratory of Dr. Lile
                                                                                                                                     Email: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1461 Std Error: 0.00
High quality sequence stop: 427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM521528 562 bp mRNA linear EST 15-FEB-2002 sak59a04.yl Gm-c1036 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1036-7303 5', mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; TcDNA library was constructed from mRNA isolated from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="somatic embryos cultured on MSD 20"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                    /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1036-550"
/clone_lib="Gm-c1036"
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99 t 2 others
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Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11arity 90.0%; Score 16.8; DB 10; 12arity 90.0%; Pred. No. 1.9e+03; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Urbana-Champaign. e-mail:
71 c 119 g 99
                                                                     4444 Forest Park Parkway, Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Public Soybean EST Project
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AW688064 576 bp mRNA linear EST 15-JUN-2000 NF004A01ST1F1000 Developing stem Medicago truncatula cDNA clone
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Eukaryota; Vilidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"vector: psport1; site_1: Not1; site_2: sal1; This cDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months cultured on MSD 20. The library was prepared using the Life Technologies pSuperScript CDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not1 restrictions site. Sal1
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1e,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tags from the Samuel Roberts Noble Foundation
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/dlone="SOYBEAN CIONE ID: Gm-c1036-7303"

/clone=lib="dm-c1046"

/tissue_type="somatic embryos.cultured on MSD 20"
Tel: 314 286 1810

Email: est@watson.wustl.edu

Finis clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact: ccu@resgen.com web site:
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99 c 141 g 130 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.8; DB 13;
Pred. No. 1.9e+03;
0; Mismatches 2;
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Insert Length: 576 Std Error: 0.00
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Unpublished (2000)
                                                                                                                                                                                                                                                Seg primer: -40RP from Gibco
High quality sequence stop: 429.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  /organism="Glycine
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90.0%;
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18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H.,
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(6SC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepare full-length cDNA libraries for rapid discovery of new denome. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,R., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.go.jp,
URE:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It
M., Konno,H., Okazaki,Y., Muramatusu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                   /note="Vector: Lambda Zap; Contains a mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Nov 9, 1999 this sequence version replaced gi:6289460.
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                       Length 576;
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RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                /dev_stage="Pooled developmental"
                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                              /organism="Medicago truncatula"
/db_xref="texon:3880"
/clone="RF004A01ST"
/clone_lib="Developing stem"
                                                                                                                                                                                                                                                                                                                                                                                       Score 16.8; DB 10
Pred. No. 1.9e+03;
0; Mismatches 2
                     Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                      internodal stem segments"
Plate: 004 row: A column: 01
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                                                                                                                                                                                                        /tissue_type="stem*
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                                                                                                                                                                                                                                                                                                                                                                                       Cuery Match 84.0%;
Best Local Similarity 90.0%;
Matches 18; Conservative
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,S., Kawai,J., Okazak
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Hayashizaki,Y.
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SOURCE
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                                                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B1335608 744 bp mRNA 11near. EST 30-JUL-2001 EST00006 Turkey Lambda ZAP Library Meleagris gallopavo cDNA clone
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
                                                                                                                                                                            CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Division of Experimental Animal Research in Riken
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae;
                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                    'clone_lib="RIKEN full-length enriched, 13 days embryo
                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roject of Genome Exploration Research Group in Riken enomic Sciences Center and Genome Science Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                  Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repared and sequenced in Mouse Genome Encyclopedia
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Pred. No. 2e+03;
0; Mismatches 2;
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Department of Veterinary PathoBiology
University of Minnesota
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="13 days embryo"
/lab_host="DH10B"
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t c 157 g 1
                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="6030408M06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="testis"
                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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Harry, D.E., Zaitlin, D.
                                                                                                                                                                                                                                                                                 prepare mouse tissues
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90.0%;
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BI519715 976 bp mRNA linear EST 29-AUG-2001 603061950T1 NIH_MGC_118 Homo saplens cDNA clone IMAGE:5211204 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning). Average insert size 1.7 kb, insert size range 1.2.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note:
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 976)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNa Library Preparation: Life Technologies, Inc.
cDNa Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 976;
  Length 947;
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Plate: LLAM11530 row: c column: 13
High quality sequence start: 22
High quality sequence stop: 835.
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Pred. No. 2.1e+03;
); Mismatches 2;
  Score 16.8; DB 12;
Pred. No. 2.1e+03;
); Mismatches 2;
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this is a NIH_MGC Library."
335 c 292 g 222 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="leukocyte"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:5211204"
                                                                                                              125 ATAACCAGAACTCCAGCCTG 144
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BG167146
BG167146.1 GI:12673849
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llarity 90.0%;
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                                                                                                                                                                                                                                                                                mRNA sequence.
BI519715
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Matches 18; Conserv
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                            /tissue_type="whole embryo"
/dev_stage="24-day"
/note="Vector: Lambda ZAP Library ZAP; RNA was isolated
/note="Vector: Lambda ZAP Library ZAP; RNA was isolated
/note="Vector: Lambda ZAP embryo using a commercially available
kit (Stratagene. CDNA library was constructed using a
Lambda ZAP (SK-, Stratagene). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 94).
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF582934 947 bp mRNA linear EST 12-DEC-200
602101384F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4224452 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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    MN 55108, USA
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Alab_host="bH10B (TI phage=resistant)"
/note="Organ: colon; Vector: pGWV-SPORTE
Site_2: Sall; Cloned unidirectionally.
                                                                                                                                                                                                                                      'clone_lib="Turkey Lambda 2AP Library'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.8; DB 13;
Pred. No. 2e+03;
                                                                                                                                                                      /organism="Meleagris gallopavo"
/db_xref="taxon:9103"
/clone="Nte041"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2e+03;
    St. Paul,
295 AS/VM, 1988 Fitch Ave, St. Paul, rel: 612 624 1287
Fax: 612 625 0204
Email: reedx054@tc.umn.edu
Seg primer: TCGAAGTTCCCCTCACTAAAGG
POLYA*Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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High quality sequence stop: 575.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: AFCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

(Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

(Applies: LLAM10247 row: c column: 17

High quality sequence stop: 652.

Location/Qualifiers

(Ab xref="tamage:4454728"

(Aclone="IMAGE:4454728"

(Aclone=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

207 c 198 g 295 t 1 others
                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                   1 (bases 1 to 1005)
NIH-MGC http://mgc.nc1.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (phage-resistant)"
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Pred. No. 2.1e+03;
0; Mismatches 2;
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90.0%;
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Best Local Similarity 90.03
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                           human.
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Search completed: July 8, 2003, 09:22:00 Job time : 1018.1 secs

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